Functional Metagenomics of Microbial Communities in Groundwater for a Bedrock Plume and Source Area

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Background/Objectives. Microbial community analysis was performed on groundwater samples from a mature remediation site. The site is a former pharmaceutical manufacturing facility that employed an underground storage tank for methylene chloride (aka dichloromethane or DCM) storage. An undetermined quantity of DCM was released from the tank and piping system over several years, and remains at depth with groundwater exhibiting concentrations at greater than 13,000,000 parts per billion (ppb) in one location. Attempts to pump and treat were unsuccessful due to low yield of the host formation, and was terminated in favor of monitored natural attenuation. Bench scale biodegradation studies demonstrated a robust capability to intrinsically biodegrade DCM at the site.

The study presented here uses metagenomics and metatranscriptomics to focus on the microbial communities in this groundwater environment responsible for the DCM biodegradation and verify biotic removal of DCM from contaminated groundwater under a variety of geochemical conditions from the source area to the distal plume extent.

Approach/Activities. This study examined the bacterial community structure and function in groundwater environments across a range of DCM concentrations and between hydrogeologic units found on the study site. Groundwater samples (n=40) were collected quarterly between October 2013 and October 2014 from 10 wells with levels of contamination ranging from 0.89 - 9,800,000 ppb. Samples were filtered and DNA was extracted from the resulting residue. This DNA was then subjected to Illumina-tag PCR and sequencing of the 16S rRNA gene.16S rRNA analysis and metatranscriptomics were conducted on 26 and 11 groundwater samples, respectively.

Results/Lessons Learned. Analysis of the 16S rRNA gene data revealed significant shifts in microbial community structure in response to varying DCM concentrations. A number of previously cited DCM-degraders (up to >20% of the bacterial community), including: Dehalobacterium, Acetobacterium and Desulfovibrio had strong positive correlations (Spearman correlation; r>0.7) with DCM concentration. Several novel taxa also correlated with DCM concentration, indicative of potentially novel DCM-degrading bacterial assemblages. Co-occurrence network analysis revealed aerobic and anaerobic bacterial taxa correlated with DCM concentration. Metatranscriptomics revealed robust expression of several xenobiotic degradation pathways within these groundwater microbial communities.
This represents the first study to leverage high-throughput sequencing to assess the comprehensive bacterial community response to varying concentrations of DCM in groundwater environments. The emerging technology and methods exploited in this study enabled the identification of potentially novel DCM-degrading consortia, and could likely do the same for other contaminants as well.