Noncompetitive Microbial Diversity Patterns in Soils: Their Causes and Implications for Bioremediation

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The determination of optimal strategies to remeditate mixed waste contamination in soils requires baseline information about the response of microbial communities under these conditions. This goal is complicated by a general lack of understanding about what forces most impact the structure of soil microbial communities, both in contaminated and pristine soils. The objectives of this study are to examine how mixed waste contamination affects the diversity and composition of soil microbial communities, and to determine the forces that most impact the structure of these communities.

Surface, vadose and saturated zone soils, collected from both contaminated and uncontaminated sites were analyzed using a 16S rDNA approach to examine microbial community structure. Both surface and vadose soils exhibited high levels of diversity with no dominance, which we characterize as a noncompetitive diversity pattern. For example, one surface sample from Dover Air Force Base yielded 886 unique rDNA clones out of 920 total. In contrast, soils from the saturated zone showed much less diversity, and were dominated by one or several community members. No differences in community diversity were observed between contaminated and noncontaminated samples, suggesting that wastes are not the key factor controlling microbial community structure at these sites.

Our examination of existing microbial communities suggests that spatial isolation at the soil surface leads to the maintenance of high levels of microbial diversity, whereas greater levels of connectiveness in the saturated zone allow for dominance by one or several community members. We tested this spatial isolation hypothesis by conducting two-species competition experiments in sand microcosms with varying levels of moisture. Competition in liquid or saturated sands resulted in dominance of the species with the most competitive growth parameters in a predictable manner. However, when the moisture content of the microcosms was lowered to increase the degree of spatial isolation and thus mimic the conditions in a surface soil, each species persisted in the microcosm in nearly equal frequency. These results suggest that spatial isolation may be a key determinant in structuring microbial soil communities.

Of concern in our community analysis is the generation of PCR artifacts during the 16S rDNA amplification and cloning. We addressed this problem by examining the severity of artifact formation in a four-species community. The degree of PCR-generated artifacts varied with the type of polymerase used, and increased with increasing PCR cycles, template concentration and species diversity. Based on these findings, an optimal strategy was devised to minimize PCR-generated artifacts in 16S-gene-based community studies.

To determine if sample size affects the observed diversity pattern, surface samples of 0.1, 0.4, 1 and 5 grams were analyzed using the 16S rDNA approach. Despite the wide range in size, each sample showed a noncompetitive diversity pattern. Surprisingly, there was little overlap among the clone libraries from these samples, suggesting that microbial diversity at the soil surface may be even higher than previously expected.