Using marine Fe mat meta-omics to gain insights into Zetaproteobacteria functional diversity, ecological interactions, and biogeochemical roles

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The Fe-oxidizing Zetaproteobacteria are chemolithoautotrophs that underpin Fe-rich hydrothermal vent mat ecosystems. This knowledge is primarily based on culture and 16S rRNA gene-based studies, so we lack a deeper understanding of the microbial ecology and functional diversity of Zetaproteobacteria and flanking communities. Zetaproteobacteria are a diverse class, with 47 OTUs found in Fe mats, and 53 OTUs in all environments, based on 97% similarity of full-length 16S rRNA gene sequences in NCBI. However, isolates only represent 8 OTUs, clustered into 3 phylotypes, so their genomes offer a limited view, and the single amplified genomes are fairly incomplete. To get a fuller view of how vent Fe mat ecosystems work, we analyzed metagenomes and metatranscriptomes of Fe mats from the Loihi Seamount and Mariana Arc, including shipboard Fe oxidation microcosm experiments. We focused on samples with a range of Zetaproteobacteria OTUs and other taxa of note. Along with many bins identified as Zetaproteobacteria, there are also novel Deltaproteobacteria, candidate Archaeal division DUSEL4, Caldithrix, Parcubacteria, Marinimicrobia, Methylococcales, Methanosarcinales (in decreasing abundance). The metagenomes contain frequent hits to the putative Fe oxidase gene, cyc2, which is one of the most highly expressed genes in the metatranscriptomes, and to RuBisCO, linking Fe oxidation and C fixation in these mats. Also present and expressed are genes for heterotrophy, fermentation, methane cycling, and denitrification. We will discuss the electron transport systems of Zetaproteobacteria, including commonalities and diversity, as well as results that show how the various Zetaproteobacteria and other microbes work together to cycle Fe, C, N, S, and P.