

## Field-Scale Evidence for Selenium Bioremediation in a Uranium-Contaminated Aquifer

Michael J. Wilkins\*, A. Lucie N'Guessan, Philip E. Long

*Pacific Northwest National Laboratory, Richland, WA, USA, 99352*

*(\*michael.wilkins@pnl.gov)*

Kenneth H. Williams

*Lawrence Berkeley National Laboratory, Berkeley, CA, USA, 94720*

Under conditions where acetate was delivered to the subsurface to facilitate bioremediation of uranium, unexpected removal of selenium was documented. Selenium was removed from solution and concentrated in its elemental form within a densely mineralized biofilm that was attached to the surface of the injection tubing used to deliver and re-circulate acetate-amended groundwater. Electron microscopy revealed close association of elemental selenium precipitates with cell surfaces, with selenium aggregates having an average particle diameter of 50-60 nm. While the concentration of total selenium in groundwater was never observed to be in excess of 1.7  $\mu\text{M}$ , the dense accumulation of elemental selenium within the biofilms over a period of just two weeks suggests an alternative source of aqueous selenium. We propose that the biostimulation of subsurface iron-reducing microorganisms – as documented by increases in ferrous iron and a *Geobacter*-dominated microbial community – liberated a formerly sorbed pool of selenium following the reductive dissolution of iron oxides. This additional pool of aqueous selenium was then available for reduction by the tubing-associated, selenium-reducing microorganisms following groundwater recirculation through the tubing. The selenium removal process appeared to be the result of a mixed microbial community within the biofilm, one capable of coupling the oxidation of acetate to the reduction of oxygen, nitrate and soluble selenium species. Phylogenetic analysis of the tubing-hosted biomass indicated a community dominated by strains of *Dechloromonas* sp. and *Thaurea* sp., with isolates exhibiting genetic similarity to the later having been shown to reduce selenate to elemental selenium under laboratory conditions. Proteogenomic analysis of the *Dechloromonas* species within these biofilm communities revealed physiological mechanisms that may allow these strains to predominate in certain niche environments during biostimulation. The presence of *Dechloromonas* sp. within the biofilm suggests that these well-known perchlorate-reducing bacteria may be critical in the selenium-removal process.

Funding for this study was provided by the Environmental Management Science Program, Office of Biological and Environmental Research, U.S. Department of Energy (DOE). Portions of the work were carried out at the Environmental Molecular Sciences Laboratory, a national scientific user facility sponsored by DOE's Office of Biological and Environmental Research and located at Pacific Northwest National Laboratory.