

Microbial glass bioalteration: Inferring mechanisms of biocorrosion from trace fossil morphology

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Volcanic glass from altered oceanic crust commonly carries textures and chemical signatures that suggest microbial involvement in its alteration with seawater. While such traces and their chemical signatures are imperfect for identifying particular microbes or their particular metabolism and geochemical effects, they offer an opportunity to constrain microbial activity in the geological record. Such constraints are commonly associated with traces of DNA and potentially distinct geochemical signatures, and they carry distinct textural characteristics that may reveal some of the functions of the microbes implicated in these processes.

There is much potential for bioalteration to significantly influence geochemical fluxes, contribute to the global biomass and it may have a role in the earliest life on earth. While there is still much uncertainty about which types of microbes are responsible, the observation of distinct textures suggest that there are at least two types of microbial activities responsible for distinct textures. In particular, we compare the development of tubular textures to the tunneling found in carbonates, and suggest a similar origin, by hyphal tunneling. This process involves the excretion of oxalic acids at the tips of fungal hyphae and the return of micronutrients back to their host cell. We suggest that glass bioalteration tunnels are caused by “drilling” of hyphae-like organelle, but we specifically do not imply that the microbe necessarily is prokaryotic. This functional interpretation may help us in our search for microbes that cause these textures. However, we caution that these organisms may be difficult to identify and to study, because they are likely to be sparsely distributed and difficult to cultivate.

Modeling of thermodynamic and kinetic controls on complex biogeochemical reaction networks

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The cycling of iron in the environment and the mobility of a number of redox-sensitive contaminants are typically controlled by complex biogeochemical reaction networks. Defensible predictions of contaminant migration and metal cycling, therefore, require mechanistic models that capture the various pathways and their rates over the entire range of redox conditions possible. Historically, modeling of microbially-mediated reactions has included only a limited range of processes, neglecting for example the coupling of reductive dissolution, secondary phase precipitation, and sorption. The rates of the microbially-mediated pathway under any given set of conditions have been treated with semi-empirical (at best) kinetic formulations. Fortunately, there is currently a growing interest in incorporating a rigorous thermodynamic framework into the kinetic models [1], while presenting more realistic treatments of the evolving microbial community structure.

In this presentation, we focus on the development of thermodynamic/kinetic models for iron cycling, uranium reduction, and sulfate reduction with application to a set of column experiments using natural sediments from the uranium bioremediation site at Old Rifle, Colorado. In the experiments, uranium-contaminated groundwater from the site is amended with variable concentrations of acetate to investigate explicitly the thermodynamic controls on the uranium, iron and sulfate reduction rates. At 3 mM acetate, uranium removal from the groundwater is almost quantitative, with only a modest decrease in the extent of removal once sulfate reduction begins at about 40 days. In contrast, uranium decreases only about 40% when 0.5 mM acetate is injected, while the onset of sulfate reduction is delayed to more than 120 days. These changes in the rates of reduction take place while pH and alkalinity affect the extent of adsorption of the uranium on solid phases within the aquifer material.

[1] Jin, Q. & Bethke, C.M. (2005) *GCA Acta* **69**, 1133-1143.