

Genomic Diversity and Ancient Origin of Magnetotactic Bacteria

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Magnetotactic bacteria (MTB) biominerlize intracellular, membrane-bounded, nano-sized magnetic mineral crystals of magnetite (Fe_3O_4) and/or greigite (Fe_3S_4) called magnetosomes and are characterized by their ability to sense and swim along geomagnetic field lines. MTB play important roles in the geochemical cycling of iron, sulfur, nitrogen and carbon. They also represent an intriguing model system for the study of microbial biominerlization and magnetoreception. Moreover, the magnetosomes can be preserved in sediment as fossil magnetosomes (or magnetofossils). Magnetofossils have been found in lacustrine and deep-sea sediments, which are stable carriers of natural remanence and may play substantial contributions to the bulk magnetization of sediments. Current phylogenetic information on MTB is based primarily on 16S rRNA gene sequences, only a small fraction of which are represented by axenic cultures. We have reconstructed draft genomes from environmental uncultivated MTB through metagenomics from both northern and southern hemispheres. These novel genomes expand greatly the coverage of MTB in the Bacteria domain, indicating that the diversity of MTB is much greater than is generally appreciated. Phylogenetic and comparative genomic analyses of all available MTB genomes have suggested a common ancient origin of iron-based magnetotaxis in the domain Bacteria that underwent lineage-specific evolution, shedding new light on the origin and evolution of magnetotactic bacteria as well as the environment of early Earth.