Genomic and magnetosome features of magnetotactic bacteria in a deep-sea hydrothermal vent chimney

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Biogenic magnetic particles are ubiquitous in the deep-sea environment. However, microorganisms responsible for the deep-sea magnet formation are largely unknown. In this study, magnetotactic bacteria were investigated mainly for a deep-sea metal sulfide chimney from South Mariana Trough. Microbial cells with teardrop-shaped magnetic particles were observed from magnetically separated chimney sample. Metagenomic analysis of microbial populations in the chimney sample revealed that most of contig sequences putatively encoding genes involved in the production of membrane-bound magnetic particles (magnetosome) were phylogenomically affiliated within Nitrospirae. A near-complete Nitrospirae genome from the chimney sample revealed the equipment of putative magnetosome genes functioning membrane invagination, protein sorting, iron transport and biomineralization. The lack of genes involved in chain alignment of magnetosomes might be consistent with poorly aligned teardrop-shaped magnetosomes observed by electron microscopy. Metabolic gene analysis showed the chemoautotrophy based H₂ as an energy source, which could be derived from hydrolysis of H₂O with Fe(II) in the metal sulfide chimney. Given the occurrence of Nitrospirae bacteria and teardrop-shaped magnetic particles in deep-sea sediments, it is suggested that Nitrospirae bacteria are important for the deep-sea magnet formation.

Keywords: deep-sea hydrothermal vent, marine sediments, magnetotactic bacteria, metal sulfide chimney, iron biogeochemistry