EGU26-8883, updated on 10 Nov 2026
https://doi.org/10.5194/egusphere-egu26-8883
EGU General Assembly 2026
© Author(s) 2026. This work is distributed under
the Creative Commons Attribution 4.0 License.

# Stratified niche partitioning of magnetotactic bacteria near a simulated oxic–anoxic transition zone

**Juan Wan**[1,2], Jiaqi Zheng[1,2], Runjia Ji[1], Sheng Yu[2], Rixiang Zhu[1], and Wei Lin[1,2]
[1]Key Laboratory of Planetary Science and Frontier Technology, Institute of Geology and Geophysics, Chinese Academy of Sciences, Beijing 100029, China
[2]College of Earth and Planetary Sciences, University of Chinese Academy of Sciences, Beijing 100049, China

Magnetotactic bacteria (MTB) are a unique group of microorganisms that biomineralize membrane-bound magnetic nanoparticles, termed magnetosomes. These magnetosomes are generally arranged into chains, enabling MTB to sense and navigate along the geomagnetic field lines and efficiently locate their preferred living zone, most commonly the oxic–anoxic transition zone (OATZ). MTB show remarkable morphological and taxonomic diversity and are widely distributed in freshwater, marine, and extreme environments, where they play important roles in the cycling of Fe, C, P, S. However, the *in situ* niches and spatiotemporal distribution patterns of different MTB lineages remain poorly understood. In this study, MTB cells were first isolated and enriched from a freshwater lake in Beijing, China, and then cultivated under simulated OATZ conditions in glass tubes. Transmission electron microscopy (TEM) observations revealed three representative MTB lineages: magnetotactic cocci (belonging to the class *Magnetococcia*) producing prismatic-shaped magnetite, magnetotactic spirilla (*Alphaproteobacteria*) forming cuboctahedral-shaped magnetite, and magnetotactic curved-rods (*Desulfovibrionia*) producing bullet-shaped crystals. During incubation, the initially formed microbial band in the OATZ developed a clear vertical stratification, with microaerobic conditions in the upper and middle layers and anaerobic conditions in the lower layer. TEM observations and metagenomic quantification demonstrated that magnetotactic cocci dominated the upper layer, magnetotactic spirilla were most abundant in the middle layer, and magnetotactic curved-rods were largely confined to the lower layer. Finally, metabolic reconstruction based on genomic data indicates that differences in oxygen-related metabolic pathways may be responsible for this vertical segregation. Collectively, our results demonstrate oxygen-driven niche partitioning among MTB lineages within the OATZ, highlighting their distinct metabolic adaptations and ecological roles.