Preliminary Program

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Q-023. DNA-Stable Isotope Probing Analysis of Bacteria Actively Involved in PCB/Biphenyl Degradation

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Knowing the identity of bacteria involved in oxidative polychlorinated biphenyl (PCB) degradation would enable accurate measurement of their spatial distribution and abundance and provide valuable information for optimizing bioremediation technology. Stable isotope probing is a potentially useful procedure for identifying bacteria actively involved in oxidative PCB/biphenyl degradation directly in soils, sediments, and enrichment cultures. The bacterial populations involved in metabolism of biphenyl in the PCB-contaminated Picatinny Arsenal (New Jersey) and River Raisin (Michigan) were investigated. Microcosms were constructed using 5 g soil in serum bottles with ^{13}C biphenyl provided as crystals on the interior surface of the microcosm bottle, and production of $^{13}CO_2$ respired from biphenyl during the 4 week incubation was measured. Biphenyl metabolism was detected within 4 weeks incubation. Soil DNA was extracted and ^{13}C-DNA separated from unlabeled community DNA by density gradient centrifugation. ^{13}C-DNA was PCR amplified using universal primers targeting 16S rRNA genes, and then amplicons were cloned and sequenced. Analyses of 16S rRNA gene sequences indicated that alpha- and beta-proteobacteria were dominant in ^{13}C-DNA from the both soil and sediment samples whereas actinobacteria were dominant in no-biphenyl control samples. Specifically, members of the genera *Ralstonia* and *Sphingomonas* were the dominant biphenyl utilizers in soil sample (Picatinny Arsenal), and members of genera *Limnobacter* and *Bradyrhizobium* were the dominant in the sediment sample (River Raisin). These DNA-SIP results suggest that in soil and sediment environment biphenyl-using microbes are mainly alpha- and beta-proteobacteria.

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