

ANALYSIS OF SOIL MICROBIAL COMMUNITIES ASSOCIATED WITH WEEDS USING DENATURING GRADIENT GEL ELECTROPHORESIS OF PCR-AMPLIFIED RIBOSOMAL RNA GENES (PCR-DGGE). Kathleen I. Anderson and Steven G. Hallett, Research Assistant and Assistant Professor, Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907.

Interactions between weeds and soilborne microbes may have numerous important agronomic impacts, and may be amenable to manipulations in integrated weed management systems. For example, soil microbial communities may play an important role in the decline of weed seedbanks by accelerating weed seed decay or by inhibiting the growth of emerging weed seedlings. Although there is significant anecdotal evidence for these impacts, they have received very little attention. This is partly due to the fact that soilborne microbes are difficult to study in detail, and effective techniques have become available only recently.

Here, we report a preliminary experiment investigating the potential for using denaturing gradient gel electrophoresis of PCR-amplified small subunit RNA genes (PCR-DGGE) to distinguish between the rhizosphere communities of different weeds growing in the same soil. Shattercane, velvetleaf, field bindweed, jimsonweed and eastern black nightshade were grown in the same field soil for 14-21 days in pots in the greenhouse. Roots were then excavated from pots and shaken roughly to dislodge loosely attached soil. DNA was then extracted from the soil that remained attached to the roots (rhizosphere soil) using a bead-beating protocol. Small regions of small-subunit ribosomal RNA genes were amplified by PCR and the PCR products were separated by DGGE.

DGGE profiles demonstrate that the rhizosphere microbial communities associated with replicate plants of the same species are very similar, but that the rhizosphere microbial communities associated with different species grown in the same soil are considerably different. The experiment demonstrates the feasibility of utilizing PCR-DGGE for the analysis of soil microbial communities associated with weeds. Additionally, this experiment demonstrates the ability of plant roots to exert a species-specific influence upon soil microbial communities. As we develop a more detailed understanding of this phenomenon, we hope we will be able to use it to design strategies to create soil microbial communities that are suppressive to weed species.