Characterizing microbial ureolytic activity in groundwater for the potential to facilitate calcite precipitation for remediation of Strontium-90

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We have been developing tools to assess ureolytic activity by native groundwater microorganisms to support the development of a novel *in situ* remediation approach for strontium-90 contamination in groundwater. In this approach, the increase in pH and alkalinity caused by urea hydrolysis drives the precipitation of calcite and co-precipitation of Sr. In aquifers that are saturated with respect to calcite (as is the case in many aquifers in the western United States), the co-precipitated metals and radionuclides are effectively removed from the aqueous phase over the long-term. Urea hydrolysis is catalyzed by the urease enzyme, which is produced by many environmental microorganisms. We have developed a quantitative PCR assay for bacterial *ure*C, the gene coding for the large catalytic subunit of urease, and applied it to groundwater and sediment samples to estimate numbers of ureolytic organisms. We are also working to develop real time reverse transcription PCR techniques to quantify mRNA transcripts of *ure*C. In addition, we have estimated *in situ* rates of urea hydrolysis using trace amounts of ^{14}C-labeled urea added to environmental samples in the laboratory. These assessment tools can aid in the initial evaluation of a particular site's suitability for the remediation approach, as well as provide indications of the effectiveness of manipulations to stimulate ureolytic activity for this purpose. We have applied these tools to samples from both the Snake River Plain Aquifer in Idaho, USA and from the Hanford 100-N site in Washington, USA. The results can also be used as inputs into a biogeochemical model to predict the extent of calcite precipitation and Sr co-precipitation at a particular site.

Influence of U(VI) on natural bacterial community of a soil sample from a uranium mining waste

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Bacteria have evolved several different mechanisms to tolerate uranium or to use U(VI) as terminal electron acceptor in anaerobic respiration. Because of this, bacteria play a major role in geomicrobiological cycling of uranium and can be used for the bioremediation of uranium-contaminated sites. In this work natural bacterial communities were investigated by the use of 16S rDNA retrievals in several soil samples from the uranium mining waste pile Haberland near the town of Johanngeorgenstadt (Saxony, Germany). Inductively coupled plasma mass spectrometry (ICP-MS) and selective sequential extraction (SSE) analysis were used for the geochemical characterization of the soil samples. The 16S rDNA analysis showed that the natural bacterial communities were predominated by α-Proteobacteria and Acidobacteria. SSE analysis demonstrated that the uranium was weakly complexed and bound by Mn(hydr)oxides or Fe(hydr)oxides. The soil samples contain in addition to uranium also other heavy metals like arsenic for example. In order to understand how U(VI) influences the structure of natural bacterial community, one of the studied samples with the lowest indigenous amount of U was supplemented with 60 mg/kg U(VI) in form of uranyl nitrate. After four weeks of incubation, SSE analysis and 16S rDNA retrieval were done in parallel. The SSE analysis demonstrated that most of the supplemented uranium was weakly complexed and remained probably bioavailable. The 16S rDNA retrieval showed that populations of *Pseudomonas*, *Arthrobacter* and *Geobacter* were stimulated by the addition of U(VI) to the soil sample. For more profound understanding of the influence of U(VI) on natural bacterial community, column experiments are running in our laboratory.