

## Using modern Fe-oxidizing microbes to unravel the evolutionary and geologic history of Fe oxidation

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Neutrophilic Fe-oxidizing microorganisms (FeOM) are key drivers of Fe cycling on modern Earth, and likely played important roles in depositing Fe oxides and associated elements in the ancient ocean. In order to better understand the roles and history of FeOM, we have been studying them in a variety of modern environments, and working with isolates in the laboratory to determine the conditions, mechanisms, and signatures of microbial Fe oxidation.

Microaerophilic FeOM appear to grow wherever Fe(II) and O<sub>2</sub> are both present. We have detected FeOM by culturing and/or 16S rRNA sequencing in groundwater seeps, streambank and coastal aquifers, a stratified estuary, soil, coastal sediments, and marine hydrothermal vents. Pure cultures allow us to connect the Fe oxidation metabolism to 16S rRNA and functional genes. Using comparative genomics, we have identified genes that represent candidates for mechanisms of Fe oxidation and biomineralization. Phylogenetic analyses give us a window into evolutionary history, suggesting horizontal transfer of key functional genes between Betaproteobacterial (freshwater) and Zetaproteobacterial (marine) FeOM. To test the roles of these genes, we have been performing transcriptomic experiments on Fe microbial mats and cultures. Linking gene function to evolution will allow us to better understand the coevolution of microbial Fe oxidation and Earth's surface chemistry.

Many microaerophilic FeOM produce Fe oxyhydroxides with distinctive morphologies that serve as biosignatures (e.g. twisted stalks in microbial mats; Krepski et al., 2013, *Geobiology* 11:457-471). These signatures correlate to specific environmental conditions, notably O<sub>2</sub> concentrations. Therefore, we have been (1) measuring the O<sub>2</sub> concentrations associated with stalk-rich microbial mats and (2) performing Fe oxidation kinetics experiments to determine preferred O<sub>2</sub> concentrations. Our results will allow us to use the Fe mineral biosignatures to interpret both the history of FeOM and oxygen evolution on Earth.