

**In vitro and in situ iron geochemistry and microbial activity at Chocolate Pots Hot Springs, Yellowstone National Park.** N. W. Fortney<sup>1,3</sup>, B. J. Converse<sup>1,3</sup>, S. He<sup>1,3</sup>, B. L. Beard<sup>1,3</sup>, C. M. Johnson<sup>1,3</sup>, E. S. Boyd<sup>2,3</sup>, and E. E. Roden<sup>1,3</sup>, <sup>1</sup>Department of Geoscience, University of Wisconsin, Madison, Wisconsin, 53706 (nfortney@wisc.edu), <sup>2</sup>Department of Microbiology and Immunology, Montana State University, Bozeman, Montana, <sup>3</sup>NASA Astrobiology Institute, USA

Microbial iron (Fe) redox cycling has been well documented in high temperature, low pH environments at Yellowstone National Park [1]. However, Fe redox cycling communities native to lower temperature, circumneutral pH hot spring environments, like Chocolate Pots (CP), have been less well studied. This study examined microbial communities and Fe geochemistry in the Fe-Si rich deposits at CP.

The current focus is on microbial dissimilatory iron reduction (DIR) and the potential for DIR to record Fe isotope signatures in the mineral deposits. Core samples were collected along the flow path at CP to determine how microbial community composition and Fe geochemistry change vertically and longitudinally moving away from the hot spring vent. Small quantities of core material were also used for in vitro Fe(III) reduction assays to assess the pathways and potential electron donor limitation of DIR. Reduction assays revealed an active DIR community proximal to the CP vent driven by endogenous electron donors, and studies with molybdate-inhibited materials indicated only minor sulfide-driven Fe(III) reduction linked to microbial sulfate reduction. These findings were reproduced in a <sup>13</sup>C-acetate stable isotope probing experiment (still in progress) aimed at identifying the active Fe(III)-reducing community in situ.

16S rRNA gene pyrosequencing of DNA extracted from CP cores and in vitro reduction assays revealed similar taxa. Of particular interest are taxa related to organisms from the newly-identified order Ignavibacteriales, which have recently been shown to have ability to reduce Fe(III) [2]. Shotgun metagenomic sequencing of Fe(III)-reducing enrichment cultures from a previous study at CP (Fortney et al., in prep) identified the presence of a porin-cytochrome complex (PCC) known to be involved in DIR in a variety of bacteria [3]. Subsequent metagenomic analysis of DNA recovered from the upper 1 cm of the core collected near the vent has revealed the presence of the same complex, suggesting its possible involvement in DIR in situ.

Preliminary iron isotope measurements of aqueous and 0.5 M HCl extractable iron phases indicate that DIR influences Fe isotopic composition in deposits within a few m of the hot spring vent. Additional measurements and analyses are underway to gain a more complete understanding of how isotopic evidence of DIR can be preserved in this unique hydrothermal

setting, which may be analogous to hydrothermal environments that are known to have existed in the distant past on Mars.

#### References:

- [1] Kozubal, M. A. et al. (2012) *Front Microbiol*, 3, 109. [2] Podosokorskaya, O. A. et al. (2013) *Environ Microbiol*, 15, 1759-1771. [3] Shi, L. et al. (2014) *Front Microbiol*, 5, 657.