Molecular Analysis of the Microbial Community Structure in Chromium Contaminated Sites before and after *In Situ* Bioreduction Stimulation by Lactate Injection

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Chromium is one of the most abundant elements on the Earth's crust, and common contaminants because of its use in many industries. A major concern about waste containing chromium is the effects that it has on human health, specially in the hexavalent state (Cr VI). Bioremediation strategies in order to reduce chromium to a less hazardous state, involves the addition of carbon sources that served as electron donor, in the presence of dissimilatory metal reducer microbes. The main focus of this research is to analyze the microbial community structure using molecular approaches in chromium contaminated soil from Hanford, Washington, before lactate biostimulation. Soil enrichments, and small scale microcosms were used to increase the biomass of the soil samples for further DNA extractions. The 16S rDNA amplicons from the total environmental DNA were obtained by using domain and group specific primers. T-RFLP and DNA micro-array technologies were used to identify and analyze the microbial community. The molecular methods on this study demonstrated the low biomass content of the samples, the non-complex community structure, and the dominance of members of the Proteobacteria and gram-positive bacterial divisions. *Geobacter* and *Desulfovibrio* were two of the metal-reducers found in both the enrichments and small scale microcosms.

Key words:

Metal-reducers
Environmental micro-array
chromium contaminated soil
microbial community structure
T-RFLP