



Q-225. Use of Geographical Information Systems to Influence the Selection of Sampling ... Page 2 of 2

Q-225. Use of Geographical Information Systems to Influence the Selection of Sampling Site Locations for the Evaluation of Microbial Diversity

W. Rice, P. Gowda;
USDA, ARS, Bushland, TX.

Soil microbial population densities can easily reach one billion cells per gram of soil; and soil microbial 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 field sites in Ochiltree and Moore counties (silty clay Sherm soil) of Texas 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. High and low crop residue soil samples 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. For the 16S V3 region primer set 341GC2-518R, an overall correct rate of classification of 85% was observed based on the user defined groups of county by crop by residue coverage. An overall correct rate of classification of 70% was observed for fungal community structure using primer set FR1GC-FF390, whereas, for the ammonia-oxidizing bacteria an overall correct rate of classification of 67% was observed when analyzed by a nested PCR assay with primers CTO189f-654r and 341GC2-518R. Crop type and residue coverage (tillage practice) can affect microbial community composition within a geographical context.

On CD-ROM ISBN 1-55581-4344 ©2007 ASM