



Microbial Community Analysis in Monosodium-methanearsonate Treated Rice Soils

Anil Somenahally¹, Terry Gentry¹, Richard Loeppert¹ and Wengui Yan²

¹Texas A&M University, College Station, TX. ²USDA-ARS, Stuttgart, AR

anil-s@tamu.edu



Abstract

This experiment was conducted in field plots at Stuttgart, AR to determine the microbial community differences between native soil and soil amended with monosodium-methanearsonate (MSMA), as part of a larger study to understand the microbial As transformations in these soils. The second objective was to determine how different water management systems (flooded and saturated) impact the soil microbial communities. The plots were either fallow or planted with the rice variety "Wells" in saturated or flooded treatments with and without MSMA application. Soil samples were collected at three different times corresponding to flooding and plant growth stages. Inter-row and rhizosphere samples were collected separately to determine differences in the microbial communities. Whole soil fatty acid methyl esters (FAMES) were analyzed in each soil sample, and PCA analyses were performed on the FAME data. The temporal changes in the microbial community were prominent. The MSMA and water regimes greatly affected the total microbial community profile. The PCA analysis of marker FAMES for bacteria and fungi revealed differences in the inter-row and rhizosphere microbial community. The statistical analysis of richness and Shannon's diversity indices further indicated the significant influence of MSMA and water regime on the soil microbial communities.

Introduction

Arsenic (As) based pesticides and defoliant, particularly monosodium-methanearsonate (MSMA), have been extensively used in cotton production throughout the southeast and south central U.S., resulting in an accumulation of As in soils of the region. Some of these same soils are used for rice production. In recent years, it has been documented that rice can accumulate As in the grain; hence, there has been increasing interest in the concentration, speciation, and transformations of arsenic in these soils and the soil and management factors that impact arsenic species transformation and uptake by rice.

Arsenic can undergo several microbial transformations in the soil, including oxidation/reduction, methylation/demethylation, and volatilization; hence microbial community analysis in these soils would be beneficial. The reduction poise due to flooding conditions affects As transformations, solubility and mobility, which in turn affect microbial interaction and community profiles. Whole soil fatty acids methyl esters (FAMES) analysis is one of several methods available for characterizing the microbial community.

Objectives

- Microbial diversity analysis in MSMA applied rice soils versus non-amended fields
- Microbial community differences among constantly flooded and the intermittently flooded rice fields

Methods

- Rice crop var. Wells was grown in Stuttgart, AR.
- Treatments 1. MSMA and No MSMA (Clean)
 2. Water regimes: Flooding and intermittent flooding (saturated)
 3. Plant (Wells) versus no plant (Fallow)

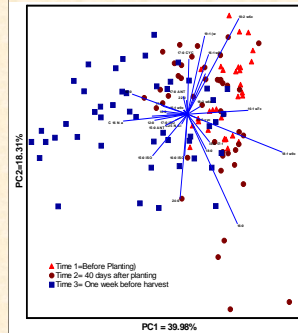
- Composite soil samples were collected in individual days plots from four replicated plots.
 - Inter-row and rhizosphere samples were collected separately from Wells plots
- Sampling time: 1. Before planting, 2. Two weeks after first flooding (~40 days after planting) and 3. One week before harvest
- Whole soil FAMES were extracted by methanol and KOH saponification followed by hexane extraction (Franzluebbers, et al., 1999).
- PC-ORD statistical software was used for principal component analysis (PCA) and diversity assessment.
- Richness (S) and Shannon's Diversity Index (H) were calculated, which are commonly used ecological tools for calculating microbial diversity.

Soil As levels (mg kg⁻¹) in the experimental plots

	No-MSMA	MSMA	
		Before application	After application
2004	7.50 ^a	17.51 ^b	21.69 ^c
2005	5.95 ^a	19.12 ^b	21.75 ^c

Results

Temporal changes in microbial community structure



- The microbial community changed over time.
- The changing redox potential and plant/microbe interactions could be the possible reasons.

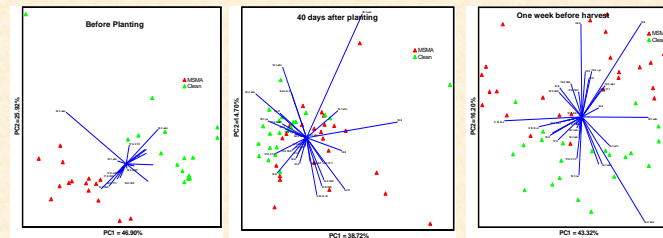
ANOVA (F statistics) in Richness and Shannon's diversity index for temporal changes in FAME

Diversity Index	F
Richness	9.87**
Shannon Diversity	12.27**

** The F value is significant at 0.01 level

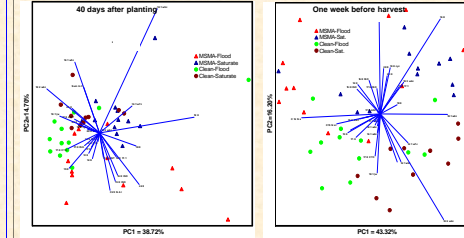
- Significant differences in the diversity indices for temporal changes in FAMES revealed that the microbial community changed during rice growth.

Microbial community differences in MSMA and non-MSMA plots



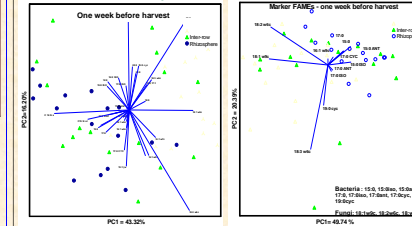
- The MSMA treated plots showed different community profiles compared to non-MSMA plots at all three times.
- The As concentration was significantly higher than non-MSMA plots.
- These fields have a history of receiving MSMA for more than 20 years. This is why even Time 1 samples showed differences in microbial community between the MSMA and non-MSMA plots.

Effect of MSMA and water regime treatments on soil microbial community profile



- Different water regimes influenced microbial diversity.
- MSMA and water regime together affected the microbial community.
- Differences are more prominent during the Time 3 samples.

Microbial community difference between inter-row and rhizosphere soil samples



- Marker FAMES analysis showed the differences in microbial community profiles among inter-row and rhizosphere samples.

Mean difference (LSD) analysis in richness and Shannon's diversity index for the effect of MSMA and water treatments on microbial community

Treatments (i versus j)	Richness			Shannon's-Diversity Index			
	Time 1	Time 2	Time 3	Time 1	Time 2	Time 3	
MSMA-Flood (1)	2	0.58	-0.67	-0.36	0.06	-0.06	-0.03
3	-0.83	-1.33*	-0.86	-0.05	-0.10*	-0.04	
4	-0.08	-1.16*	0.14	-0.02	-0.06	0.06	
MSMA-Sat. (2)	3	-1.41*	-0.67	-0.50	-0.12	-0.05	-0.01
4	-0.67	-0.50	0.50	-0.08	0.00	0.09*	
Clean-Flood (3)	4	0.75	0.17	1.00*	0.04	0.05	0.09*

Clean Sat.=4

* The mean difference is significant at 0.05 level.

Mean difference (LSD) analysis of Shannon's diversity index for the effect of MSMA and water treatments on microbial community using only marker FAMES

Treatments	Time 1	Time 2	Time 3	
MSMA-Flood (1)	2	0.01*	0.02*	0.01*
3	-0.00	-0.00	-0.00	
4	0.00	0.01	0.00	
MSMA-Sat. (2)	3	-0.01*	-0.03*	-0.01*
4	-0.00	-0.01*	-0.00	
Clean-Flood (3)	4	0.00	0.01*	0.00

Clean Sat.=4

* The mean difference is significant at 0.05 level.

Conclusions

- MSMA treated rice plots showed different community profiles compared to the non-MSMA plots.
- Microbial communities differed in constant flooding versus saturated plots. The reducing conditions affect As solubility, which in turn might also have impacted microbial community structure. As(III), is more prevalent under reduced conditions, which is more toxic and more mobile.

Future Work

- DNA fingerprinting and sequencing to study specific bacterial species involved in As transformations
- As speciation in soil

References

A.J. Franzluebbers, N. Nazih, J.A. Stuedemann, J.J. Fuhrmann, H.H. Schomberg and P.G. Harteld. 1999. Soil Carbon and Nitrogen Pools under Low- and High-Endophyte-Infected Tall Fescue. *Soil Science Society of America Journal*. 63:1687-1694.