Biogeochemistry of microbial communities associated with diffusion limited reduction of U(VI) and NO_3^- as co-contaminants in natural sediments and soils

Eoin Brodie[2], Terry C. Hazen[1], Jiamin M. Wan[1], Tetsu K. Tokunaga[1], Joern Larsen[1], Keith Olson[1], Dominique Joyner[1], Gary L. Andersen[1], Mary Firestone[1,2].

[1]Lawrence Berkeley National Laboratory, Berkeley, California
[2]University of California, Berkeley, California

The primary objective of this research is to study the coupled transport and biogeochemistry of U(VI) and NO_3^-. The redox reactions of these co-occurring contaminants are investigated in realistically heterogeneous model systems. We used direct measurements within diffusion-limited domains at the mesoscale (defined as the typical diffusion-limited scale, ranging from about 10^{-4} to 10^{-1} m). It is within these diffusion-limited domains that large gradients in microbial activity, chemical potentials, reaction rates, and transport rates can coexist. Thus, the dynamics at this mesoscale can control redox-dependent biotransformations in nature. Column experiments were performed using contrasting sediment types, a neutral pH sediment from the Oak Ridge FRC, TN and an alkaline sediment from Altamont Pass, CA. Both sediments were uniformly contaminated with U(VI) and NO_3^- solutions and organic carbon (TSB at 800, 80, 0 mg/L) was supplied from the surface via diffusion. In sediments receiving high OC loads, significant U(VI) reduction occurred in the upper regions, while deeper zones retained U primarily as U(VI). Redox conditions and uranium speciation were consistent with the spatial pattern of microbial activity. Carbon limitation of U(VI) reduction resulted from the interaction between microbial carbon consumption and diffusive supply of carbon. Alterations in bacterial community structure between columns and individual zones were assessed using a fingerprinting approach (TRFLP). T-RFLP analysis indicated dynamic bacterial ribotypes between redox zones and column treatments which we investigated further using previously developed but optimized photolithographic oligonucleotide arrays custom designed for 16S sequence identification. Using this approach we were able to determine the predominant sequence types (OTUs) associated with zones differing in redox and mineralogy.