Impact of agricultural land management practices on bacterial community composition and diversity in soils from Michigan, Georgia, and Kansas.

Mark A. Williams[1]*, Kamlesh Jangid[2], Alan J. Franzluebbers[3], Michael B. Jenkins[3], Dinku Endale[3], David C. Coleman[4] and William B. Whitman[2]

[1]Plant and Soil Sciences, Mississippi State University, MS State, MS 39762; [2]Dep. of Microbiology, University of Georgia, Athens GA 30602;
[3]USDA-ARS, 1420 Experiment Station Road, Watkinsville GA 30677; [4]Institute of Ecology, University of Georgia, Athens GA 30602

Introduction

The structure and diversity of soil microorganisms are directly influenced by changes in the soil environment. Agricultural land management tremendously impacts agro-ecosystems and affects soil microbial communities. However, it is not known how strongly the composition and structure of communities are impacted, and whether these impacts are consistent across biogeographic locations. The results in this poster are part of a larger study looking at the affect of several land management practices on microbial communtiies. The poster presents work that investigated the composition and structure of soil microbial communities in conventionally tilled cropland and "native" soils in three separate geographic regions (MI, KS, and GA, USA).

Study Sites

1. **The J. Phil Campbell, Sr., Natural Resource Conservation Center, Watkinsville, Georgia. Soils are sandy loams (fine, kaolinitic thermic Typic Kanhpludult). The forested plots were planted to loblolly pine in the 1860's and now contain a mixture of loblolly and deciduous species. The tilled plots have grown several different crops (corn, soybean, sorgham, cotton) and have been maintained for decades.**

2. **Kellogg Biological Station, Long-Term Ecological Research Network, Kellogg, Michigan. Soils are sandy loams. Forested conifer plantations are 40 to 60 years of age. The decades long tillage experiment is cropped with corn-soybean-wheat rotations.**

3. **Konza Prairie Biological Station, Long-Term Ecological Research Network, Manhattan, KS. Soils are silt loams (mesic Typic Arguidolls). The native prairie was annually burned for the past several decades and has never been plowed. The tilled plots have been cultivated for >50 years and managed for soybean, wheat, and grain sorgham production.**

Fig 1. Photograph of representative plots of the two treatments

Experimental Setup & Methods

Mineral soil was collected from three replicate plots (~10 by 30m) at the 1-10 cm depth in both the Winter (Dec-Feb) and Summer (July-Sep) of 2005-2006. DNA was extracted from 10 g of soil using the PowerMax Soil DNA isolation kit (MOBIO Labs). After purification, the DNA was inventoried and stored at -80 C. Fifteen cycle-PCR reactions were used to amplify the rRNA genes. The PCR products were cloned immediately after amplification and libraries were produced using the TOPO TA cloning kit from Invitrogen. Well isolated colonies were then picked, incubated for growth, and submitted in blocks for sequencing to the Molecular Genomics Instrumentation Facility, University of Georgia.

OTU distribution with treatment

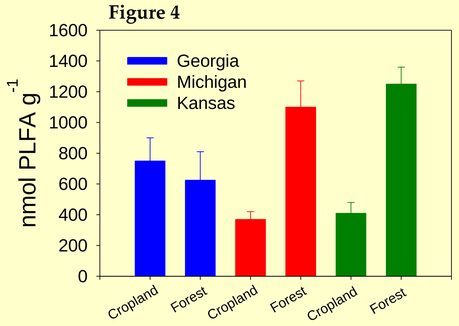
Table 1

OTU #	OTU size[a]	Georgia		Michigan		Kansas	
		Cropland	Forest	Cropland	Forest	Cropland	Prairie
2	35	5[b]	1	1	1	0	0
4	33	16	0	0	0	0	0
11	74	6	3	1	6	0	0
14	33	4	1	1	1	0	0
27	34	7	2	2	1	0	0
28	189	2	0	9	3	12	8
38	73	2	3	1	6	1	0
42	38	3	0	0	0	3	0
56	79	5	0	2	2	6	1
59	168	1	4	2	6	1	4
69	38	4	8	0	7	0	1
117	109	0	8	1	7	3	3
180	45	0	0	0	2	1	0
230	252	0	0	8	0	11	2
244	30	0	0	1	0	0	0
256	58	0	3	0	1	1	4
266	54	0	0	1	3	0	2
267	76	0	0	1	0	2	6
308	42	0	0	2	0	1	0
312	64	0	0	6	1	0	4
315	56	0	0	2	2	0	0
371	33	0	4	0	5	0	0
396	36	0	0	0	1	0	4
398	68	0	0	2	0	3	9
415	42	0	0	0	2	0	0
510	41	0	1	0	3	0	0
554	35	0	9	0	3	0	2
588	37	0	0	0	0	1	0
594	72	0	0	2	2	1	4
625	39	0	0	0	2	0	0
665	46	0	9	0	2	0	0
760	52	0	0	0	0	2	2
795	60	0	0	3	0	1	2
1378	46	0	0	3	1	0	3
1380	53	0	0	2	0	3	8
1381	36	0	0	2	1	1	1
1390	38	0	0	1	4	1	0
1465	41	0	0	1	0	2	3
1469	34	0	0	1	0	0	2
1705	35	0	0	0	0	2	3

[a] The OTU'shown represent only those with n>30. The data shown here summarize only two of the seven treatments from the entire study. OTU's were formed at D=0.03.
[b] To highlight the primary differences in the dominant bacterial members, the OTU's with n>1 are highlighted.

Microbial biomass (PLFA)

Figure 4



NMS Analysis of bacterial and microbial communities

Figure 2 (16S rDNA)

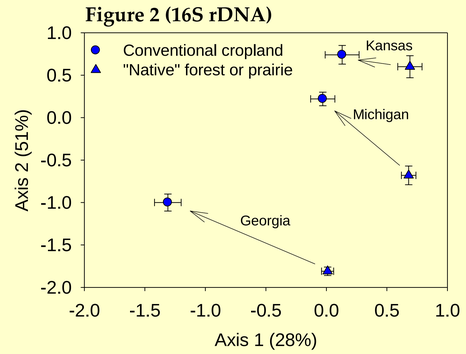
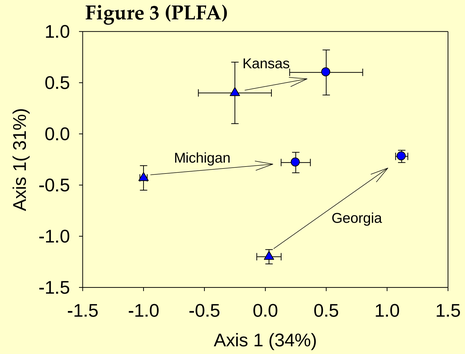


Figure 3 (PLFA)



The NMS ordination plot of the of the compositional and structural changes in soil microbial communities. For Figure 2, the groupings used to separate communities were based on the relative proportion of each of the 200 most abundant OTUs (n>10). The OTUs were formed using the average neighbor algorithm in DOTUR at a distance of 0.03 (Schloss and Handelsman, 2005). For Figure 3 groupings used to separate communities were based on the mol % of 44 fatty acids. Percentages denote the amount of variability associated with each axis. The arrow shows the apparent direction of community change, associated with the cropping of "native" soil.

SOIL EFFECTS: The distribution of the dominant operational taxonomic units (OTU), reflecting those groups with greater than 30 members and representing approximately 25% of the OTU's deterimined in the study **(Table 1)**, support the broader differences indicated by multivariate and univariate statistical analysis **(Figure 2)**. For one, the bacterial communities associated with all of the soils tended to be structurally different, regardless of treatment. However, the bacterial communities in the Georgia soils were distinctly different from those found in MI and KS. Analysis of PLFA **(Figure 3)** corroborated differences detected using 16S rDNA.

CROPPING EFFECTS: The effects of cropping (as depicted by arrows) on the soil microbial communities were large, though somewhat smaller than the effects of soil type **(Figure 2 and 3)**. Regardless of the exact characteristics of the change, both the rDNA based and PLFA based measurements suggested that cropping induced a similar directional trajectory on the communities. The change in bacterial communities due to cropping are also apparent in **Table 1**. For example, OTU's 28 and 230 showed increases, while 69, 117, 256, and 554 showed decreases due to cropping in all three soils. However, the consistent nature of the differences between cropping systems is not always apparent in Table 1. This Table only shows the OTU's with the largest number of members, representing about 25% of the total OTU's in our samples. Thus, a more thorough analysis of the rare OTU's may shed further light on the nature of the community changes due to cropping.

Diversity Indices

Table 2

Diversity Index[a]	Georgia		Michigan		Kansas	
	Cropped	Forest	Cropped	Forest	Cropped	Prairie
S[b]	107	142	199	174	166	182
N[c]	259	277	273	280	235	272
Eveness	2.15	2.12	2.2	2.2	2.2	2.2
H/Hmax	0.79	0.81	0.9	0.88	0.9	0.9
Simpson (1/D)	71	77	191	168	127	176
Chao 1	125	382	770	492	587	679
95 % lci	115	269	529	354	401	458
95 % hci	145	546	1093	682	846	981

[a] Calculations were based on OTUs formed using DOTUR (Schloss and Handelsman, 2005) at *D*= 0.03; [b] Total number of OTUs; [c] Total number of clones in the library; [d] Minimum and maximum eveness values were 0 & 2.3, respectively; [e] Chao1= S + $n_1^2/2n_2$, where n_2 is the number of clones that occur twice; [f] 95% lower and [g] higher confidence interval for Chao1 estimator.

The soils in MI and KS showed substantially greater diversity and richness of bacterial communities than those in GA. Clearly, cropping had a negative impact on the richness of the bacterial communities in the GA, but not the KS or MI soils **(Table 2)**. In KS, but not the GA or MI soils, cropping negatively impacted the community diversity. In light of the substantial reduction in bacterial community richness in the GA soils but not KS or MI soils due cropping, it is surprising that the effects of cropping on microbial biomass **(Figure 4)** showed an opposite trend. There was little change in microbial biomass in GA, but substantial reductions in MI and KS soils. For the Georiga soil, this would suggest that perhaps the major changes in bacterial communities due to cropping occurred among the rare members. In MI and KS, cropping may have a more widespread impact on the bacterial community.

Conclusions

This work seems to suggest that cropping and conventional tillage alter the soil microbial communities in native soils in some consistent ways, regardless of geography or soil type **(Figure 2 and 3)**. Soil bacterial communities in the three locations are different, however there are also important similarities. Both the similarities and differences between the communities needs further investigation. The relationship between the loss of community biomass **(Figure 4)** and changes in diversity and richness of the bacterial communities **(Table 2)** also needs further study to understand which members are impacted most by disturbance and land management.

References

1. Schloss, P.D., Handelsman, J. 2005. Applied and Environmental Microbiology 71: 1501-1506.

Acknowledgement

This work was supported by the USDA-NRI Soil Processes Competitive Grants Program.