

## Pushing the limits of AMS measurements of cosmogenic radioisotopes in natural systems

M. JANZEN<sup>1</sup> AND A. GALINDO-URIBARRI<sup>1,2</sup>

<sup>1</sup>Department of Earth and Planetary Sciences, University of Tennessee, TN 37996, United States (mjanzen1@utk.edu)

<sup>2</sup>Physics Division, Oak Ridge National Laboratory, P.O. Box 2008, MS 6368, Oak Ridge, TN 37831, United States (uribbarri@ornl.gov)

Pushing the detection limits of cosmogenic radioisotopes using Accelerator Mass Spectrometry (AMS) techniques will be extremely advantageous to the field of earth sciences. In the late 1970's research in earth sciences was revolutionized by the use of AMS to achieve isotopic levels many orders of magnitude lower than conventional mass spectrometers. In earth sciences AMS techniques are most commonly employed for the measurement of cosmogenic radioisotopes. These isotopes are most useful for quantifying processes at Earth's surface. At the Holifield Radioactive Ion Beam Facility (HRIBF) we have exceptional capabilities owing to the unique set up including the highest operating voltage electrostatic accelerator in the world, the 25-MV Tandem, as well as unique beam transport components and peripheral equipment. This system allows for the detection of extremely rare isotopes and effectively remove isobar interferences. Recent measurements on <sup>36</sup>Cl/Cl ratios within seawater samples have shown that the levels of detection can be pushed as far as 10<sup>-16</sup> [1]. Recent developments of new AMS methods such as photodetachments of negative ions may allow us to push the limits even further and increase the range of radioisotopes that can be detected [2]. I will describe an on-going research program at HRIBF that includes identifying natural systems where this extra sensitivity could make a difference. Measurements at the limit of sensitivity will contribute to constrain the predictions from cosmogenic production models at Earth's surface.

[1] A. Galindo-Uribarri *et al.* (2007) *Nucl. Instr. Meth. B* **259**, 123. [2] A. Galindo-Uribarri *et al.* (2010) *Nucl. Instr. Meth. B* **268**, 834.

## Linking geochemistry to microbial community structure and function in sulfidic geothermal systems of Yellowstone National Park

Z.J. JAY<sup>1</sup>, B. PLANER-FRIEDRICH<sup>2</sup>, D.B. RUSCH<sup>3</sup>  
AND W.P. INSKEEP<sup>1\*</sup>

<sup>1</sup>Department of Land Resources & Environmental Sciences, Montana State University, Bozeman, MT 59717, USA  
(\*correspondence: binskeep@montana.edu)

<sup>2</sup>University of Bayreuth, Bayreuth, Germany

<sup>3</sup>J. Craig Venter Institute, Rockville, MD 20850, USA

Analysis of metagenome sequence from high-temperature microbial communities in Yellowstone National Park (YNP) suggests the importance of heterotrophic, S-respiring crenarchaeal populations in sub-oxic sulfidic sediments. The primary goal of this study was to determine the role of Thermoproteales and Desulfurococcales populations in S and C cycling in these communities using both molecular and culture methods. Metagenome sequence was obtained from three sub-oxic, elemental S-dominated hot springs in YNP: Monarch Geyser (80° C, pH 4), Cistern Spr. (CS; 76° C, pH 5) and Joseph's Coat HS (JCHS; 80° C, pH 6). Major sequence assemblies from these sites resulted in nearly complete consensus genomes of *Acidilobus*, *Vulcanisaeta* and *Caldivirga*-like organisms in all sites, *Thermoproteus/Pyrobaculum* spp. in JCHS and CS, and two different Sulfolobales phylotypes in CS. Several enzymes and transporters involved in protein, carbohydrate, and lipid catabolism were identified. The predominant community members all contain bd-ubiquinol oxidase genes and lack any evidence for heme-copper oxidases often associated with aerobic respiration. The expression of genes involved in anaerobic respiration, including novel S reductases in the dimethylsulfoxide (DMSO) molybdopterin family, NAD (P)H:S<sup>0</sup> oxidoreductases, and nitric oxide reductases, was studied using RT-PCR to estimate the activity of these processes in each habitat. Results from molecular analyses of field samples were compared to controlled experiments using a *Pyrobaculum* sp. isolated from JCHS that is capable of growing anaerobically on S<sup>0</sup>, using yeast extract as a C and energy source. This organism contains a novel DMSO reductase, highly related to gene sequences identified in the JCHS metagenome. The effect of S<sup>0</sup> particle size on microbial growth was evaluated in concert with the expression of novel DMSO reductases. These data provide insight regarding the structure and function of high-temperature microbial communities, and the role of specific phylotypes in S and C cycling in sub-oxic, sulfidic geothermal systems.