A Study of Microbial Communities from Till and No-Till Missouri Soils Using Genetic Fingerprinting

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In agriculture, soil microbial communities can have a significant impact on plant growth and strongly influence the characteristics and health of the soil itself. Turning the top layer of soil over prior to planting, or tilling, has been a popular tool in the past for cultivating crops. However, excessive tilling can have negative effects. Tilling disrupts soil structure, creates hardpans, disturbs natural microbial communities, causes loss of nitrogen and organic matter, releases stored carbon and exposes the soil to erosion. This project examines soil samples from tilled and no-till fields to explore the impacts of tilling on microbial biodiversity in farm soil. Soil cores extracted from adjacent fields under different tillage practices were profiled for type, texture, pH, nutrients, organic matter and active carbon. No-till and till soil samples from different depths into the soil cores were used to generate a bacterial isolate collection. Degenerate DNA primers were used to amplify 16S rRNA genes from a subset of isolates. Subsequent DNA sequence analysis was performed for microbe identification. Whole soil DNA was also isolated from till and no-till samples and a second set of 16S DNA primers, one including a GC clamp at its 5' end, was used to amplify ~500 bp PCR fragments for denaturing gradient gel electrophoresis (DGGE). This type of analysis revealed differences in microbial community structure. Results from DNA sequencing and DGGE indicate that tilling affects the soil microbiome and disrupts natural microbial communities involved in plant growth and soil health.

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