Scientific Focus Areas (SFA)

Interconnected Cycling of Fe, S, and C in the Terrestrial Subsurface: New Paths and Opportunities for Coupling Biotic and Abiotic Processes

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The biogeochemical cycling of Fe, S, and C in the terrestrial subsurface affects contaminant mobility, nutrient availability, and the chemistry of groundwater. Predicting the flow of electrons through these elements, particularly in the context of the Rifle IFRC, requires a fundamental, molecular-level understanding of the coupled biotic and abiotic processes responsible for these transformations.

In bioreactor experiments, we show that at pH 9, dissimilatory metal-reducing bacteria (DMRB) can respire S(0) but not goethite because the reduction of the latter is not thermodynamically favorable under oligotrophic conditions. Because the reaction of HS- with Fe(III) minerals produces S(0), DMRB in alkaline aquifers may require active respiration by sulfate-reducing bacteria (SRB) to respire. Under these conditions, Fe(III) reduction will proceed via S(0)-mediated electron-shuttling pathways through a mutualistic partnership between DMRB and SRB rather than the direct enzymatic reduction of Fe(III) minerals by DMRB alone.

In separate experiments, we investigate how the nature of organic C plays a critical role in determining the mechanism by which Fe(III) minerals are reduced. In microcosms containing both ferrihydrite and sulfate as electron acceptors and amended with acetate or lactate, we found that both acceptors were reduced simultaneously and that lactate promoted more rapid reduction. When glucose was used as the sole electron donor, however, ferrihydrite was reduced without a concomitant reduction of sulfate. The production of acetate per mol of glucose consumed differed between replicate bottles, as did the amount of total C recovered as organic acids, causing significant differences in the pH between the glucose-fed microcosms and variations in the total accumulation of aqueous Fe(II).

Because elements such as Fe, S, and C can cycle rapidly between different valence states in subsurface environments, actual pathways of electron flow are difficult to determine from geochemical measurements alone. By reconstructing the genomes of microorganisms that catalyze these processes from a metagenome, we can begin to unravel the metabolic networks active in these environments. We reconstructed the complete 2.4 Mb genome of a previously uncultivated epsilonproteobacterium by assembling short-read shotgun metagenomic data using a complexity reduction approach. Genomic evidence suggests that the organism is a chemolithoautotrophic diazotroph capable of deriving energy for growth by microaerophilic or nitrate-/nitric oxide-dependent oxidation of S(0), sulfide, sulfite, or H2. At steady-state, these critical but transient metabolites often exist at only minute and difficult to measure concentrations, underscoring the critical role of genomic analysis in understanding the geochemistry of complex subsurface environments.