

ASA-CSSA-SSSA | 2007 International Annual Meetings
November 4–8 • New Orleans, Louisiana
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Wednesday, November 7, 2007
292-16

Fungal and Bacterial Community Structure Downwind Of a Cattle Feedyard.

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Soils provide a complex microhabitat for harboring a diverse group of microorganisms. The interaction of soil type, crop type, agroecosystem, and land management practices may all influence agricultural bacterial communities. In a previous study, we documented the long-term environmental impacts of beef cattle concentrated animal feeding operations (CAFOs) on soil bacterial communities on lands that are adjacent to CAFOs. The potential environmental effects of beef cattle CAFOs airborne manure particles and dusts on plant vegetation and soil nutrients such as carbon, nitrogen and phosphorus in native pastureland in the agroecosystem of the high plains of Texas have been evaluated. A linear gradient (from west to east) was identified for vegetation changes, dust and manure particle loads, while an exponential soil phosphorus (P) gradient was observed. The order of influence that we observed is that soil depth > soil P > vegetative class in determining soil bacterial community structure and that these environmental influences are largely independent of one another. The objective of this study was to evaluate the effects of soil depth, soil P and vegetation change on fungal community structure. DGGE-PCR employing a 'universal' fungal specific 18S PCR primer set was used in this study. We used principal components analysis combined with discriminant analysis to reveal the interaction of soil depth, soil P and vegetation class on soil fungal community structure. Soil depth was observed to most strongly influence fungal community structure. This result is similar to that previously seen for bacterial community structure. However, in contrast to bacterial community structure the effect of soil P on fungal community structure was negligible while plant vegetation composition had a moderate effect on fungal populations.

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