



The microbial sulfur cycle

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Sulfur is one example of an element whose transformation and fate in the environment are critically dependent upon microbial activities. Sulfur is the 10th most abundant element in the universe and the sixth most abundant element in microbial biomass. By virtue of its chemical properties, particularly the wide range of stable redox states, sulfur plays important roles in central biochemistry as a structural element, redox center, and carbon carrier. In addition, redox reactions involving reduced and oxidized inorganic sulfur compounds can be utilized by microbes for the generation and conservation of biochemical energy. Microbial transformation of both inorganic and organic sulfur compounds has had a profound effect on the properties of the biosphere and continues to affect geochemistry today.

While sulfur microbiology has a rich history, the last decade has changed our views on many aspects of microbially driven biogeochemical cycles, including the global sulfur cycle, in that tremendous advances in methods, techniques, and approaches have enabled the discovery of novel processes and characterization of the organisms and molecular mechanisms that facilitate them. This progress is documented in a collection of 20 articles at the leading edge of sulfur microbiology, focusing on microbes, reactions, and compounds of geochemical significance. Whether students or peer researchers in the field, it is the intent of this Research Topic issue to reach a wide audience whose interests and expertise spans from the molecular biochemistry of single enzymes and their reactions through pure culture physiology and genetic analysis to community level metagenomics and metatranscriptomics. This collection is especially timely given the recent publication describing one of the oldest microfossils to date that likely lived a sulfur-dependent chemolithoautotrophic lifestyle (Wacey et al., 2011). Microbial sulfur cycling may have had a hand in starting it all.

This collection of papers can be viewed as falling roughly into four clusters that deal with enzymes/activities, organisms/pathways/comparative approaches, symbiosis, and environments:

- At the level of enzymes and activities, new data are reported on a variety of systems. Structural analyses are reported for a disproportionating sulfur oxygenase/reductase and a dissimilatory sulfite reductase. Two independent papers focus on tetrathionate hydrolase, one of bacterial and one of archeal origin. Electron flow for the Sor pathway of thiosulfate oxidation has been further defined in *Sinorhizobium meliloti*. Finally, another article provides the first functional evidence in a phototrophic bacterium for the function of a quinone-interacting membrane-bound oxidoreductase that participates in the oxidation of sulfite.
- At the level of pathways and organisms, detailed reviews have been produced. For the sulfate reducing bacteria, the foci are metabolic flexibility, energy metabolism, and electron

flow. In the phototrophic bacteria, putative sulfur oxidation pathways in sequenced *Chlorobi* are examined. Finally, the latest developments in microbial pathways for the degradation of DMSP, an extremely important component of the marine sulfur cycle are summarized. Three research articles focus on the regulation of sulfur oxidation genes in the purple sulfur bacterium *Allochromatium vinosum*, growth on tetrathionate vs. S(0) in *Acidithiobacillus caldus* and new *Mycobacteria* isolates from sandstone monuments that appear to grow as sulfur oxidizers.

- Multi-organism interactions and symbiosis encompass the third category. Papers on exclusively prokaryotic symbioses and those that cross domain boundaries involving microbial eukaryotes and the symbionts of marine fauna provide a broad perspective in this arena grounded in the application of traditional (label tracing experiments to examine substrate exchange) and cutting edge (transcriptomic analysis of uncultured microbial symbionts) techniques.
- Finally, this issue presents three papers on sulfur cycling at the level of ecosystems and communities. Two extreme environments are examined. Sorokin et al. (2011) summarize their long track record of work in soda lakes that combine high salinity with high pH. Both the reductive and oxidative arms of the sulfur cycle are discussed, and new insights into sulfidogenesis are presented for these fascinating systems. Yang et al. (2011) compare microbial communities and chemolithoautotrophic activity in relatively understudied freshwater hydrothermal vents in Yellowstone Lake. Finally, Luther et al. (2011) present a detailed analysis of the chemical parameters that influence abiotic oxidation of sulfide in natural environments. Sulfide oxidizing microbes must compete with this abiotic process and this report analyzes both literature and fresh experimental data to show that biotic sulfide oxidation will almost always occur at significantly faster rates due to kinetic restrictions on abiotic oxidation. Biology rules after all, as should be evident not just from this paper, but from the entire collection presented here.

Together, these papers represent the forefront of research of this field. We hope you enjoy them as much as we enjoyed working with this talented group of researchers to put this volume together.

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