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## Recent Work

### Title

Identification of Different Relationships Between Contaminated Groundwater Samples Based Upon Extensive Geochemical Data or Multiple Gene Sequences from Microbial Communities

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## Identification of Different Relationships Between Contaminated Groundwater Samples Based Upon Extensive Geochemical Data or Multiple Gene Sequences from Microbial Communities

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Clonal libraries of multiple genes (SSU rRNA gene, *nirK*, *nirS*, *amoA*, *pmoA*, and *dsrAB*) were constructed from groundwater samples (n=6) that varied in degrees of contamination. The sites were in proximity to a concentration plume, and over one hundred geochemical parameters were measured for the groundwater samples and included pH, anions, cations, heavy metals, organic contaminants, and TOC (total organic carbon). Principle components analyses (PCA) were used to compare the relationships between the sites with respect to the unique (n=785) operational taxonomic unit (OTU) distributions within the different clonal libraries. When geochemical characteristics were analyzed, the data suggested that the samples could be differentiated based upon pH, nitrate, sulfate, nickel, aluminum, and uranium. Similar relationships between the sites were observed when 107 analytes were used, but more resolution was achieved between the more contaminated sites. In addition, a majority of the variance between the acidic samples could be accounted for by tetrachloroethene, <sup>99</sup>Tc, SO<sub>4</sub>, Al, Th and 1,1,2-trichloro-1,2,2-trifluoroethane. The analysis based on the phylogenetic marker (SSU rRNA gene) resulted in different groupings for background and the two circum neutral sites compared to the geochemical analysis, and analyses of the OTU distributions for the functional genes each predicted different relationships between the sites. A tripartite PCA explained 76% of the variance, and grouped the background sample with the three, heavily contaminated sites. When all gene OTUs were used in the analyses, the sites were more similar than in any other comparison, 94% of the observed variance could be explained, the background site was grouped with the contaminated sites, and possible key populations were identified by factor analysis. The data suggested that even though the background site was phylogenetically and geochemically distinct from the acidic sites, the extreme conditions of the acidic samples might be more analogous to the limiting nutrient conditions of the background site.