How do microbes make minerals in the environment? Tracking iron and sulfur biomineralization using meta-omics and microscopy

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Much of our knowledge on microbial mineralization comes from observations of biomineralization in the laboratory. If our model organisms are representative, these lab-based approaches can give great insight into microbial roles in natural systems. However, the picture can be more complex, with diverse, uncultured consortia working together within biomineralizing environments. To link our isolate-based work to in situ processes, we have been studying Fe oxyhydroxide and S(0) biomineralization in Fe-rich deep sea hydrothermal vents and sulfidic caves. We have coupled field experiments with culturing, imaging, metagenomics, and metatranscriptomics. We will present colonization experiments conducted at the Frassasi Cave system, in which we studied S(0)-forming bacteria by microscopy, genome-resolved metagenomics, and metatranscriptomics. This allowed us to follow biomineralization by uncultured organisms, and connect community ecology, gene expression, and biogeochemical functions as biofilms matured. We will also discuss work on Fe-mineralizing mats at Loihi Seamount, Mid-Atlantic Ridge, and Marianas. These mats are built by different Zetaproteobacteria, distinct from isolated species, and more diverse. We have used meta-omics of *in situ* samples and shipboard Fe-amended incubations to demonstrate that the *cyc2* gene is a marker of Fe oxidation, and therefore Fe biomineralization. Using this gene, we were able to identify other possible Fe-oxidizing taxa within the mats, not previously known as FeOB. In all, this work has allowed us to better understand ecology of biomineralization in model environmental systems, and develop genetic markers of biomineralization. This knowledge can be used in more complex systems to evaluate the roles of biomineralizing organisms in key biogeochemical processes.