DGGE Analysis for Soil Bacterial Diversity. (S03-deng194353-Poster)

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Abstract:

Experimental limitations have hindered the ability to characterize the diverse microbial community and to link a microbial community structure to its ecological functions. DGGE analyses of rDNA permit description of soil microbial fingerprints as well as identification of individual microorganisms inhabiting in the environment. We examined the DGGE fingerprints of the highly variable V9 region of 16S rDNA in six soils that were under different management practices. Microbial diversity and community structure were affected by soil management practices as evidenced by changes in the DGGE banding patterns. Based on similarity matching of 99 sequences obtained from one of the soils with those in the database, 84 showed similarity only to uncultured bacterial 16S rDNA or less than 95% matching. The ones matched with sequences in the database were mostly affiliated to Proteobacteria. Phylogenetic analyses revealed six major clusters and grouped into five major taxa: bacteroidetes, alpha proteobacteria, beta proteobacteria, gamma proteobacteria, and acidobacteria. Most of the sequences remain unclassified.

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