

Microbial Composition Analysis in TCE Dechlorination and Competitive Electron-Accepting Processes during Bioremediation

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Groundwater and soil contamination caused by chlorinated compounds such as TCE and PCE is of great environmental concern. Considering the slow rate of natural bioattenuation of chlorinated solvents at many sites that may cause the accumulation of toxic intermediates, remediation strategies involving biostimulation and bioaugmentation are often required for effective treatment. Past operations at Hill Air Force Base (AFB) in Utah resulted in the contamination of soil and groundwater by chlorinated solvents including trichloroethylene (TCE). Column study was carried out at the Utah Water Research Laboratory in order to evaluate the potential treatability of OU5 soil and groundwater via bioremediation.

Treatments in the column study were constructed using OU5 site soil, and TCE and carbon donor amended groundwater from OU5. Two whey columns, two emulsified oil columns, two emulsified oil plus surfactant columns, and two No Carbon control columns have been operating for more than 1000 days. Partial dechlorination is observed in all donor amended columns, and complete transformation from TCE to cis-DCE is being achieved in the whey columns. Significant iron reduction and methanogenesis is also observed in the whey columns but not in the columns amended with emulsified oil. Microbial community analysis using clone library and Automated Ribosomal Intergenic Spacer Analysis (ARISA) procedure revealed that column biostimulation greatly changed the composition of the iron-reducing bacterial community in the original OU5 sediments, and obvious changes in microbial community composition along the depth of columns were observed in response to biostimulation. Potentially competitive microbial populations stimulated by whey, emulsified oil and emulsified oil plus surfactant (Partial $\approx 50\%$ Dechlorination to cis-DCE) are obviously different, which indicates that the nature of the selected carbon donor affects microbial community composition, and can impact the effectiveness of TCE bioremediation. Although the *vcrA* gene, the gene encoding vinyl chloride reductase, has been detected in all of the columns using real-time PCR (RTPCR), no complete dechlorination was observed. Further study on competitive electron accepting processes and gene expression are therefore necessary to optimize bioremediation strategies. Molecular tools, including RTPCR, ARISA, and clone library development, are being used in this study to track the changes in microbial community composition in response to bioaugmentation, to identify the prevalence of interacting communities and genes encoding key enzymes, and to evaluate reductive dechlorination and potentially competitive electron accepting processes in order to optimize remediation strategies.

Details of community structure analysis following biostimulation will be compared to that in response to bioaugmentation, and optimal remediation strategies developed from these results will be highlighted.