DIVERSITY AND ACTIVITY OF SULFUR-CYCLING CHEMOAUTOTROPHIC MICROBIAL MATS OF THE PALOS VERDES HYDROTHERMAL VENT FIELD, CA. P. Miranda[1], M. Thao[2], C. Martinez[2], R. Hatzenpichler[3], V. Orphan[3], L. Stevens[1] and J. Dillon[2], [1]Dept. of Geological Sciences, California State University – Long Beach, 1250 Bellflower Blvd. Long Beach, CA 90840, pjmiranda09@gmail.com, [2]Dept. of Biological Sciences, California State University – Long Beach, 1250 Bellflower Blvd. Long Beach, CA 90840, jesse.dillon@csulb.edu, [3]Div. of Geological and Planetary Sciences, California Institute of Technology, 1200 E. California Blvd. Pasadena, CA 91106.

Abstract: Hydrothermal vents are biogeochemical hotspots at rock-water interfaces where magmatic processes expel geothermally-heated subsurface fluids into cold seawater. These hydrothermal systems exhibit substantial geochemical variability, operating over a range of spatial scales, from meters to millimeters, leading to the formation of gradients and creating microniche landscapes. These extreme ecosystems support flourishing chemosynthetically-driven populations [1] where H_2, Fe^{2+} or HS^- are oxidized. This complex hydrothermal trophic structure is maintained by a variety of metabolic groups including iron-oxidizers, methanogens, hydrogen-oxidizers and/or sulfide-oxidizers, etc. that often form microbial mats or biofilms [2]. Microbial mats are consortial biofilm communities that support complex microscale ecosystems and depend on redox reactions for metabolism and growth. Although, these chemosynthetic microbial mat communities are often found in extreme environments on the modern Earth, they were much more widespread in the marine realm for the first 1-2 billion years of life on Earth [3] where, their metabolic activities altered ocean-atmospheric composition and planetary chemistry [4]. These hydrothermal microbial mat ecosystems were likely key architects of Earth's early biogeochemical cycles [5]. Thus, chemosynthetic microbial communities, especially sulfur-cyclers, have been major drivers of ecosystem dynamics and environmental processes on a planetary-scale for over 3.5 billion years. Additionally, the impact of these metabolic relationships and biogeochemical pathways can be leveraged for astrobiological applications. In particular to studies of the "Red Planet," since conditions on Mars and on the early Earth are considered to be similar. Furthermore, if it were discovered that Mars hosted life, it would likely manifest in microbial form. As such, modern sulfur-cycling microbial mats are excellent model systems for studying the biogeochemical processes that have driven the evolution of life and the habitability of Earth. Which, in turn would provide insight into astrobiological studies, from planetary geochemical evolution to the existence of life on Mars.

Although these communities have long been studied in deep-sea hydrothermal settings, the remote nature of these vents makes investigations difficult, infrequent and expensive. The White Point (WP) shallow-sea hydrothermal vent field along the southern California coast is an excellent near-shore system in which to study biogeochemical processes and to explore abiotic (geological/ecological) influences on these hydrothermal microbial ecosystems. This study focuses on the chemolithoautotrophic sulfur-cycling microbial mats that inhabit WP. We studied the diversity, micron-scale spatial associations and metabolic activity of these mat communities via PCR-amplification of 16S rRNA and *aprA* genes, Fluorescent *in situ* Hybridization (FISH) microscopy and sulfate-reduction rate measurements. Sequencing analysis revealed a diverse group of sulfur-cycling bacteria, including relatives of known sulfur-oxidizing lineages (e.g. *Marithrix, Sulfurovum*) as well as sulfate-/sulfur-reducing lineages, especially *Desulfuromusa*. FISH microscopy revealed close physical associations between sulfur-oxidizing and sulfate-/sulfur-reducing bacteria, while activity studies showed high rates of biological sulfate reduction. Comparisons of the WP microbial mat sequences with molecular data from other hydrothermal vent microbial communities indicate that they are very similar. This suggests that the WP hydrothermal sulfur-vent microbial mat environment is a suitable model system for studying the fluid-rock dynamics of "thiobiotic" communities and sulfur biogeochemistry of hydrothermal vent systems. Furthermore, hydrothermal environments are important astrobiological targets because, they are the most likely location for life to be identified on Mars and they may provide valuable information into biogeochemical processes that may have influenced the potential habitability of the Martian landscape.

References:

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