Analysis of Microbial Rhizosphere and Phyllosphere Populations from Different Growth Environments as Determined by DGGE. (S03-ibekwe174911-Poster)

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Abstract:

The effects of two contrasting soils on the development of rhizosphere and phyllosphere microbial communities were analyzed to determine the influence of plant age on community composition. Nucleic acids were extracted from rhizosphere and phyllosphere samples at different stages of development. PCR was used to amplify 16S ribosomal DNA (rDNA) and the products were subjected to denaturing gradient gel electrophoresis (DGGE). Prominent DGGE bands were excised and sequenced to gain insight into the identities of predominantly present (PCR) bacterial populations. The majority of DGGE band sequences were related to bacterial genera previously associated with the rhizosphere and phyllosphere such as Pseudomonas, Comamonas, Acetobacter, Bacillus and Arthrobacter. The PCR-DGGE patterns observed for rhizosphere samples were more complex than those obtained from bulk soil and phyllosphere.

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