

**USING ENVIRONMENTAL MOLECULAR DIAGNOSTICS TO ASSESS  
BIOREMEDIATION POTENTIAL AT A BTEX CONTAMINATED SITE**

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A microbial study was conducted at a refinery to investigate the biodegradation of benzene, toluene, ethylbenzene, and xylene (BTEX) contamination under existing site conditions. Twenty five Bio-Trap<sup>®</sup> samplers were deployed in monitoring wells throughout the site to collect integrated samples of the active microbial community. The Bio-Traps<sup>®</sup> were recovered for analysis after a 30 day incubation period, molecular biomarkers were extracted from the samples for analysis. Groundwater samples were also collected from the wells and analyzed for geochemistry and contaminant concentrations. Chemical, geochemical, and microbiological data provided multiple lines of evidence to evaluate biodegradation occurring at the site. The diversity of the microbial community, total biomass, and the presence of taxonomic groups and functional genes involved in hydrocarbon degradation were quantified using phospholipid fatty acid (PLFA) analysis of extracted lipids and qPCR analysis of extracted DNA. These results point to a significant, diverse microbial community active in site groundwater. Correlations between BTEX concentrations and microbial and geochemical lines of evidence suggest that hydrocarbon biodegradation is occurring via aerobic oxidation, methanogenesis, sulfate reduction, and possibly Fe<sup>+3</sup> reduction. Hydrocarbon biodegradation in groundwater is likely limited by availability of electron acceptors and nitrogen and phosphorus nutrients, which are essential for microbial growth.

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