



5-9 October 2008 Houston Texas

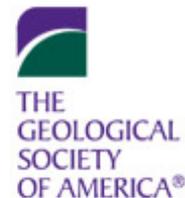
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[745-15 Influence of Cotton Crop Development and Level of Irrigation of Microbial Community Structure.](#)

Wednesday, 8 October 2008

George R. Brown Convention Center, Exhibit Hall E

William C. Rice , *USDA-ARS, Bushland, TX*

Susan O'shaughnessy , *USDA-ARS, Bushland, TX*

Steve Evett , *USDA-ARS, Bushland, TX*

Soil microbial population densities can easily reach one billion cells per gram of soil; and soil microbial diversity has been shown to exceed fifty thousand individual species per gram of soil. Soil type and underlying soil structure are considered primary determinants of microbial community structure in soils. Disturbance of soil due to agricultural practices (tillage) has been shown to reduce or alter microbial diversity while long term agricultural production also can influence microbial diversity. The objective of this study was to evaluate the effects of cotton crop development and four levels of irrigation (0, 33, 67 and 100 % of well-irrigated crop water demand) on microbial community structure during the course of the growing season. We used denaturing gradient gel electrophoresis-polymerase chain reaction (DGGE-PCR) assay employing universal PCR primers that target prokaryotic (16S) and eukaryotic (18S) ribosomal genes and other non 16S DNA primer sets to evaluate microbial diversity. Community DNA samples were obtained from four sampling dates beginning at planting and ending prior to harvest. Both cotton crop development and the level of irrigation influenced general microbial community structure. Microbial diversity tended to increase overtime and was positively influenced by the level of irrigation.

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