Microbial Fe(III) oxide reduction potential in Chocolate Pots hot springs, Yellowstone National Park

NATHANIEL W. FORTNEY[1,3], ERIC E. RODEN[1,3]
AND ERIC S. BOYD[2,3]

[1]University of Wisconsin-Madison, Madison, Wisconsin, 53706, USA
(nfortney@wisc.edu, eroden@geology.wisc.edu)
[2]Montana State University, Bozeman, Montana, 59717, USA
(eboyd@montana.edu)
[3]NASA Astrobiology Institute, USA

Previous research into microbial dissimilatory iron reduction (DIR) in Yellowstone National Park (YNP) has focused on high temperature, low pH environments where soluble Fe(III) is utilized as an electron acceptor for respiration. Much less attention has been paid to DIR in lower temperature, circumneutral pH environments, where solid phase Fe(III) oxides are the dominant forms of ferric iron. This study explored the potential for microbial Fe(III) oxide reduction in warm (ca. 40-50°C), circumneutral pH Chocolate Pots hot springs (CP), YNP. Endogenous microbial communities reduced native CP Fe(III) oxides, as documented by most probable number (MPN) enumerations and enrichment culture studies. Enrichment cultures demonstrated sustained DIR tied to acetate and lactate or H_2 oxidation. These cultures have also exhibited growth through reduction of synthetic amorphous Fe(III) oxides and oxidation of either acetate or lactate alone. The extent to which bacterial sulfate reduction contributed to DIR was explored by eliminating sulfate from the culture media and inhibiting sulfate reduction with molybdate. Results indicate that bacterial sulfate reduction does not contribute substantially to observed rates of DIR. Genomic DNA was extracted from the enrichment cultures for 16S rRNA gene pyrosequencing. The results showed that dominant bacterial sequences were closely related to the well known Fe(III) reducer *Geobacter metallireducens*. Additional taxa included relatives of *Desulfohalobium* and *Thermodesulfovibrio*, although their involvement in DIR is unknown. Future studies will include metagenomic and Fe isotopic analyses of enrichment cultures, *in vitro* DIR experiments, and materials obtained from vertical sediment cores collected along the flow path. These studies will provide a snapshot of the coupled geochemical-microbial reaction system through time and space, demonstrating how genomic and isotopic properties change with depth and distance along the flow path. Our analyses will offer the first detailed insight into how internal Fe redox cycling may control the Fe isotope composition of a Fe-rich, neutral pH geothermal environment.