Geological Controls on H_2 Cycling in Yellowstone National Park Hot Spring Communities

Melody R. Lindsay[1], Matthew R. Urschel[1], Kirsten E. Fristad[2], Kristopher M. Fecteau[3], Everett L. Shock[3,4], Tori M. Hoehler[2], Eric S. Boyd[1]

[1]Montana State University, Department of Microbiology and Immunology, Bozeman, MT, [2]NASA Ames Research Center, Moffett Field, CA, [3]Arizona State University, Department of Chemistry and Biochemistry, Tempe, AZ, [4]Arizona State University, School of Earth and Space Exploration, Tempe, AZ

Background

The interaction between crustal rocks rich in iron (e.g., basalts, peridotites) and water generates hydrogen (H_2) via several processes collectively known as serpentinization. These reactions are widespread and were likely active early during Earth's history; comparable processes can be expected on other rocky planets that have liquid water. The H_2 produced through these water-rock interactions likely had an integral role in supporting ancient chemoautotrophic metabolisms.

The influence of lithogenic H_2 on the distribution of H_2-dependent chemoautotrophic metabolisms and the microbial communities they support can be explored through the integration of geochemical, molecular, and physiological data in modern early earth analog systems. In particular, such relationships can be explored in the accessible hot springs in Yellowstone National Park (YNP) (Fig. 1) which provide a range of lithogenic H_2 sources that have been suggested to support diverse H_2 metabolizing microbial communities. Gradients in oxidant availability due to differences in subsurface geology (Fig. 2) may dictate the nature of H_2 metabolisms in geothermal communities in YNP.

We hypothesize that chemotrophic organisms involved in H_2 metabolism have diversified to capitalize on available gradients in oxidants

***Goal 1*: Integrate geochemical, molecular and physiological approaches to link populations with chemotrophic H_2 transformation activities in YNP hot springs**

***Goal 2*: Determine the extent to which H_2 metabolic activity is coupled with various oxidants and their availability (e.g. CO_2, SO_4, NO_3, O_2)**

***Goal 3*: Quantify the extent to which distribution and diversity of hydrogenase genes reflects availability of oxidants**

Site Location

Sampling Locations: **Roadside West (RW) Spring** and **Roadside East (RE)** (Fig. 3, Fig. 4) are a paired set of hot springs (Fig. 2) which were chosen because they are likely to exhibit differences in the availability of H_2-metabolism supporting metabolisms.

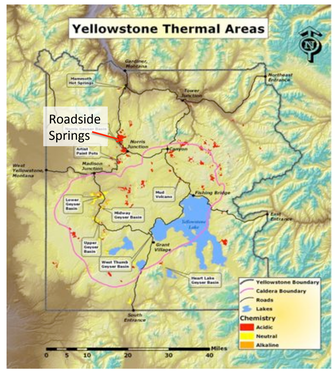

Figure 1. Location of Roadside Springs in YNP.

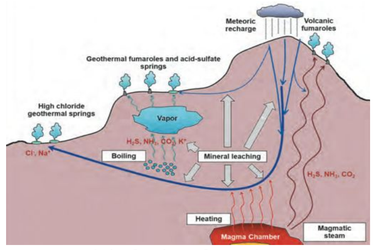

Figure 2. Model of subsurface phase separation leading to acidic and alkaline springs.

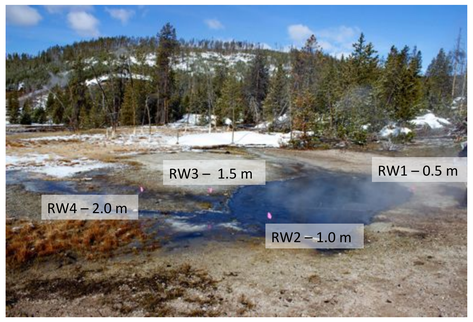

Figure 3. RW spring source and outflow channel

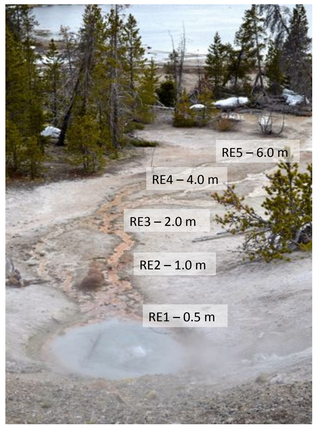

Figure 4. RE spring source and outflow channel

Acknowledgements: Funds for this project were provided by NASA Exobiology and Evolutionary Biology Grant #NNX13AI11G, and travel funds to attend this conference were provided by a SETI Institute Travel Grant and a MSU Thermal Biology Institute Turner Foundation Award.

Methods

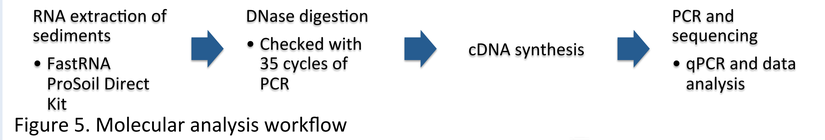

Figure 5. Molecular analysis workflow

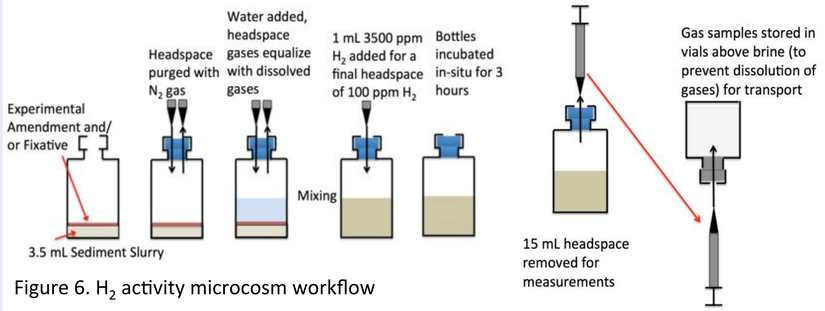

Figure 6. H_2 activity microcosm workflow

Results – Aqueous and Gas Phase Geochemistry

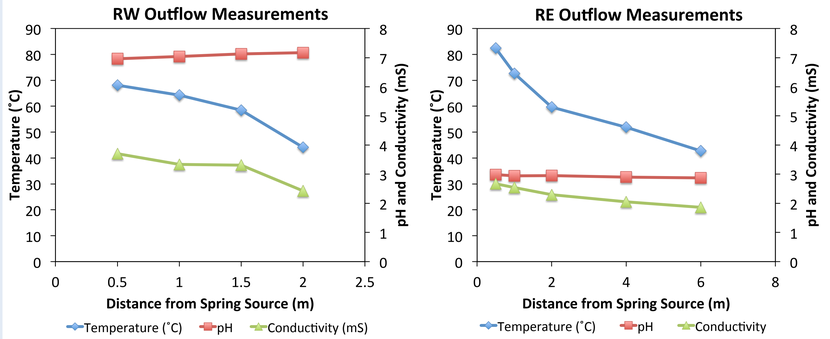

Figure 7. Fluid temperature, pH and conductivity measured down RW and RE outflow channels.

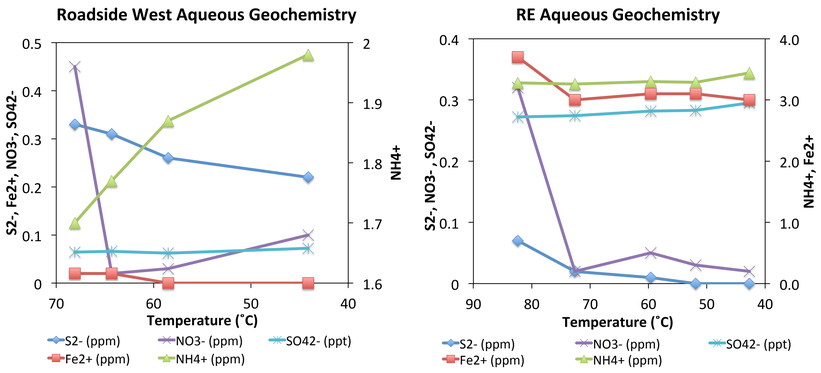

Figure 8. Geochemical gradients; specifically sulfide, iron, nitrate, sulfate, and ammonia as measured down RW and RE outflow channels.

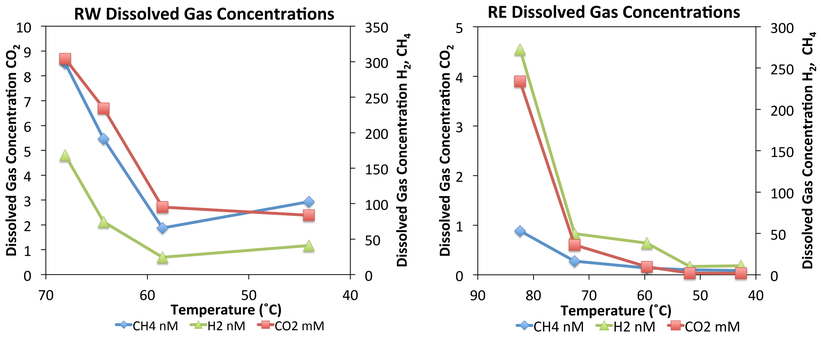

Figure 9. Gradients in dissolved gases (CH_4, CO_2, H_2) along the RW and RE outflow channels.

Results – Microbial Activities

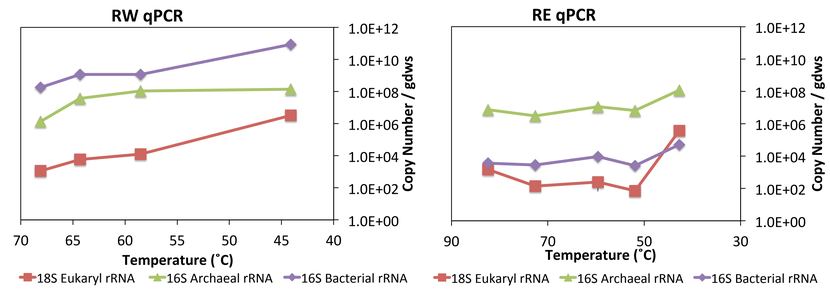

Figure 10. Abundance of bacterial, archaeal, and eukaryal SSU rRNA transcripts in the RW and RE outflow channels.

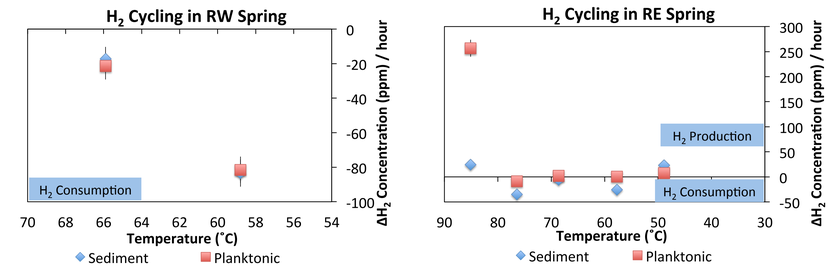

Figure 11. Net change in H_2 concentration during a 1 hour incubation, indicating H_2 production or H_2 consumption in planktonic and sediment-associated microbial communities.

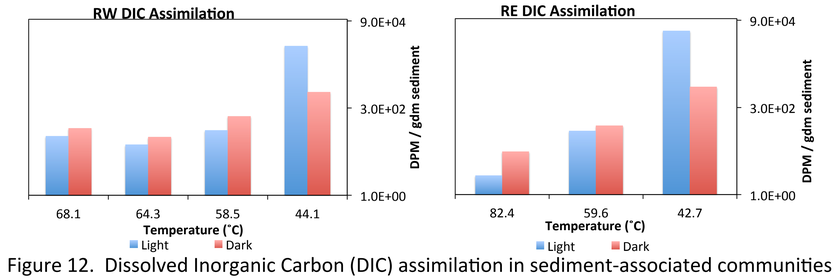

Figure 12. Dissolved Inorganic Carbon (DIC) assimilation in sediment-associated communities from RW and RE incubated at different temperatures along the outflow channel.

Conclusions

- SSU rRNA transcript abundance increases as temperature decreases and as pH becomes more neutral, which may reflect decreased maintenance energy demands at lower temperature or more circumneutral pH
- Decreasing levels of some substrates (e.g. NO_3^-) down RE and RW outflow channels (Fig. 8) could reveal the preferred e- acceptors coupled with H_2 oxidation.
- While most communities were net sinks for H_2, one (RE1) was a net source of H_2 suggesting a role for biology in producing H_2 in hot spring communities
- The abundance of the bacterial 16S rRNA transcripts along the RW outflow channel correlates with net H_2 consumption activities, while the abundance of archaeal 16S rRNA transcripts along the RE outflow channel suggests that archaea have a role in net H_2 production activities.
- Rates of CO_2 fixation and the abundance of SSU transcripts are correlated and exhibit a marked increase as the communities transition from chemotrophic to phototrophic metabolisms.

Future/Ongoing Work

- Ongoing multiple probable number assays and sequencing of SSU rRNA and hydrogenase transcripts will provide insight into the preferred redox partner(s) for H_2 metabolisms, the identity of the active species in these hot spring microbial communities, and the activity and identity of hydrogenases responsible for H_2 metabolism in YNP hot springs.
- Phylogenetic analyses of SSU rRNA and hydrogenase transcripts when integrated with geochemical and physiological assays will provide a mechanism to examine the extent to which the diversification of hydrogenases and H_2- cycling microbial communities reflect available energy gradients in this early earth analog system.