INCORPORATING QPCR QUANTIFICATION OF AROMATIC OXYGENASE GENES INTO SITE CHARACTERIZATION AND MANAGEMENT

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Demonstration of biodegradation as a treatment mechanism particularly under monitored natural attenuation (MNA) conditions depends on converging lines of chemical, geochemical, and biological evidence to support a decision. Quantitative polymerase chain reaction (qPCR) enumeration of aromatic oxygenase genes was combined with contaminant trend analysis to evaluate the feasibility of MNA at two BTEX-impacted sites and the effectiveness of ORC® injection at a third site. At MNA Site A, phenol hydroxylase (PHE), ring hydroxylating toluene monooxygenase (RMO), and toluene monooxygenase (TOL) genes on the order of at least 106 copies/L combined with stable benzene concentrations suggested MNA would be effective at the site. Conversely, the quantification of aromatic oxygenase genes in downgradient, sentinel wells combined with increasing benzene concentrations within the plume indicated MNA would not be appropriate at MNA site B. At ORC Site C, aromatic oxygenase genes were detected under MNA conditions but low DO levels and benzene biodegradation rates indicated MNA would not meet site objectives in an acceptable timeframe. After ORC injection, DO levels increased, BTEX concentrations decreased, and copies of PHE increased. Following depletion of ORC or available BTEX, aromatic oxygenase genes were not detected until MNA conditions were re-established.

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