

Correlations of magnetosome-related genes in Nitrospirae genomes to magnetosome geometry and redox stratification in deep-sea environments

*Shinsaku Nakano¹, Shingo Kato², Mariko Kouduka¹, Toshitsugu Yamazaki³, Yohey Suzuki¹

1. Graduate School of Science, The University of Tokyo, 2. RIKEN, 3. Atmosphere and Ocean Research Institute, The University of Tokyo

Biogenic magnetic particles are ubiquitously found in deep-sea sediments and important carriers of rock magnetism for reconstructing the Earth's past regarding sediment age and geomagnetic field. However, microorganisms responsible for the formation of magnetic particles are largely unknown in the deep-sea environment, because of the difficulty in sampling, cultivation, and magnetic separation of magnetotactic cells for single-cell genomics. In this study, deep-sea sediments from Japan Sea and a metal sulfide chimney from South Mariana Trough were subjected to magnetic separation and subsequent electron microscopic observations. Although teardrop-shaped magnetite (Fe₃O₄) particles without microbial cells and 16S rRNA gene sequences related to magnetotactic Nitrospirae species were previously obtained from Japan Sea sediments with a redox zonation enriched with dissolved Fe(II) (the iron boundary), no magnetotactic cells were observed after the magnetic separation. From the metal sulfide chimney, magnetotactic cells were observed with teardrop-shaped magnetite particles. Metagenomic analysis of the chimney sample revealed that contig sequences encoding genes involved in the formation of magnetosome, membrane-bound magnetic particles, were mostly affiliated within Nitrospirae based on sequence similarity. Previous studies have reported that magnetosome-related genes are clustered together as the magnetosome island (MAI) in known magnetotactic bacteria. However, those genes were scattered in a near-complete Nitrospirae genome reconstructed from the chimney sample. Although magnetotactic bacteria are generally considered to align magnetic particles into a chain for efficiently moving in a vertical redox zonation by orienting the cell along the geomagnetic field, Nitrospirae-affiliated genes involved in chain formation were not found in the near-complete Nitrospirae genome from the chimney with a horizontal redox zonation. Comparative analysis of near-complete Nitrospirae genomes available from public databases revealed that the chain-related genes were found in the genomes from terrestrial deep aquifers and deep-sea sediments with a vertical redox zonation. As the Nitrospirae species associated with teardrop magnetite and the iron boundary in Japan Sea was closely related to Nitrospirae species with the chain-related genes, the presence of the chain-related genes appears to be correlated with a vertical redox zonation. In addition, our results suggest that the Nitrospirae species without MAI are responsible for the production of teardrop magnetite in deep-sea environment, and that teardrop magnetite is a paleoredox indicator especially for the iron boundary.

Keywords: magnetotactic bacteria, metal sulfide chimney, magnetofossil, remnant magnetization