Long term impact of tillage and crop rotation on soil microbial diversity and soil health

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Introduction

Soil health provides an overall picture of soil functionality that includes chemical, physical and biological features necessary for long-term, sustainable productivity. Although considerable focus has been given to the chemical and physical property impacts on soil quality, proposals for sustainable land use have shown that there is a lack of much research on the assessment of "soil quality" from a soil microbiological point of view (Pankhurst, *et al.*, 1997). Healthy soil maintains diverse microbial communities that have been shown to control plant diseases, effectively recycle plant nutrients, improve soil structure and improve overall crop production (Doran & Zeiss, 2000, Anderson, 2003). However, there is a lack of knowledge regarding the effect of tillage, crop rotation and residue management on soil microbial diversity and vice versa under major crop rotation systems. A three-year (2013 -2015) study was initiated to evaluate the effects of tillage, crop rotation and residue management on soil biodiversity to establish strategies to achieve soils that effectively support sustainable agriculture.

Objectives

- To evaluate the effects of tillage, crop rotation and residue management on soil microbial biodiversity in a corn-soybean rotation system.
- To identify tillage and residue management combinations that would provide optimum soil biodiversity for sustainable soybean farming.

Methods

Study Site: The study was established on a Marietta loam soil (non-irrigated) at the North Mississippi Research and Extension Center, Verona, MS; and another site on Bosket very fine sandy loam and Dubbs silt loam soils (irrigated) at the Delta Research and Extension Center, Stoneville, MS.

Experimental Design: Split Plot

Main Plot : Corn Crop Residue Management

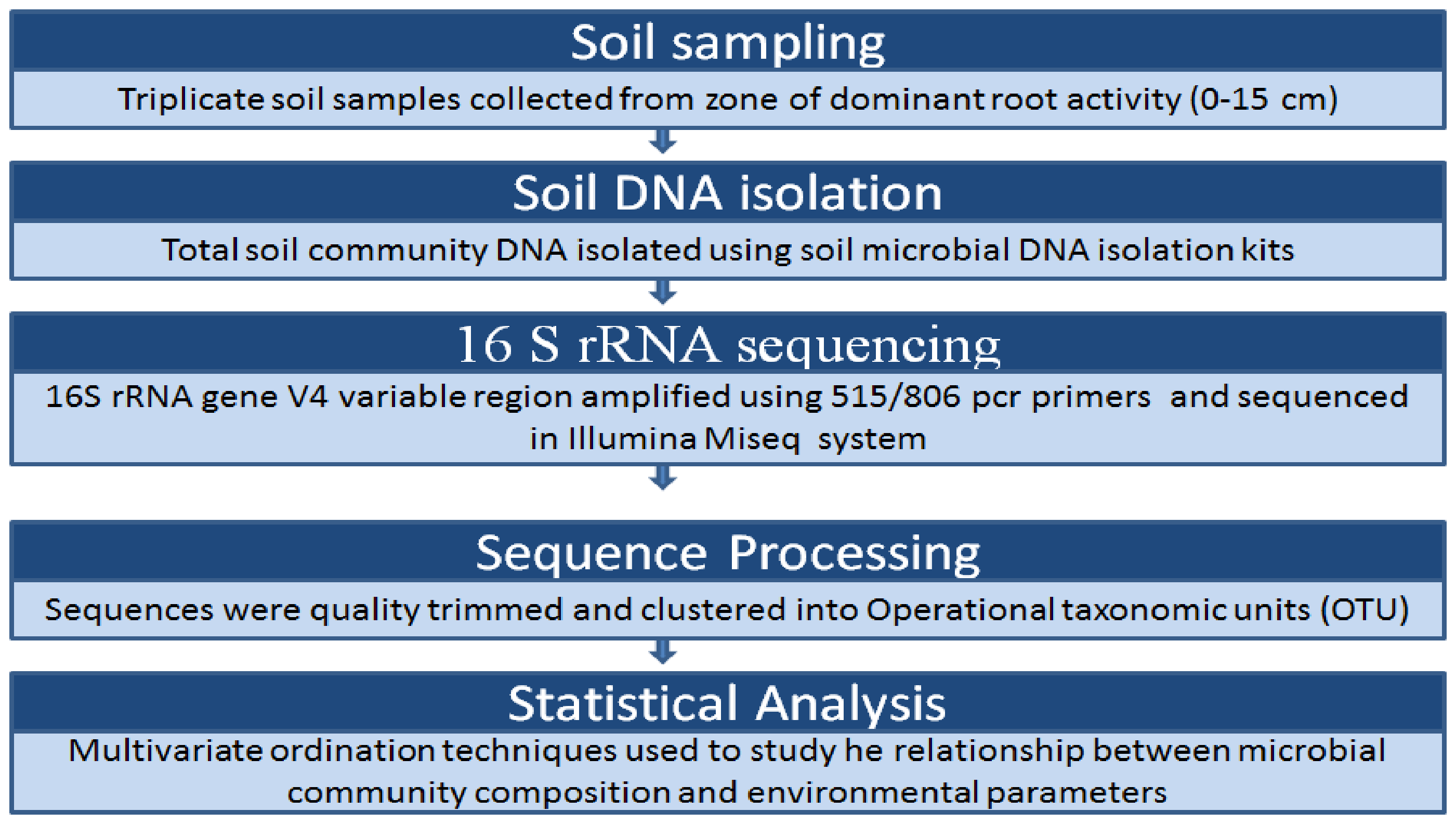
Burn (Corn residue before planting Soybean)

No-burn (Corn residue before planting Soybean)

Sub-plot : Tillage Systems

1. No-tillage (old beds) (NT)
2. Annual fall bed-roller (BR)
3. Annual fall disk (2X) Fb TerraTill® (D + TT)
4. Annual fall TerraTill (TT)

Soil DNA Sequencing Approach:



Soil sampling

Triplicate soil samples collected from zone of dominant root activity (0-15 cm)

Soil DNA isolation

Total soil community DNA isolated using soil microbial DNA isolation kits

16 S rRNA sequencing

16S rRNA gene V4 variable region amplified using 515/806 pcr primers and sequenced in Illumina Miseq system

Sequence Processing

Sequences were quality trimmed and clustered into Operational taxonomic units (OTU)

Statistical Analysis

Multivariate ordination techniques used to study he relationship between microbial community composition and environmental parameters

Results

Table 1: Mantel test correlations between the bacterial community distribution and selected soil characteristics at both the locations

Variable	Mantel Test *	
	r_M	P-value
Tillage Treatments	0.32	<0.0001
Soil Physico-chemical characteristics	0.19	0.07
Residue management	-0.010	0.486

* Mantel test of relationship between bacterial community similarity matrix, tillage treatments, residue management and environmental characteristics. r_M Standardized Mantel statistic

Fig 1: Bray-Curtis ordination plot showing the relationship between tillage management, location and bacterial community composition

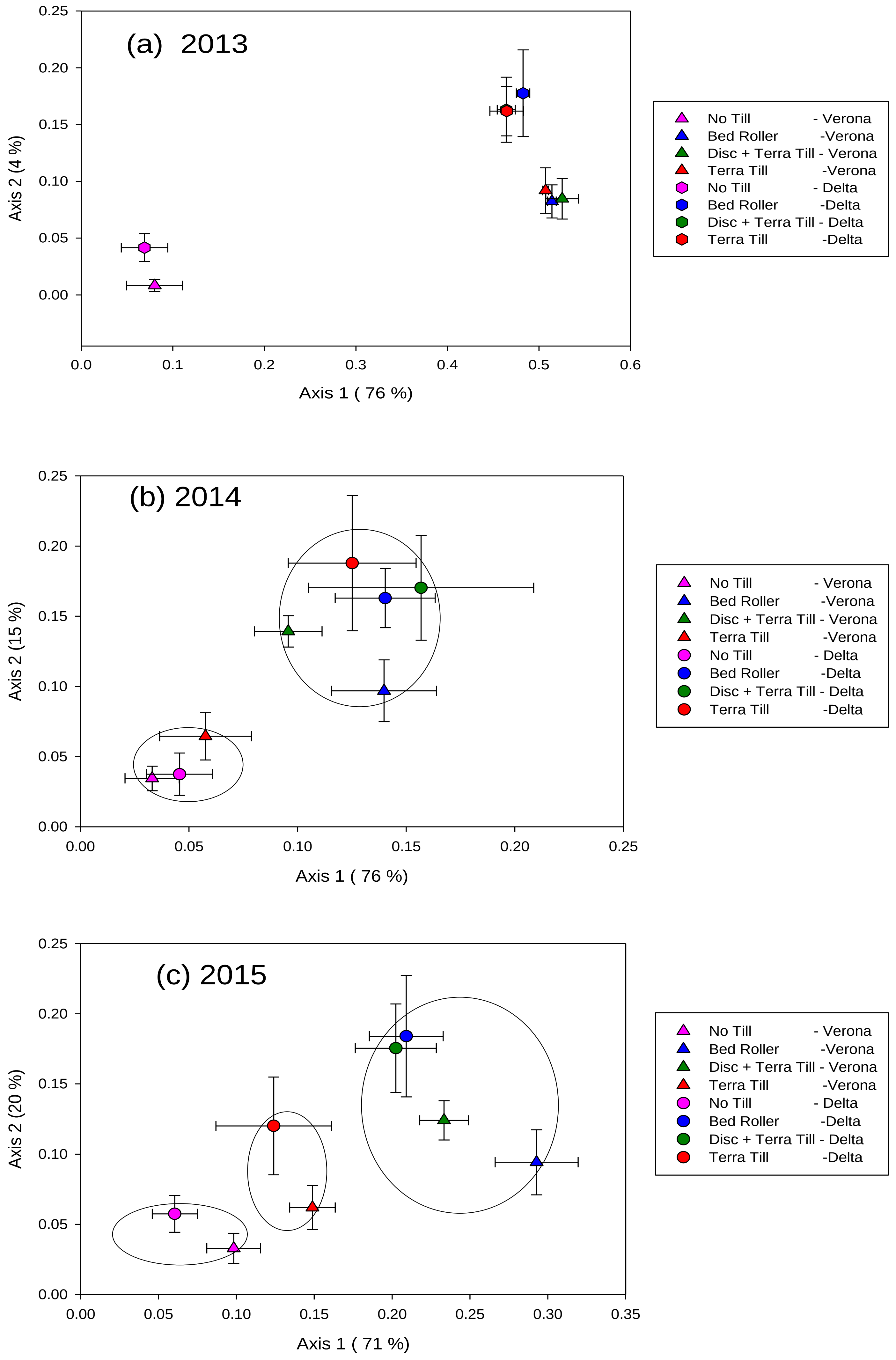


Table 2. The Simpson diversity index of soil bacterial community across tillage treatment plots for (2013-2015), Verona and Stoneville, MS.

	--------------- Verona ------------------			-------------- Stoneville --------------		
Tillage	**2013**	**2014**	**2015**	**2013**	**2014**	**2015**
NT	205 a	211 a	216 a	211 a	223 a	234 a
BR	134 b	142 b	141 b	129 b	144 b	139 b
D + TT	125 b	126 b	136 b	142 ab	139 b	151 b
TT	189 ab	210 a	217 a	192 a	189 a	202 a

-Numbers in a column followed by the same letters are not significantly different at 5% probability level.

Discussion

- Crop residue (burn vs no-burn) management did not have any effect on the soil chemical characteristics. The interaction between tillage and residue management was also not significant.
- A simple Mantel test showed that there was significant correlation between bacterial community distribution and tillage treatments (rM = 0.32, $p < 0.0001$) followed by soil physico-chemical characteristics (Table 1).
- The distribution of 200 most abundant OTUs (Operational taxonomic Units- Bacterial species groups) across the treatment plots showed strong relationship between the bacterial community change and tillage management for all the three years (Fig 1)
- Bacterial community change showed a trend in which the bacterial community structure at the conservation-till plots (NT and TT) were significantly different from the conventionally-tilled plots (BR, D+TT) sites as explained by the axis of maximum variability over the rotation years (Fig 1: a, b and c)
- Bacterial diversity was considerably higher in No-till and Terra Till plots (Table 2). This trend was more prominent from the second year. This indicated that a more diverse group of soil bacterial community inhabited the conservation-till plots, which might have had abundant functional microorganisms.
- *Proteobacteria* were more abundant in the conventionally tilled plots than the conservation-till plots (Data not shown). These groups are efficient decomposers and mineralize the available C more quickly than other groups

Summary

The results suggest that tillage had a profound effect on biomass and composition of soil microbial communities. Bacterial community composition were significantly different in soils under conservation-tillage compared to that in soils under ridge tillage, which resulted in distinct soil microbial community structure. The results showed that the tillage effect on composition of soil microbial communities was very pronounced in the short term, but the effect of crop rotation was probably built in the long term.

Future Research

Future research will focus on the impact of these microbial diversity changes on soil health attributes under corn-soybean production systems and the functional significance of the microbial diversity changes in these production systems.

References

Anderson T-H (2003) Microbial eco-physiological indicators to asses soil quality. *Agriculture, Ecosystems & Environment* **98**: 285-293.

Doran JW & Zeiss MR (2000) Soil health and sustainability: managing the biotic component of soil quality. *Applied Soil Ecology* **15**: 3-11.

Pankhurst C, Doube BM & Gupta V (1997) *Biological indicators of soil health*. Cab International.