

Iron microbial mat morphological and genetic signatures: clues to the ecology and mechanisms of chemolithotrophic iron-oxidizers in freshwater and marine environments

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Microbial mats are formed by microorganisms working in coordinated symbiosis, often benefitting the community by controlling the local geochemical or physical environment. Thus, the ecology of the mat depends on the individual roles of microbes organized into niches within a larger architecture. Chemolithotrophic Fe-oxidizing bacteria (FeOB) form distinctive Fe oxyhydroxide biominerals which constitute the building blocks of the mat. In recent years, we have made progress in determining the overall mat community composition and the metabolism of Fe-oxidizing isolates. However, we know very little about the structural arrangement of the community within the mat or the genetic mechanisms responsible for biomineral and therefore mat formation. Understanding both physical mat structure and formation mechanisms is important to unravelling FeOB evolution, the biogeochemistry and ecology of Fe-rich habitats, and ultimately interpreting FeOB biosignatures in the rock record.

Mats in freshwater and marine environments contain strikingly similar biomineral morphologies, yet they are formed by phylogenetically distinct microorganisms. This suggests that the overall architecture and underlying genetics of freshwater and marine mats has evolved to serve particular roles specific to Fe oxidation. Thus, we conducted a comparative study of freshwater mats from Spruce Point, Maine, and marine mats from hydrothermal vents at Loihi Seamount, Hawaii. We have developed a new approach to sampling Fe mats in order to preserve the delicate structure for analysis by confocal and scanning electron microscopy.

Our analyses of these intact mats show that freshwater and marine mats are similarly initiated by a single type of structure-former. These ecosystem engineers form either a hollow sheath or a twisted stalk biomineral during mat formation, with a highly directional structure. These microbes appear to be the vanguard organisms that anchor the community within oxygen/Fe(II) gradients, further allowing for community succession in the mat interior as evidenced by other mineralized morphologies. Patterns in biomineral thickness and directionality were indicative of redox gradients and temporal changes in the geochemical environment. These observations show that the FeOB create the structure of the environment for the entire microbial community, acting as environmental engineers. Furthermore, they leave behind distinctive signatures of environmental conditions (e.g. presence of oxygen, hydrothermal pulsing), which can be recorded in the rock record.

The structural similarity between mat habitats is also supported by the analysis of FeOB genetics. Between freshwater and marine FeOB isolates, we have identified several gene targets involved in electron transport and Fe oxide structure formation. SSU ribosomal RNA molecular marker analyses of discrete mat samples (also analyzed for structure) suggest that the most active Fe oxidizers are relatively low abundance keystone species. Therefore, we conducted experiments to stimulate mat structure formation and study mRNA expression patterns in order to test which genes are involved. By combining our knowledge of the structural architecture with the genetics of Fe mat formation, we have been able to provide a more comprehensive picture of mat development, from the mechanism of formation to the production of easily recognizable biosignatures.