LABORATORY, FIELD, AND MODELING STUDIES OF AEROBIC COMETABOLISM OF CAHS BY BUTANE-UTILIZING MICROORGANISMS

Lewis Semprini[1], Mark E. Dolan[1], Maureen Mathias[1], Gary D. Hopkins2, and Perry L. McCarty[2]

[1]Dept. of Civil, Construction and Environmental Engineering, Oregon State University, Corvallis, OR 97331

[2]Dept. of Civil and Environmental Engineering, Stanford University, Stanford, CA 94305

The ability of butane-utilizing microorganisms to aerobically cometabolize a mixture of chlorinated aliphatic hydrocarbons (CAHs) in laboratory microcosms and in an in-situ field demonstration was modeled using parameter values measured in laboratory experiments. The butane grown culture was inoculated into soil and groundwater microcosms and exposed to butane with several repeated additions of 1,1,1-trichloroethane (TCA), 1,1-dichloroethylene (1,1-DCE), and 1,1-dichloroethane (1,1-DCA) at aqueous concentrations of 200 μg/L, 100 μg/L, and 200 μg/L, respectively. The utilization of butane and the transformation of the CAH mixture in the batch microcosms were simulated using differential equations accounting for Michaelis-Menten kinetics with cell growth and decay, substrate utilization, transformation product toxicity, and substrate inhibition of CAH transformation. Both competitive inhibition kinetics and mixed inhibition kinetics, determined in prior laboratory studies, were included in the model construct. The equations were solved simultaneously using fourth-order Runge-Kutta numerical integration. The batch microcosm experimental results were simulated well with parameter values determined independently in culture kinetic studies, with some minor adjustments. Having adequately defined the parameter values from laboratory studies, the biotransformation model was combined with 1-D advective-dispersive transport to simulate the results of in-situ bioremediation tests conducted at the Moffett Field Test Facility in CA. The butane-utilizing culture was injected into a 7 m subsurface test site and exposed to alternating pulses of oxygen and butane, along with TCA (150 μg/L), 1,1-DCE (50 μg/L) and 1,1-DCA (150 μg/L). The model simulated well the transient transformation of the CAHs in response to different butane and oxygen pulse cycles and injection concentrations. Model simulations correlated well with field results and indicated that better remediation performance was achieved when more butane and oxygen were injected in the field test plot with short pulse cycles. 1,1-DCE was the most effectively transformed, followed by 1,1-DCA, and TCA, consistent with model predictions. The model simulations also indicated that as time proceeded, indigenous microorganisms were likely responsible for the effective transformation of 1,1-DCE and limited transformation of 1,1-DCA and TCA. This was consistent with PCR based molecular analysis of the microbial population that was stimulated.