Identification of Corn Rhizosphere Bacteria Potentially Important in Crop Growth Under Different Agronomic Treatments. (S03bulinski171115-Oral)

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Abstract:

The relationship between monoculture yield decline and the rhizosphere community has always been difficult to assess. Principal components analysis (PCA) and analysis of variance (ANOVA) were used to identify statistically important bacterial populations in the rhizosphere of corn plants grown under different agronomic treatments (no-till, plow, monoculture and rotation with soybeans combinations). Rhizosphere bacterial communities of corn collected in 1998-2000 were analyzed by denaturing gradient gel electrophoresis (DGGE) of 16S rRNA PCR products. Cluster analysis using PCA revealed that in all three years, profiles grouped according to agronomic treatment. ANOVA was used to identify the bands that significantly contributed to the variation associated with the agronomic treatment effects. Three bands were found to be significant consistently over three years in early growth stages of monoculture corn treatments. DNA sequence determination

revealed they belonged to the groups Proteobacteria and Cytophaga-Flavobacterium-Bacteroides (CFB). Yield decline and the presence of these bands over three field seasons suggest there is an association between the two observations.

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