

## **USE OF GEOGRAPHICAL INFORMATION SYSTEMS TO INFLUENCE SELECTION OF SAMPLING SITE LOCATIONS FOR THE EVALUATION OF MICROBIAL DIVERSITY**

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### **ABSTRACT**

Microbial soil population densities can easily reach one billion cells per gram of soil; and microbial soil diversity has been estimated to reach ten 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 crop type and residue on soil microbial populations. We used denaturing gradient gel electrophoresis-polymerase chain reaction (DGGE-PCR) assay employing universal PCR primers that target prokaryotic and eukaryotic ribosomal genes and other primer sets to evaluate microbial diversity. Field survey and soil samples were obtained from 41 field sites in Ochiltree County (silty clay Sherm soil) on the same day as a Landsat 5 satellite passed overhead during the 2005 planting season. Tillage information (crop coverage) was used to classify sorghum and wheat into high and low crop residue categories. Three high and low crop residues were selected for each crop type. Community DNA samples were prepared and subjected to various community analysis using DGGE-PCR and other PCR based assays. An interaction between crop type, crop residue coverage and geographical distance was observed. Crop type affected microbial community composition approximately 60 % of the time. This suggests that additional long term agricultural production information is required to successfully predict microbial community composition.