Revisited multicomponent chemical geothermometry: application to the Dixie Valley geothermal area

L. PEIFFER*, C. WANNER, N. SPYCHER, E. SONNENTHAL, B.M. KENNEDY

Lawrence Berkeley National Laboratory, Berkeley, USA, lpeiffer@lbl.gov (* presenting author)

The multicomponent chemical geothermometry method [1,2] involves computing the saturation indices of potential reservoir minerals over a range of temperatures, given a known geothermal fluid composition, then inferring reservoir temperature from the clustering of mineral saturation indices near zero. This method was automated as a stand-alone computer program (geoT), easing its application and allowing optimization of model input parameters using parameter-estimation software [3]. The code can process simultaneously multiple water compositions, and correct for dilution and mixing effects as well as gas loss. The temperature of the reservoir is estimated from statistical analysis of computed mineral saturation indices. One difficulty of the method is that it is sensitive to potentially erroneous Al chemical analyses, an issue which can be partly resolved by resorting to computed Al concentrations assuming equilibration with selected Al-bearing minerals [2].

The geothermometry method and new code are being tested on geothermal fluids from Dixie Valley (Nevada, USA) using an extensive set of water and gas analyses [4]. These data include total and dissolved ("ionized") Al analyses in filtered (0.45 and 0.2 μm) and unfiltered water samples, allowing testing the effect of these various reported Al concentrations on predicted temperatures. A set of minerals prevailing in the geothermal reservoir was assumed based on XRD data from well cuttings [5]. Gas analyses were added back to the well waters, and increased salinity effects caused by the reinjection of flashed brines into the reservoir were also considered. Using "ionized" Al concentrations in unfiltered samples, reservoir temperatures of ~250°C were obtained. These temperatures were similar to values obtained by computing Al concentrations assuming equilibrium with Al minerals (albite, microcline, muscovite). These temperatures seem reliable because they are consistent with measured downhole water temperatures. In contrast, the 0.2-μ filtered Al analyses led to lower computed temperatures close to sampling temperatures (160°–180°C) and corresponding to different equilibrated minerals. In this case, the 0.2-μ filtered Al concentrations appear too low, apparently reflecting the filtering-out of colloidal Al formed by cooling. Hot spring waters from the wider Dixie Valley area were also investigated. The lack of consistency between their reconstructed equilibrium temperatures, as well as significant differences in their chemical composition may indicate that Dixie Valley hosts several distinct reservoirs. Batch geochemical modelling and reactive transport simulations are being conducted to understand processes affecting the deep geothermal fluids on their way to the surface and to characterize the hydrologic relations between the deep reservoir and the superficial hot springs.

References
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Evolutionary Response of S Isotope Fractionation by Sulfate Reducing Microorganisms

ANDRÉ PELLERIN[1]*, NADIA MYKYTCZUK[2], REBECCA AUSTIN[1], GRANT M. ZANE[3], LYLE WHYTE[2], JUDY D. WALL[3], AND BOSWELL WING[1]

[1]Department of Earth and Planetary Sciences, McGill University, Montréal, Canada, andre.pellerin@mail.mcgill.ca (* presenting author), boswell.wing@mcgill.ca, rebecca.austin@mail.mcgill.ca
[2]Department of Natural Resource Science, McGill University, St-Anne de Bellevue, Canada, nadia.mykytczuk@mail.mcgill.ca, lyle.whyte@mcgill.ca
[3]University of Missouri, Biochemistry Division, Columbia, USA, WallJ@missouri.edu, zaneg@missouri.edu

Microbial sulfur isotope fractionation is controlled by the energy metabolism of sulfate reducing microorganisms. It represents a well-defined and precisely measurable characteristic of the phenotype of the microorganism. As such, it is dependent both on the underlying genotype and on the response of that genotype to variability in the local environment. Since genotype and environment have both changed throughout Earth's history, the geological record of biogenic S isotopes must reflect the influence of both environmental change and molecular evolution. However, the basic interplay between microbial evolution and S isotope fractionation has not been examined.

We investigated the evolutionary response of S isotope fractionation in the sulfate-reducing bacterium *Desulfovibrio vulgaris* Hildenborough (DvH). Two bacteria – the wild type DvH as well as a mutant derived from that strain in which one copy of a gene putatively encoding lactate dehydrogenase was deleted and replaced with an antibiotic resistance cassette were used as model organisms. In defined media (sulfate and lactate limited) at 33°C, ancestral wild type and mutant DvH exhibit fractionation factors that reproducibly differ by 0.5‰. We serially transferred six replicate lines of the wild type and six replicate lines of the mutant for 600 generations in batch cultures. Over the course of the experiments, we assayed fitness through direct competition experiments between the ancestral mutant and descendant wild-type strains (or vice versa). In these competition experiments, we used qPCR to monitor the relative abundance of the mutant through a unique genetic barcode associated with the antibiotic resistant cassette. After 300 generations, the descendant strains were markedly more fit than their ancestors, with relative growth rate increases of nearly 30%. This means that the descendant strains have a clear selective advantage in the defined media, illustrating that DvH can undergo evolutionary adaptation on laboratory timescales.

Despite the clear evidence for evolutionary changes over the course of our experiment, isotopic assays of the descendant wild-type and mutant strains reveal that the 0.5‰ difference in their fractionation factors is conserved. Preservation of such a small isotope effect implies that the sulfate reducing energy metabolism is remarkably robust to the selective pressures of our experimental setup.