

Unveiling Microbial Responses to Coupled S-Fe Cycles in Yellowstone's Hydrothermal Features: Insights from Metagenomics and Geochemical Analysis for Astrobiology

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Understanding the interplay between biological and non-biological processes in elemental cycles is crucial for elucidating habitable environments both on Earth and beyond. In this study, we investigate the sulfur-iron (S-Fe) metabolizing organisms within Yellowstone National Park's hydrothermal features, leveraging metagenomics and geochemical analyses to unveil their interaction and shed light on astrobiological implications.

Yellowstone's unique geothermal features offer a natural laboratory to study biogeochemical processes relevant to early Earth and primitive planetary bodies. Despite previous predictions suggesting limited metabolic energy yield from S-Fe metabolisms[1], our preliminary results reveal the presence of sulfate reducers across diverse habitats within Yellowstone, as evidenced by the detection of *dsr* genes. Notably, key genes associated with sulfate reduction (*dsr*, *apr*, and *sat*) have been identified in previous studies[2], indicating the feasibility of sulfate reduction in various environments.

Metagenomic sequencing has provided a foundational dataset, which we plan to integrate with geochemical analyses. Our focus includes annotating genes related to sulfate reduction (*dsrA*) and iron cycling (*MtrCAB*, *OmcA*) to identify key functional genes associated with these processes. Additionally, we aim to explore a diverse range of metabolic pathways, such as sulfate reduction, methanogenesis, carbon fixation, iron cycling, hydrogen metabolism, and sulfur oxidation, to elucidate microbial roles comprehensively.

Future analyses will involve network analysis to uncover potential syntrophic relationships and metabolic pathway reconstruction to infer microbial functions. Integration with geochemical data will facilitate exploring correlations between functional genes, microbial taxa, and environmental conditions, enhancing our understanding of the ecological significance of the S-Fe cycle.

Sulfate reduction, an ancient metabolic pathway central to Earth's sulfur biogeochemical cycles, holds implications for astrobiology. Enzymes like dissimilatory sulfite reductase are pivotal in this process, suggesting the possibility of sulfate reduction in environments with hydrothermal activity, such as Europa's icy ocean worlds.

Finally, we aim to analyze enzymes as potential biomarkers of sulfate-reducing organisms on other planets, exploring astrobiological implications by juxtaposing our findings with data from planetary analogues and investigating gene markers as potential biosignatures.