

Microbial interactions with sulfide and arsenite in an acidic geothermal spring in Yellowstone National Park

SETH D'IMPERIO, CORINNE LEHR AND
TIMOTHY R. MCDERMOTT

Dept. Land Resources and Environmental Sciences, and
Thermal Biology Institute Montana State University,
Bozeman, MT 59717 (sethd@mymail.msu.montana.edu;
clehr@montana.edu; timmcd@m.montana.edu)

We are studying the ecophysiology of microbial populations inhabiting an acid-sulfate-chloride geothermal spring in Norris Geysir Basin, Yellowstone National Park. Source water temperature ranges from 63 to 73 °C and pH between 3.1 to 3.3. Electron donors present at concentrations capable of supporting chemolithoautotrophic-based primary production include Fe(II), H₂, H₂S, and As(III). The spring is chemostat-like in that the bioavailability of these energy sources is constant, although absolute concentrations can vary somewhat, and aqueous chemistry measurements have revealed the presence of numerous chemical (and temperature) gradients occurring as a function of distance from the point of spring discharge. In-field assays demonstrate significant microbial oxidation of As(III), but only in specific zones in the spring outflow channel where H₂S is depleted. We are combining biogeochemical measurements, phylogenetic analysis, and pure culture experiments to model *in situ* As(III)-H₂S-microbe interactions in order to explain the apparent zonation of the As(III) oxidation. An As(III)-oxidizing *Hydrogenobaculum* strain was isolated and used to show that sulfide inhibits As(III) oxidation. Additional in-field experiments re-examined As(III) oxidation in the spring mats by manipulating H₂S concentrations and found that the microorganisms in the spring mats appear enzymatically equipped to oxidize As(III), but are inhibited to do so if appreciable dissolved H₂S is present ($\geq 5\text{-}10 \mu\text{M H}_2\text{S}$). H₂S appears to not be toxic, but rather acts as a reversible, competitive inhibitor of the As(III) oxidase enzyme, an example of a geochemical control on a microbial process.

The Vulcano hydrothermal system: Microbial community structure, novel isolates, and geochemical energy sources

J. P. AMEND, K. L. ROGERS, A. RUSCH AND C. GAMMON

Department of Earth & Planetary Sciences, Washington
University, St. Louis, MO 63130 USA
(amend@levee.wustl.edu, rogers@levee.wustl.edu)

The hydrothermal system of Vulcano Island, Italy is arguably the best-studied shallow marine vent environment in the world. This system is the type locality for some of the most famous hyper-thermophiles, including *Thermotoga maritima*, *Aquifex aeolicus*, and *Archaeoglobus fulgidus*. In addition, geochemical analyses and modeling have revealed hundreds of energy-yielding redox reactions that could support autotrophic and heterotrophic communities.

We have applied several techniques to characterize the interface of hydrothermal geochemistry and microbial diversity at Vulcano. Using geochemically-designed media, we isolated the first O₂-tolerant member of the archaeal order Thermococcales (*Palaeococcus helgesonii*) and a novel thermophilic, autotrophic, sulfate-reducing bacterium that is only 92% identical in its 16S rRNA gene sequence to any cultivated organism. The prokaryotic communities in three Vulcano sediment samples, determined by fluorescent *in situ* hybridization (FISH), were dominated by Archaea (60-80% of probe-detected cells). However, the abundances of specific archaeal groups range significantly across the sites: 11-16% for the Thermococcales, 6-15% for the Archaeoglobales and 17-26% for the Crenarchaeota. In one case, the disappearance of the aerobe, *Aquifex*, from the microbial community corresponded to a marked decline in O₂. Diverse archaeal communities were also noted in 16S rRNA gene surveys. Archaeal diversity in a thermal well consisted of 17 unique phylotypes and was dominated by a group of uncultured, deeply-branching Crenarchaeota. In contrast, a thermal vent with similar temperature and pH contained 6 unique archaeal phylotypes, all distinct from those found in the well. Documented compositional and energetic diversity appears to be directly linked to prokaryotic community structure and diversity.