Effect of Land Management on Soil Bacterial Community Composition and Diversity in the Southern Piedmont, USA

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Introduction

Soil bacteria are the most abundant and diverse group of organisms in soil and play a critical role in terrestrial ecosystems and global biogeochemical cycles. However, the activity and diversity of soil microorganisms are directly influenced by changes in the soil environment. Agricultural land management trajectories impact agro-ecosystems and affect the diversity and structure of soil microbial communities.

The project was carried out to investigate the effects of cropping systems on the composition of soil microbial communities in agricultural soils using the 16S rRNA gene library approach.

The J. Phil Campbell, Sr., Natural Resource Conservation Center (SPC/NRC), Wakulla Springs, Georgia, USA
1. By 10 by 30 m plots with Cecil sandy loam soil conventionally cropped with corn since 1981.
2. Control neighboring forest in an upland field with Cecil sandy loam soil with lobolly pine plantation protected from cultivation since the 1890s.
3. Plots conventionally cultivated with various rowcrops prior to grassland establishment in 1991.

Study Site

Effects of agricultural land management practices on prokaryotic diversity are well described. Soil microorganisms and seven management systems at the J. Phil Campbell, Sr. Natural Resource Conservation Center near Wakulla Springs, Georgia. Community DNA was extracted from soil, and the prokaryotic community composition and diversity were assessed using 165 rRNA gene clone libraries and phospholipid fatty acid (PLFA) analyses. The resulting 3706 sequences formed 3330 operational taxonomic units (OTUs) with a Chao1 estimated total richness of 3114 OTUs at 87% sequence similarity. Specific associations between certain OTUs and soil types were noted. The Acidobacteria and the Firmicutes were the two most abundant taxa in all soil libraries. The forest soils contained the highest numbers of Acidobacteria, the paddy fields treated with crop residues and pasture soils contained the least. The UHSMTU analyses indicated that the bacterial communities from soils under all seven treatments were significantly different.

However, those from the forest were clearly distinct from the others. Statistical modeling revealed that the p. - r. - and u. - Proteobacteria were abundant in ungrazed and cropped soils, whereas the numbers of ~Proteobacteria decreased in the cropped soils. With the addition of inorganic fertilizer, the Acidobacteria and ~Proteobacteria increased in abundance. In contrast, the p. - r. - and u. - Proteobacteria were significantly decreased. Similarly, the relative abundance of the Gammaproteobacteria and the p. - and u. - Proteobacteria was higher in the summer than in the winter. Analyses of the mid PLFA profile indicated that the fungi were relatively more abundant in the forest. Bacteria dominated the grazed and cropped soils. Seasonal effects on mol % PLFA were also observed. The microbial biomass was 1.3-fold in winter than in the summer. These results suggest that agricultural land management practices such as inorganic fertilizer, paddy field management, grazing or season affect the microbial community structure.

Comparison with Ungrazed and Grazed pasture

Type of treatment

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<th>Diversity Index</th>
<th>A1</th>
<th>A2</th>
<th>B1</th>
<th>B2</th>
<th>C1</th>
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<th>D2</th>
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<tr>
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<td>715</td>
<td>763</td>
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<tr>
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The sequencing was carried out at the Molecular Genetics Instrumentation Facility, University of Georgia.

Conclusions

We present four significant findings. Agriculture has a significant impact on both the diversity and structure of soil microbial communities. UHSMTU analyses indicated that the bacterial communities from soils under all seven treatments were significantly different. The agricultural soils (A1, B1 and C1) had higher bacterial diversity than the forest. Forest soils (D1) contained the highest numbers of Acidobacteria. Second, there was a significant influence of litter-fertilization amendments on microbial community in agricultural soils. The Acidobacteria were the least abundant in paddy litter amended soils (A2 and B2), r.-Proteobacteria were significantly absent in soils cropped with inorganic fertilizer (A1). The differences between various treatments were specifically attributed to the distribution of Acidobacteria and Proteobacteria present in those soils. The application of paddy litter specifically altered the composition of these two taxonomic groups. Third, the relatively minor change in microbial communities due to season as compared to both the field and litter-fertilizer amendment. Secondly, but a larger response to PLFA, perhaps a result of physiological changes rather than community structure per se. Lastly, there were specific associations between some of the most abundant OTUs with certain soil types and/or fertilizer amendments. These findings contribute significantly towards understanding the specificity of the changes in soil microbial communities as a result of long-term agricultural land management.

References


Acknowledgement

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Prepared by: