Microbial Metabolism in Serpentinite Fluids

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Serpentinization is the process in which ultramafic rocks, characteristic of the upper mantle, react with water liberating mantle carbon and reducing power to potenially support chemosynthetic microbial communities. These communities may be important mediators of carbon and energy exchange between the deep Earth and the surface biosphere. Our work focuses on the Coast Range Ophiolite Microbial Observatory (CROMO) in Northern California where subsurface fluids are accessible through a series of wells. Preliminary analyses indicate that the highly basic fluids (pH 9-12) have low microbial diversity, but there is limited knowledge about the metabolic capabilities of these communties. Metagenomic data from similar serpentine environments [1] have identified Betaproteobacteria belonging to the order Burkholderiales and Gram-positive bacteria from the phylum Clostridiales, as key components of the serpentine microbiome.

In an effort to better characterize the microbial community, metabolism, and geochemistry at CROMO, fluids from two representative wells (N08B and CSWold) were sampled during a recent field campaign. The wells selected can be differentiated in that N08B had cell counts ranging from 10^5-10^6 cells mL^{-1} of fluid, and abundance of the Betaproteobacterium *Hydrogenophaga*. In contrast, fluids from CSWold have lower cell counts (~10^3 cells mL^{-1}) and an abundance of *Dethiobacter*, a taxon within the phylum *Clostridiales*. Geochemical characterization of the fluids includes measurements of dissolved gases (H_2, CO, CH_4), dissolved inorganic and organic carbon, volatile fatty acids, and nutrients. Microcosm experiments were conducted with the purpose of monitoring carbon fixation and metabolism of small organic compounds, such as acetate, while tracing changes in fluid chemistry and microbial community composition. These experiments are expected to provide insight into the biogeochemical dynamics of the serpentinite subsurface at CROMO and represent a first step for developing RNA based Stable Isotope Probing (RNA-SIP) experiments to trace microbial activity at this site.

[1] Brazelton *et al*. (2012) Frontiers in Microbiology 2:268

Experimentally quantifying metabasalt dissolution kinetics at 25°C and pH 2-12

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Despite the large number of studies reporting individual minerals dissolution rates, less is known about the dissolution rates of whole rocks. This lack of data motivated this study of the dissolution kinetics of a metabasalt from the Mt. Reventino area (Southern Italy). Experiments were performed on crushed and sieved metabasalt at 25°C using mixed-flow reactors. The interpretation of our experiments takes account of the contributions of the dissolution of each distinct mineral to model the chemical evolution of the aqueous phase. Individual mineral surface areas were estimated by distributing the total crushed rock BET surface area among the different minerals present in the metabasalt (chlorite, amphibole, epidote, albite, and phengite) as a function of their modal abundances. Then, by adopting the literature dissolution rate of epidote [1], the temporal evolution of cation concentrations were used to retrieve the dissolution rates of the other minerals. Dissolution rates for chlorite, amphibole, albite, and phengite retrieved from the pH 2 experiments are within an order of magnitude from each other. This observation contrasts with corresponding rates reported in the literature and suggests that mineral dissolution rates are affected by presence of other minerals in multi-phase rocks.

[1] Marini (2007) In *Thermodynamics, Kinetics and Reaction Path Modeling*, 470.

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