Response of Microbial Diversity and Community Structure to Management Practices of Prairie Soils

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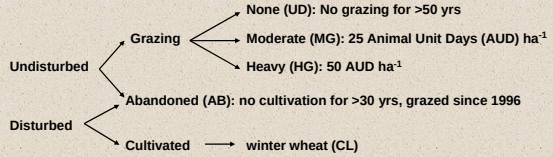
ABSTRACT

A diverse community of microorganisms governs soil processes. Revealing changes in soil biota induced by management may help the development of management strategies to improve the productivity and sustainability of soil ecosystems. The main objective was to evaluate the effects of long-term management practices on the diversity and structure of the soil microbial communities as determined by Fatty Acid Methyl Ester (FAME) analysis. Five long-term (more than 30 years) treatments were evaluated, including undisturbed, set-aside from cultivation, moderately grazed, heavily grazed, and winter wheat (*Triticum aestivum* L.). The non-cultivated systems had the highest microbial biomass and the highest proportions of fungal and protozoan biomarkers. The undisturbed system had higher proportion of Gram-positive bacteria, while the grazed systems favored fast growing microorganisms such as Gram-negative bacteria. In the cultivated system, the microbial community also was dominated by Gram-negative bacteria, and higher proportions of cyclopropyl fatty acids that indicated nutritional stress. The correlations between enzyme activities and microbial biomass were stronger than between enzyme activities and phenotypic groups of organisms (Gram-positive and Gram-negative bacteria, actinomycetes, fungi, and protozoa), suggesting that the size of the microbial community rather than its composition had more impact on the enzyme functional capacity of the soil ecosystem.

OBJECTIVE

To determine impacts of long-term management practices in semiarid mixed prairie soil ecosystems of Southern Great Plains on the diversity and structure of microbial communities and to link microbial community structure to its functional diversity expressed through soil enzymatic activity.

TREATMENTS



MATERIALS AND METHODS

- Surface (0 to 0.10 m) composite soil samples (35 to 45 cores) were obtained from nine randomly selected plots (0.5 ha each) which served as field replications for each treatment. A total of 45 soil samples were obtained. Field-moist soils were sieved (2 mm) and stored at 4ºC until analysis for soil microbial properties and enzyme activities. A portion of each sample was freeze dried, and stored at -20ºC for Fatty Acid Methyl Ester (FAME) analysis.
- Soils of all treatments had neutral to alkaline pH values (7.2 to 7.6), texture that varied from Loam to Silt loam and organic C contents between 0.97 and 2.15%. Results showed that management practices affected several abiotic and biotic properties of the prairie soil ecosystems. When compared to the UD, MG did not significantly affect organic C, total N and P contents, and microbial biomass and activity. Values of these properties were followed by those in the HG and AB systems, and were lowest in the CL ones. Similar pattern was observed for most of the enzyme activities involved in C, N, and P cycling.
- Fatty acids (FA) were extracted from the soils using the procedure for pure culture isolates as previously applied for soil analyses (Acosta-Martínez et al., 2004), and consisted of four steps: (i) saponification, (ii) methylation (esterification), (iii) extraction of the FAMEs, and (iv) washing of the solvent extract. The organic phase containing FAMEs was analyzed in a 6890 GC Series II, equipped with a flame ionization detector and a fused silica capillary column. Peaks in a sample were identified by comparison to standard FA (Microbial ID, Newark, Del.) and their relative peak areas (% over total detected areas) were determined with respect to other FA in a sample using the MIS Aerobe method of the Microbial Identification System (MIDI, MIS, Microbial ID, Inc., Newark, DE).
- Interpretation of the FAME profiles was aided by the use of fatty acid markers that tend to be abundant in particular groups of organisms (Cavigelli et al., 1995; Zelles, 1999). Phenotypic microbial groups: Gram(+) bacteria: *i*14:0, *i*15:0, *a*15:0, *i*16:0, 17:0, *i*17:0, *a*17:0, *i*19:0, and *i*20:0; Gram(-) bacteria: 14:1ω5*c*, 15:1ω6*c*, 16:1ω9*c*, 16:1ω5*c*, 17:1ω8*c*, 17:1ω6*c*, *cy*17:0, 18:1ω7*c*, 18:1ω5*c*, and *cy*19:0; Actinomycetes: 10*me*16:0, 10*me*17:0, and 10*me*18:0; Fungi: 18:1ω9*c*, 18:2ω6*c*, 18:3ω6*c*, 20:1ω9*c* and 20:2ω6*c*; Mycorrhizae: 18:1ω9*c*, 18:3ω6*c*; Protozoa: 20:4ω6*c*.

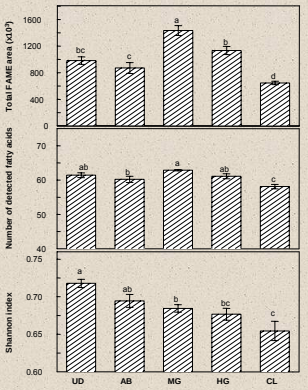


Figure 1. Effect of management practices on total area, number of detected fatty acids and Shannon diversity index determined by FAME analysis. Columns are means ± *SE*. Different letters indicate significantly different means according to *LSD* test at *P*≤0.05, *n* = 9.

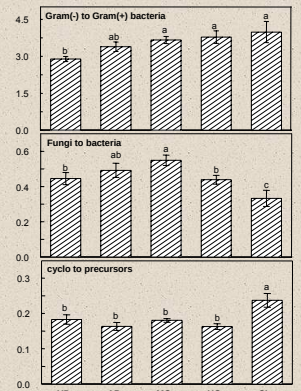


Figure 3. Effect of management practices on soil microbial community composition and on the ratio of cyclopropyl fatty acids to their precursors [(*cy*17+*cy*19)/(16:1ω7*c*+18:1ω7*c*)]. Columns are means ± *SE*. Different letters indicate significantly different means according to *LSD* test at *P*≤0.05, *n* = 9.

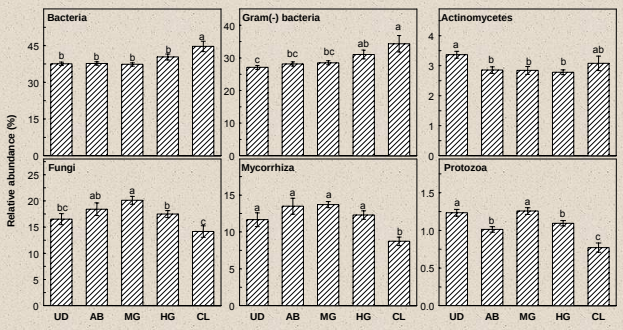


Figure 2. Effect of management practices on the relative abundance of phenotypic microbial groups. Columns are means ± *SE*. Different letters indicate significantly different means according to *LSD* test at *P*≤0.05, *n* = 9.

Table 1. Correlation coefficients (*r*) of the number of detected fatty acids, total area, and phenotypic groups of microorganisms revealed by FAME analysis with selected soil properties (*n* = 45).

Soil property	Detected fatty acids	Total area	Bacteria		Actino-mycetes	Fungi	Mycor-rhizae	Protozoa
			Gram(+)	Gram(-)				
Organic C	0.63 ***	0.63 ***	0.75 ***	0.48 ***	0.69 ***	0.48 ***	0.46 **	0.71 ***
Total N	0.59 ***	0.63 ***	0.73 ***	0.52 ***	0.71 ***	0.46 **	0.44 **	0.70 ***
Inorganic P	0.39 **	0.39 **	-0.12	-0.09	0.20	0.06	0.05	0.27
Organic P	-0.32 *	-0.25	-0.20	-0.07	-0.16	-0.34 *	-0.40 **	-0.29
Microbial C	0.63 ***	0.73 ***	0.77 ***	0.60 ***	0.73 ***	0.61 ***	0.61 ***	0.79 ***
Microbial N	0.57 ***	0.67 ***	0.72 ***	0.55 ***	0.70 ***	0.53 ***	0.54 ***	0.73 ***
Microbial P	0.68 ***	0.72 ***	0.79 ***	0.63 ***	0.74 ***	0.56 ***	0.56 ***	0.78 ***
Dehydroge-nase activity	0.33 *	0.49 ***	0.56 ***	0.39 **	0.55 ***	0.36 *	0.39 **	0.54 ***

Table 2. Relationships (*r* values) between phenotypic groups of microorganisms revealed by FAME analysis and enzyme activities (*n* = 45).

Enzyme activities	Bacteria		Actino-mycetes	Fungi	Mycor-rhizae	Protozoa
	Gram (+)	Gram (-)				
α-glucosidase	0.15	0.01	0.17	0.09	0.10	0.21
β-glucosidase	0.29	-0.04	0.29	0.16	0.18	0.28
α-galactosidase	0.36 *	0.06	0.35 *	0.29	0.29	0.42 **
β-galactosidase	0.35 *	0.09	0.36 *	0.29	0.29	0.39 **
Cellulase	0.27	-0.01	0.26	0.17	0.20	0.30 *
Invertase	0.25	0.49 ***	0.23	0.44 **	0.39 **	0.33 *
β-glucosaminidase	0.48 ***	0.39 **	0.44 **	0.59 ***	0.58 ***	0.62 ***
Urease	0.41 **	0.17	0.41 **	0.34 *	0.33 *	0.46 **
L-asparaginase	0.36 *	0.19	0.32 *	0.29	0.30 *	0.38 **
L-glutaminase	0.58 ***	0.50 ***	0.51 ***	0.60 ***	0.61 ***	0.64 ***
Protease	0.09	0.17	0.04	-0.01	-0.03	0.01
Nitrare Reductase	-0.02	-0.18	-0.01	-0.06	-0.04	-0.05
Acid phosphomonoesterase	0.35 *	0.14	0.30 *	0.34 *	0.34 *	0.37 *
Alk. Phosphomonoesterase	0.33 *	0.12	0.32 *	0.24	0.26	0.40 **
Phosphodiesterase	0.47 **	0.37 *	0.44 **	0.45 **	0.46 **	0.60 ***
Inorganic pyrophosphatase	0.23	0.16	0.16	0.27	0.25	0.25

Phenotypic groups of microorganisms estimated as the sum of proportions (%) of fatty acid biomarkers multiplied by the total area determined from the chromatograph of each sample. Enzyme activities were expressed as mg product per g dry soil per incubation time. *P<0.1; **P<0.05; ***P<0.001.

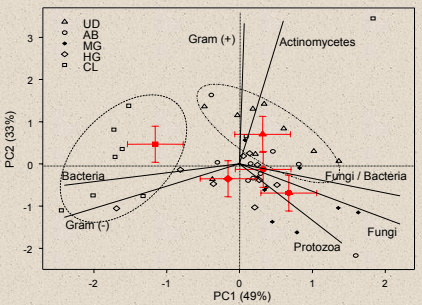


Figure 4. Gabriel biplot and principal component analysis (PCA) of phenotypic microbial groups. Rays that have small angles with a PC axis contribute more to that PC. Rays that have small angles with each other are positively correlated. Red markers in the PCA plot represent treatment means (*n* = 9). Horizontal and vertical error bars are based on 95% confidence intervals for PC1 and PC2, respectively.

SUMMARY

- High variability in the uncultivated soils favored development of diverse habitats that harbor a wide-range of microbial groups with relatively high proportion of Gram(+) microorganisms in the community.
- Changes in the ratio of Gram(-) to Gram(+) signify different types of plant residues and organic inputs in the soil systems evaluated. The long-term stability of the uncultivated systems and the presence of more complex (recalcitrant) organic materials promoted fungi, actinomycetes, and Gram(+) bacteria, resulting in significantly higher fungal to bacterial biomass ratios than the cultivated soils.
- When compared with the undisturbed system, grazing, especially at moderate intensity, increased microbial abundance and the proportion of fungi -especially mycorrhizae- in the community, but did not significantly affect the relative abundance of protozoa.
- Cultivation, physical disruption, and monoculture cropping system led to significant reduction in microbial abundance and diversity, promoted dominance of bacteria, in particular Gram(-) bacteria, while reducing the biomass of fungi and actinomycetes.
- During successional development, microbial diversity increased, accompanied by increasing proportion of fungal and slow growing microorganisms.
- The phenotypic groups of microorganisms were correlated with most soil chemical and microbial properties evaluated. The significant correlations between microbial biomass and the total abundance of fatty acids further suggested that fatty acids provide a measure of microbial biomass.
- That some enzymes tested correlated with several phenotypic groups implied differential contributions of different microbial groups to the detected enzyme activities and indicated potential functional redundancy in soil microbial communities. These findings suggest resilience of the microbial community in performing ecosystem functions
- In general, the correlations of enzyme activities with total microbial biomass were stronger than with any phenotypic group of microorganisms. It seems that the functional capacity of the soil ecosystem depended more on the size of the microbial community rather than on its structure.