

How microbes oxidize Fe(II)

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Microbial Fe oxidation is increasingly being recognized in a wide variety of terrestrial and marine environments, including groundwater, lakes, estuaries, sediments, hydrothermal vents, weathering rocks, and the rhizosphere. This is due in part to novel culture techniques, which have resulted in new enrichments and isolates, and also due to new molecular approaches, which give us insight into uncultured Fe-oxidizing bacteria (FeOB). But unlike many other metabolisms, we have yet to systematically analyze the enzymatic mechanisms of Fe oxidation, its taxonomic breadth, and the evolutionary relationships.

Recent work has begun to reveal a set of key genes involved in Fe oxidation, notably *cyc2*, which encodes the outer membrane cytochrome [1-3]. Originally biochemically characterized as an Fe oxidase in the acidophilic FeOB *Acidithiobacillus ferrooxidans* (e.g. [4]), we have found over 800 homologs in isolate genomes and metagenome-assembled genomes. Homologs of *cyc2* are found in chemolithotrophic (both acidophilic and neutrophilic), and phototrophic FeOB, as well as many organisms not known to oxidize Fe. In addition to mining existing genomic data, we have been analyzing the genomes of new chemolithotrophic FeOB isolates, as well as metagenomes and metatranscriptomes of Zetaproteobacteria-dominated Fe microbial mats from deep sea hydrothermal vents (e.g. Loihi seamount, Marianas Arc). I will discuss our efforts to piece together the electron transport systems of FeOB, to understand the commonalities and diversity, as well as our work to demonstrate Cyc2 function in neutrophilic chemolithotrophs. Ultimately, we aim to give a window into evolutionary relationships of FeOB, in the context of the existing microfossil record and the history of Fe and O₂ on Earth.

References:

[1] Barco *et al.* (2015) *AEM* 81:5927; [2] Kato *et al.* (2015) *Frontiers Microbiol.* 6:1265; [3] Chiu *et al.*, in review; [4] Castelle *et al.* (2008) *J. Biol. Chem.* 283:25803.