

Meta-'omics and the geobiology of giant sulfur bacteria

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Sulfur-oxidizing bacteria of the family *Beggiatoaceae* are lithotrophs that generally live at redox interfaces between hydrogen sulfide and oxygen or nitrate. In sulfidic sediments such as those found at methane seeps and oxygen minimum zones, sulfur bacteria are thought to be important for the geochemical cycling of carbon, sulfur, nitrogen, and phosphorus. Bacteria of the genus *Thiomargarita* are the largest of these sulfur bacteria with individual cells attaining millimetric diameters. *Thiomargarita*-like bacteria remain uncultivated and their metabolisms and physiologies are incompletely understood. Despite the current inability to maintain growth of *Thiomargarita* in the lab, culture independent approaches have the potential to provide new insights into the physiologies and ecologies of these enigmatic organisms and shed new light on their geobiological roles in diverse ecosystems.

For example, the hydrolysis of polyphosphate by *Thiomargarita* and the resulting release of orthophosphate into pore waters, has been linked to the formation of phosphorites [1]. Metagenomic investigations of *Thiomargarita nelsonii* show the presence of genes involved in polyphosphate metabolism in the *Thiomargarita* genome, as well as genes involved in coupling sulfur oxidation to both denitrification and nitrate-reducing ammonification. Interestingly, in a separate metatranscriptomic analysis of *Thiomargarita*-like bacteria (*Ca.* *Thiopilula*) from Barbados seep sediment incubations shows gene expression related to sulfide oxidation linked to nitrate reduction [2], but no polyphosphate-related transcripts from *Ca.* *Thiopilula* were recovered [3]. Phosphate was released in the incubation, potentially from polyphosphate-metabolizing bacteria outside of the family *Beggiatoaceae*. These results illustrate the metabolic complexities of natural environments and some of the challenges inherent in linking genomes to geobiological processes.

[1] Schulz, H.N., Schulz, H.D., (2005), *Science* **307**, 416-418.

[2] Jones, D.S. et al., (In press) *Applied and Environmental Microbiology* [3] Jones, D.S. et al., (In review), *ISME Journal*.