

BIO-SEP® BIO-TRAP STABLE ISOTOPE PROBING: A NEW TOOL FOR CHARACTERIZING BIODEGRADATION POTENTIAL AND THE ASSOCIATED MICROBIAL ECOLOGY

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Microorganisms have a dramatic role in the fate of hazardous materials released into the environment. Complex biodegradation pathways involved in the biological processing of toxic compounds often require the support of multiple organisms interacting as a consortium. Despite their importance and vast diversity, the taxonomic identity of the microorganisms involved in consortia processes is largely unknown. The objective of this poster is to demonstrate how the coupling of molecular biological methods with stable-isotope abundance in biomarkers can provide a cultivation-independent method for linking the identity of bacteria with their function in the environment. Stable carbon isotope analysis can be performed using Bio-Sep® bio-traps containing labeled target compound as a means to investigate microorganisms involved in biodegradation of hazardous materials as well as degradation rates. The bio-traps attract indigenous microorganisms by providing a carbon source to a microbial community that is pre-adapted to *in situ* biodegradation of the specific target compound. Specific microbial populations will metabolize the isotopically labeled substrates, and ¹³C –enriched biomarkers will allow the target group of microorganisms to be characterized taxonomically, functionally and for metabolic status. ¹³C -DNA from microorganisms involved in the biodegradation can be separated by density-gradient centrifugation. Thus, the target group of microorganisms can be characterized through gene probing and sequence analysis. Phospholipid fatty acids can also be efficiently extracted from Bio-Sep® beads to provide a means for discerning viable biomass, community

composition and metabolic status of the community involved in biodegradation. Isotopically-enriched fatty acids produced during the growth of metabolically distinct microbial groups on a ^{13}C -enriched carbon source can be resolved from the ^{12}C -pool through the use of GC-c-IRMS. Stable-isotope probing thus offers a powerful new technique for identifying microbial communities actively involved in specific metabolic processes in the contaminated subsurface.