# Oak Ridge Source Zone Sediment

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The stimulation of microbial uranium reduction at the field scale presents several challenges relative to the bench scale. First, bioremediation in the field will take place in the presence of heterogeneous sediment, which contains multiple components that can react geochemically with uranium. Next, a complex and changing community of bacteria will be responsible for uranium reduction in subsurface environments, not single strains or enrichments studied in the laboratory. Finally, multiple electron donors and acceptors are potentially available in a field setting, which complicates predictions regarding microbial metabolism. To investigate these issues, community fingerprinting and x-ray absorption spectroscopy were used to analyze microbial uranium reduction in a heterogeneous environment. Microcosms were established containing sediment samples from Area 3 of the Oak Ridge Field Research Center, ethanol, denitrified synthetic groundwater, and, as an inoculum, the effluent of a denitrifying fluidized bed reactor.

In most microcosms, soluble U(VI) and ethanol concentration decreased as acetate accumulated. Uranium associated with the solid phase was also reduced, as indicated by x-ray absorption near-edge structure (XANES) spectroscopy of sediment from sacrificed microcosms. This transformation was apparently mediated either directly or indirectly by bacterial activity, as uranium was not reduced in sterilized microcosms. Little iron was reduced during this time, but sulfate reduction proceeded concurrently with uranium reduction. Sulfate reduction may have been favored due to greater bioavailability of soluble sulfate over ferric iron, or due to greater initial numbers of sulfate-reducing bacteria than iron-reducing bacteria. As these factors are relevant to the Oak Ridge source zone, sulfate-reducing bacteria may reduce uranium in the field. Results indicated that, under sediment and groundwater conditions representative of the source zone during treatment, the amendment of ethanol can stimulate uranium reduction.

In other microcosms, however, soluble U(VI) concentration rebounded or leveled off after an initial decrease. XANES analysis revealed the reduction of sediment-associated uranium in these microcosms was also incomplete. A rebound in soluble uranium concentration implies the rate of uranium desorption from sediment exceeded the rate of its bioreduction. Biomass growth may have been inhibited in these microcosms, as little DNA was obtained from tubes in which uranium reduction ceased. Differences in patterns of uranium reduction between replicate microcosms highlight the significance of sediment and/or inoculum heterogeneity.

Changes in the microbial community upon biostimulation were monitored with terminal restriction fragment length polymorphism (T-RFLP) analysis. A comparison of T-RFLP profiles indicated a significant shift in community structure occurred as uranium was reduced. In addition, profiles showed that different community members were dominant in microcosms with complete versus incomplete uranium reduction. Further work is needed to elucidate the impact of microbial community composition on the function of uranium reduction.