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## Revisiting biogenic iron sulfide minerals

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Throughout Earth's history, the burial of iron sulfide minerals and organic carbon has governed the oxygen concentrations in the Earth's atmosphere. On modern Earth, sulfate-reducing microorganisms (SRM) are the major source of dissolved sulfide in low-temperature sedimentary environments, though their role in iron sulfide mineral formation is assumed to be limited to providing dissolved sulfide to the Fe-S system. Here we present data that challenge that assumption, and posit that SRM also play a role in the nucleation and growth of iron sulfide minerals by providing both organic templates for nucleation and organic material which informs mineralization [1].

Using the deep-sea sulfate-reducing bacterium *Desulfovibrio hydrothermalis* AM13 [2], and a combination of microscopy and spectroscopy, we demonstrate that iron sulfide minerals precipitated in the presence of SRM bear unexpected physical characteristics that will potentially affect their reactivity and transformation. "Biogenic" iron sulfide minerals have larger crystal sizes and aggregate much more than abiotic minerals formed in similar conditions without the presence of microbial cells. Moreover, upon forming in the presence of SRM, iron sulfide minerals become associated with organic carbon, potentially preserving labile organic material from degradation.

We propose that the physical and chemical characteristics conferred to iron sulfide minerals by SRM not only play a role in preserving organic carbon in sedimentary environments, but also could serve as biosignatures for microbial life in anoxic environments.

[1] A. Picard, A. Gartman, P.R. Girguis. What do we really know about the role of microorganisms in iron sulfide mineral formation? *Frontiers in Earth Science* (2016), 4:68.

[2] D. Alazard, S. Dukan, A. Urios, F. Verhe, N. Bouabida, F. Morel, P. Thomas, J.L. Garcia and B. Ollivier, *Desulfovibrio hydrothermalis* sp. nov., a novel sulfate-reducing bacterium isolated from hydrothermal vents, *Int. J. Syst. Evol. Microbiol.*, 53 (2003) 173-178.