

Soil Microbiome Characteristics Associated with Long-Term Potato Cropping System Management Practices

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INTRODUCTION

Potato cropping system practices substantially affect soil microbial communities and the development of soilborne diseases. Cropping systems incorporating soil health management practices, such as longer rotations, disease-suppressive crops, cover crops and green manures, reduced tillage, and/or organic amendments can potentially alter the soil microbiome, reduce soilborne potato diseases, and increase productivity. Since soil microbiology is closely associated with most soil processes, it is important to know and understand the effects of changes in cropping practices over time on soil microbiology. In this research, we examined different approaches to crop management and incorporation of soil health practices into enhanced potato cropping systems. This research follows previous studies on the effects of different 3-yr potato cropping systems designed to address management goals of soil conservation, soil improvement, and disease suppression. Previously, we evaluated these systems for effects on soil properties, tuber yield, soilborne diseases, and economic viability. In this research update, preliminary analyses of cropping system effects on the soil microbiome following long-term cropping practices through taxonomic identification of the composition of bacterial and fungal communities using high throughput amplicon sequencing of DNA extracted from soil are presented.

MATERIALS AND METHODS

Potato cropping system trials examining different approaches to crop management and incorporation of soil health management practices were established in Presque Isle, ME, in 2004, and continued (with modifications in 2013) through 2018, comprising a RCB design (5 blocks) with Cropping System (CS) as the primary factor (treatment plots 3.6 x 15.2 m each). CS consisted of 5 different systems (SQ, SC, SI, DS, and PP) with different management goals and characteristics as listed in Table 1. Soil microbiome characteristics were determined through taxonomic identification from 16S rDNA (bacterial – primer set 515F-806R) and ITS2 (fungal – primer set ITS3-ITS4) region amplicon sequencing using the Illumina HiSeq 2500 system with paired end reads of 250bp length. Soil DNA was extracted using PowerSoil kits (MoBio, Inc) from 3 subsamples/plot of a composite plot soil sample collected in the Spring of 2017. After quality control (reads merged, cleaned, filtered), Operational Taxonomic Units (OTUs) were determined and taxonomy (kingdom, phylum, class, order, family, genus, species) assigned using standard procedures (Uparse, Mothur, MUSCLE software – SILVA database). Sequence abundance was normalized and analyzed for various alpha and beta diversity indices among cropping systems.

RESULTS

Soil fungal and bacterial community characteristics were distinctly different among cropping systems, as first indicated by richness and diversity of OTUs (Table 2). Fungal taxonomy also revealed distinct differences among cropping systems at all taxonomic levels, with SI showing higher abundance of Zygomycetes, DS more Basidiomycetes, and PP and SQ more Ascomycetes and Chytridiomycetes (Figure 1), with significant differences in relative abundances right down to genus level (and PP and SQ showing higher levels of potato pathogens) (Figure 2). In addition, there were several highly abundant unidentified OTUs specifically associated with individual cropping systems. Bacterial taxonomy also demonstrated significant differences among cropping systems at all taxonomic levels, with SI resulting in greater abundance of the phyla Actinobacteria, Bacteroidetes, and Nitrospirae, DS also more Actinobacteria as well as Firmicutes, SC more Acidobacteria, Verrucomicrobia, and Armatimonadetes, SQ more Proteobacteria, Acidobacteria, and Latescibacteria, and PP more Proetobacteria and Gemmatimonadetes (Figure 3), with numerous genera distinctly associated with different cropping systems (Figure 4). Multivariate analyses (PCA) of overall taxonomic characteristics shows the clustering of CS, representing the differences in community characteristics among cropping systems for both fungi and bacteria (Figures 5 and 6). Work is continuing to understand the importance of these differences and their specific relationships to and potential for managing such properties as crop productivity and disease suppression.

Table 1. Names, descriptions, and features of the cropping systems used to address specific management goals.

Abbrev.	Name of system	Original rotation (2004-2012)	Modified rotation (2013-2018) – (Comments)
SQ	Standard 2-yr rotation	Barley (Red clover) - Potato	No change - Typical rotation – Status Quo (Control)
SC	Soil Conserving (3-yr)	Barley (Timothy) - Timothy	Barley (Ryegrass) – Canola/Winter Rye cover
SI	Soil Improving (3-yr)	SC plus compost amendment	Barley (Ryegrass) – Canola (History of compost)
DS	Disease-Suppressive (3-yr)	Mustard GM/ Rapeseed cover Sudangrass GM/ Rye cover	Barley (Ryegrass) – Mustard GM/Rapeseed cover (Disease-suppressive green manure and cover crop)
PP	Continuous potato	Potato - Potato	No change - Non-rotation control

Figure 1. Fungal taxonomic composition at the phylum level for soils from different cropping systems (Spring sampling)

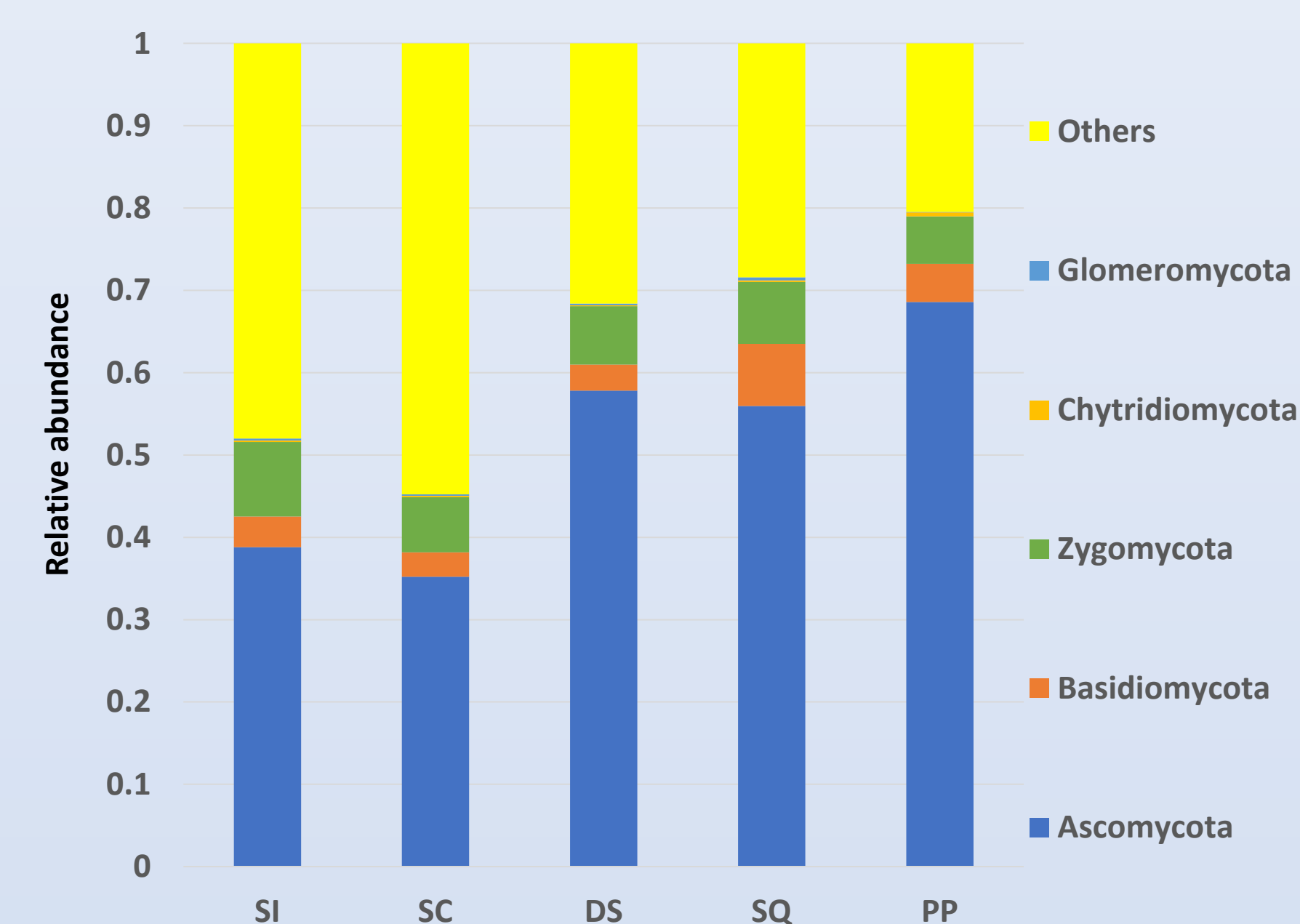


Figure 2. Abundance heatmap of top 40 fungal genera by cropping system

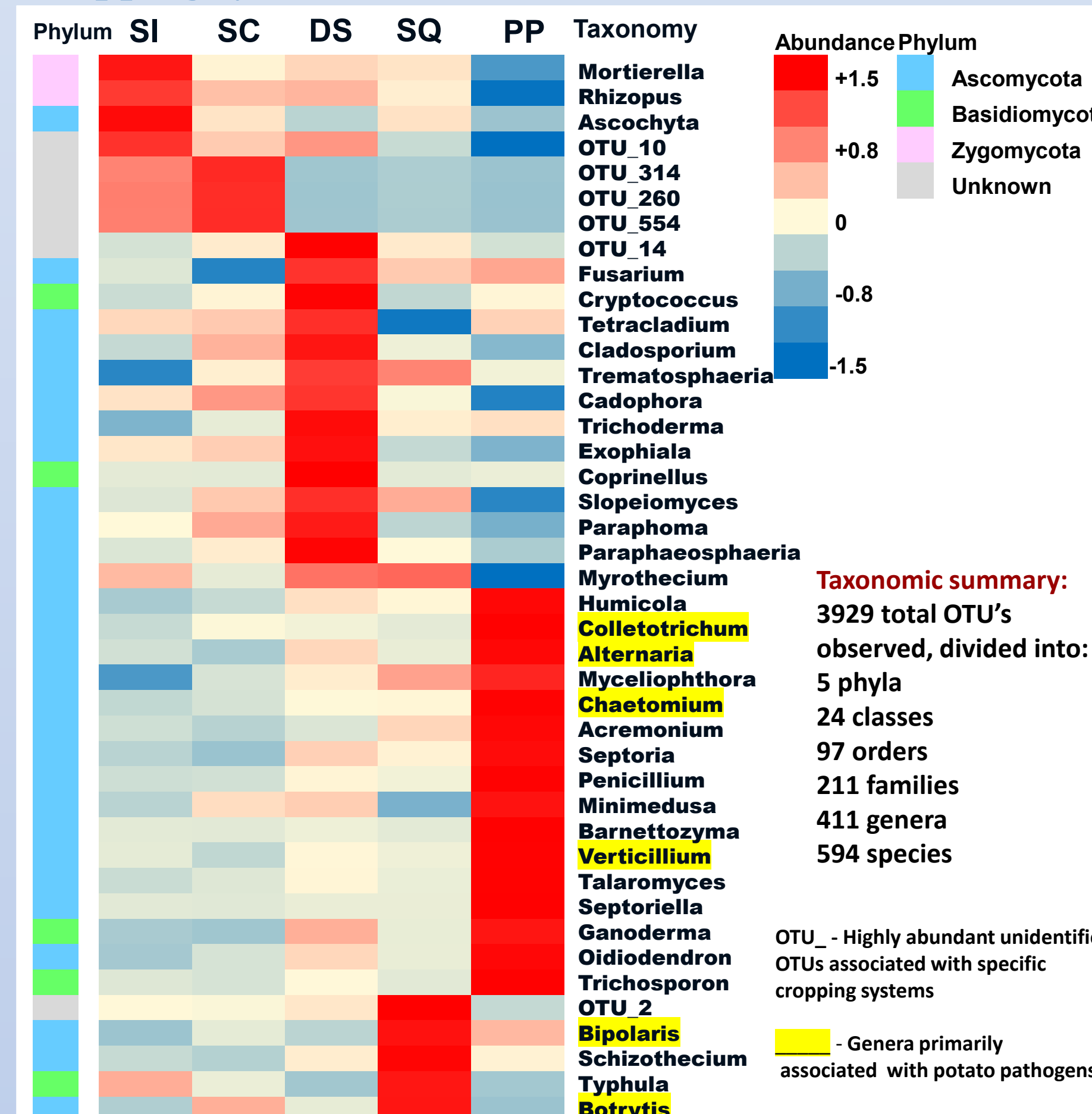


Figure 3. Bacterial taxonomic composition at the phylum level for soils from different cropping systems (Spring sampling)

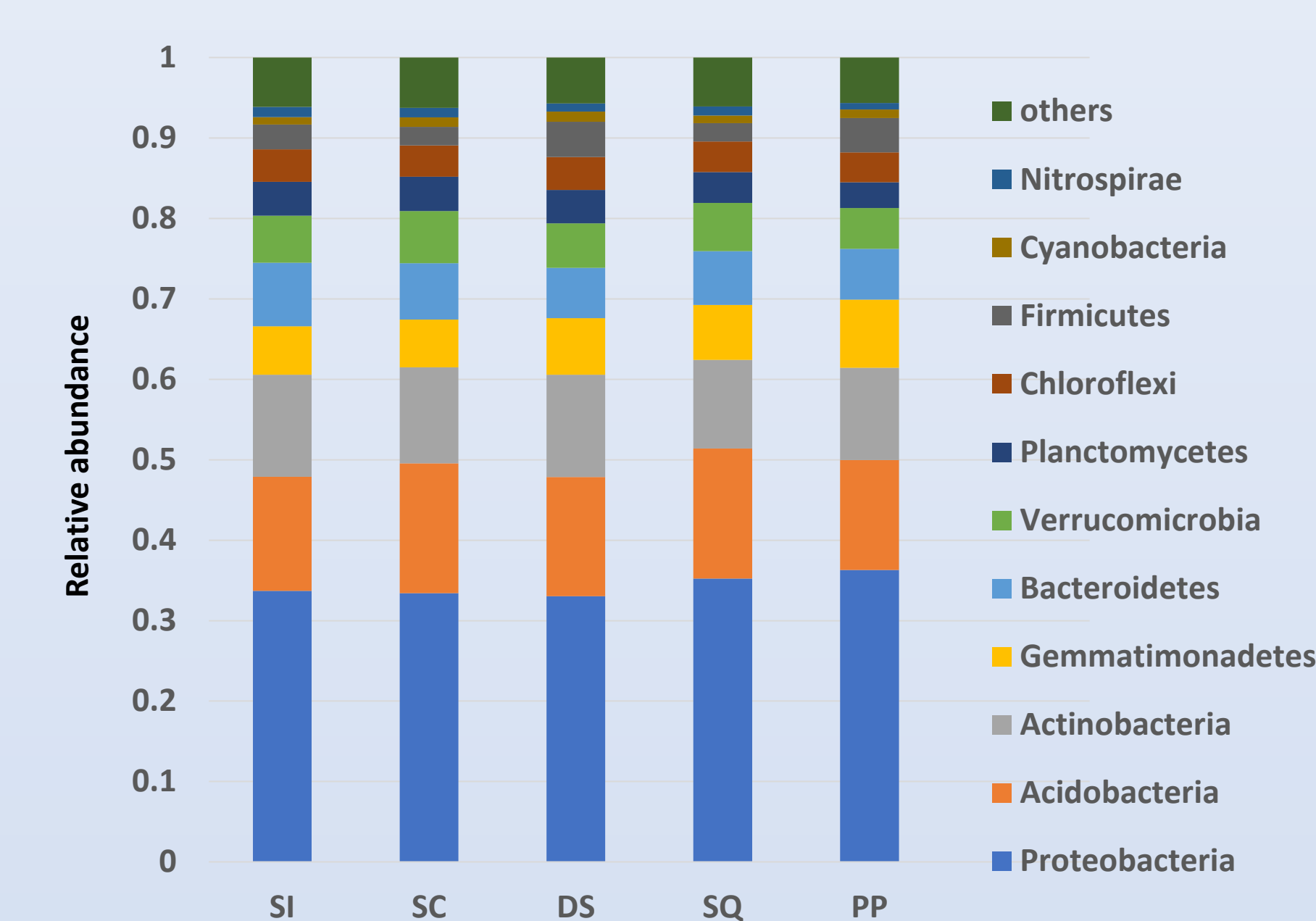
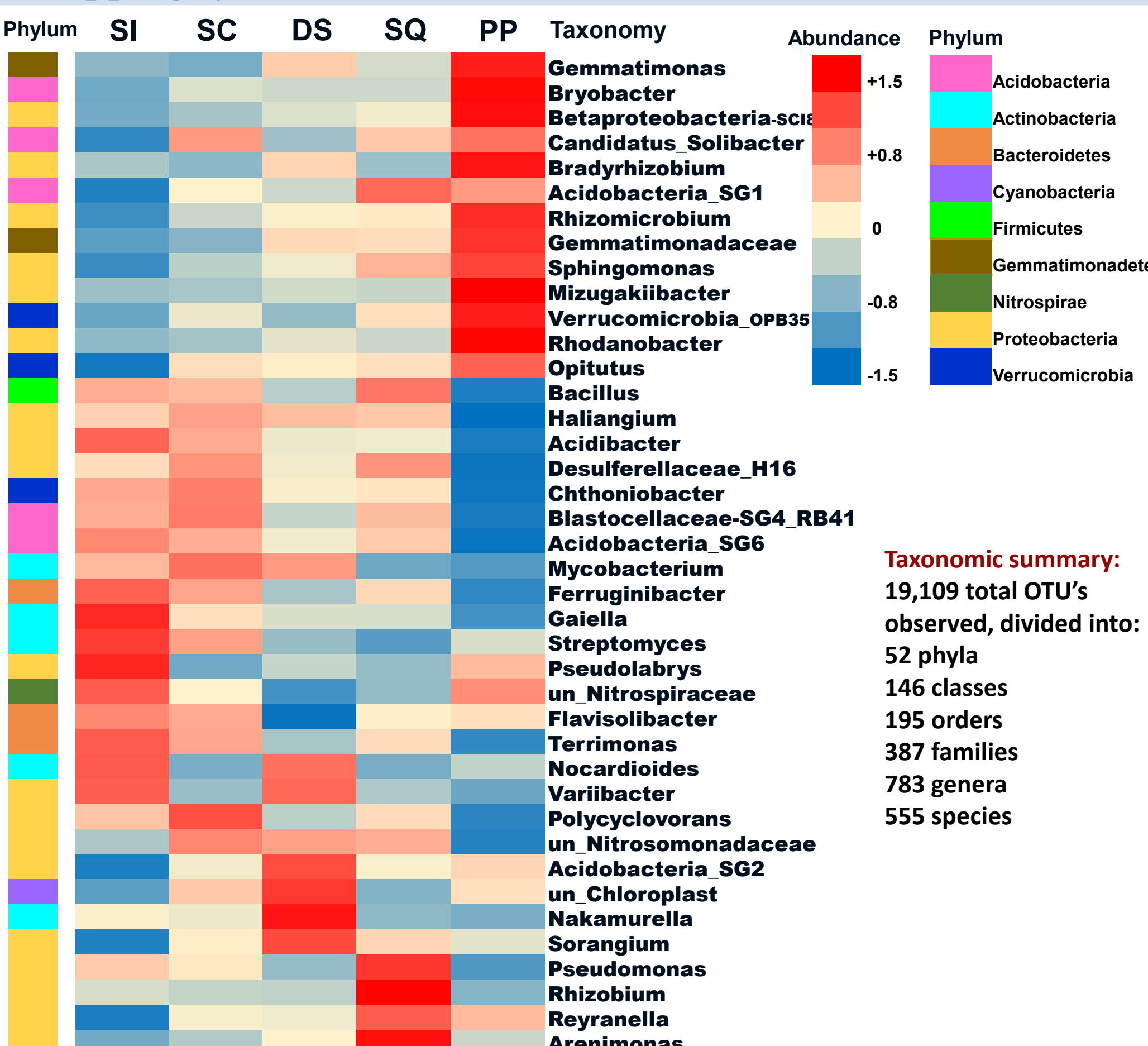


Figure 4. Abundance heatmap of top 40 bacterial genera by cropping system



CONCLUSIONS

- > Cropping systems incorporating soil health management practices (longer rotations, cover crops and green manures, organic amendments, and conservation tillage) affected soil microbial communities in distinctly different ways.
- > Differences in soil microbial composition result from the specific combinations of crops and practices in the cropping systems and may be related to effects on productivity, disease suppression, and sustainability.
- > Taxonomic identification of the specific fungi and bacteria associated with the different cropping systems provide the means to further explore these relationships for future development of actively managed beneficial soil microbial communities

Table 2. Soil microbial community characteristics as affected by cropping system – Average total number Operational Taxonomic Units (OTUs) and Shannon Diversity Index.

Cropping System	Fungal		Bacterial	
	# OTUs	Shannon	# OTUs	Shannon
SI	1401 a	5.89 bc	6772 a	10.98 a
SC	1366 a	5.70 cd	6804 a	10.96 ab
DS	1270 b	6.42 a	6594 b	10.89 bc
SQ	1251 bc	5.41 d	6614 b	10.86 c
PP	1187 c	6.11 ab	6229 c	10.55 d

Figure 5. Cropping system effect on soil fungal community composition (Principal components analysis)

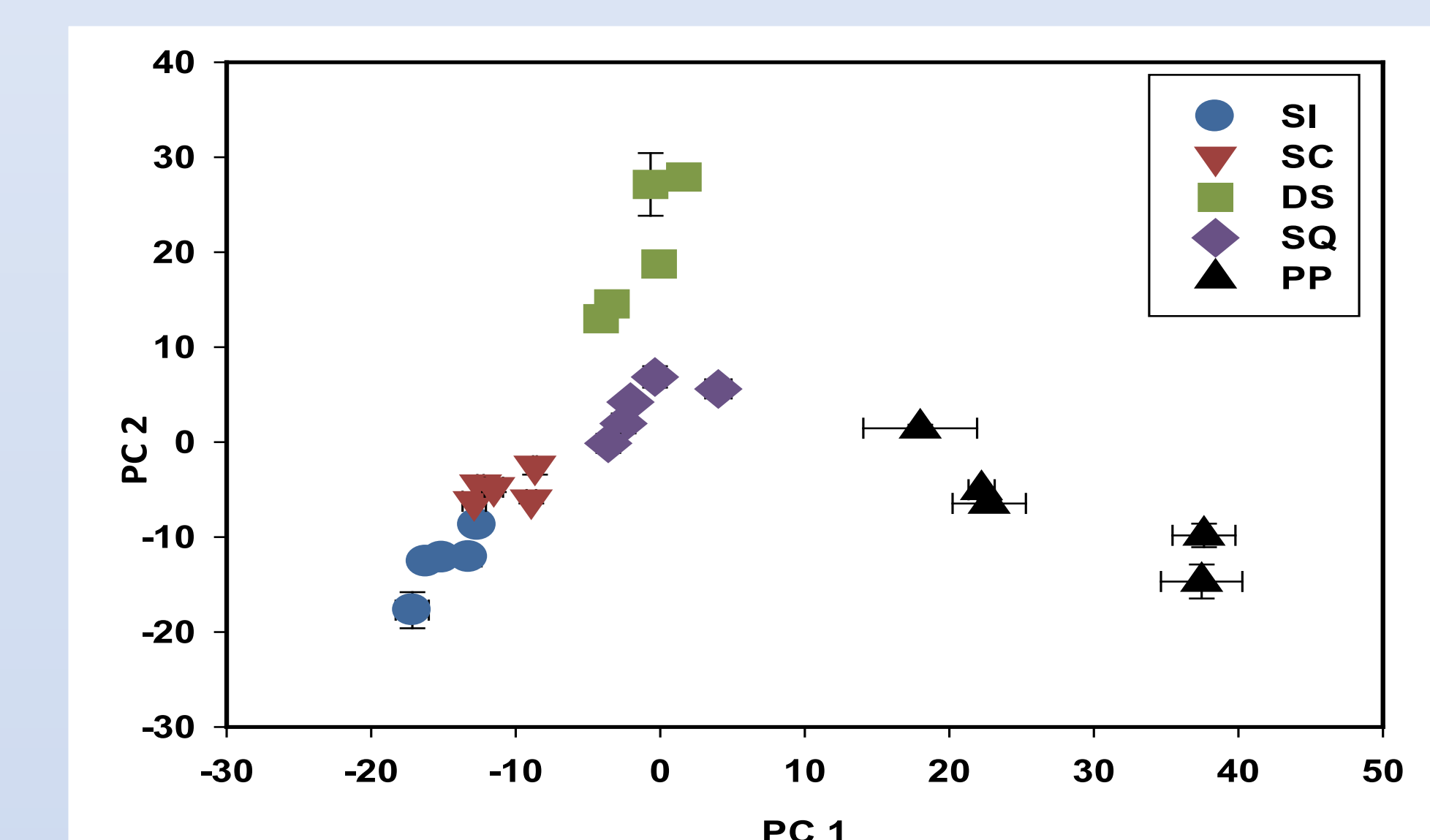


Figure 6. Cropping system effect on soil bacterial community composition (Principal components analysis)

