Late Stage Degradation Rates for TCE Daughter Products Correlated with Microbial Community Composition Determined by NGS Analysis

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Background/Objectives. Groundwater at a manufacturing facility in Portland, Oregon was impacted by TCE and manufactured gas plant waste (primarily naphthalene, BTEX, PAHs, and cyanide). In situ chemical reduction enhanced bioremediation for source area treatment was implemented in 2009, with demonstrated success in 2013. Implementation consisted of a 150 foot-long permeable reactive barrier (PRB) consisting of EHC® and bioaugmented with KB-1® installed at 40-112 feet bgs using direct-push technology. Groundwater data were collected from 23 monitoring wells upgradient, within and downgradient of the PRB. Early results confirmed 99.99% TCE mass removal within one year, with many wells below the USEPA MCL. Residual concentrations of cis-dichloroethene (cDCE) and vinyl chloride (TCE degradation products) were observed, with delayed decreases in degradation. To supplement conventional monitoring parameters, next generation sequencing (NGS) was performed to characterize microbial community structure and to provide further insights into remediation performance at specific wells.

Approach/Activities. The objective of the work was to evaluate a significant time-series data set to identify potential correlations between CVOC degradation rates and NGS data describing the microbial community growth and characteristics. Degradation rates for cDCE and VC (observed from 2010 through 2016) were estimated using first-order slope analysis. The delay (relative to amendment injection and source TCE depletion) was also measured and considered, and half-lives for degradation rates were estimated. NGS data, including a total of 279 DNA samples extracted from monitoring well groundwater (2009 through 2014 were sequenced using an Illumina® platform with 16S rRNA gene targeted universal primers. Sequences were merged with FLASH, de-multiplexed, quality checked and clustered into operational taxonomic units (OTUs), often equated to "microbial species", using the UPARSE pipeline. Ribosomal database classifier was used for taxonomic assignment of OTUs.

Results/Lessons Learned. Substantial microbial diversity was identified at the site, but in most samples, dechlorinators comprised a high proportion of OTUs including *Dehalococcoides*, *Dehalogenimonas* and *Geobacter* with lower abundances of *Dehalobacter* and *Dehalobacterium*. Other anaerobes including sulfate reducers and methanogens were detected in most samples. Degradation rates, and the delay times for end-stage degradation (depletion of TCE source as indicated by declining/non-detect cis-DCE concentrations) were estimated and correlated to the relative abundance of dechlorinating bacteria. The impact of geochemical factors including pH, contaminant profile, electron donor status on microbial community structure were also analyzed and will be discussed in the context of optimizing remediation performance for the occasionally recalcitrant degradation products. Ultimately, NGS data were found to be a productive enhancement of the data set for confirming long-term reliability of the remediation technology.