

# Unlocking Gene Networks Behind Magnetosome Formation in Magnetotactic Bacteria

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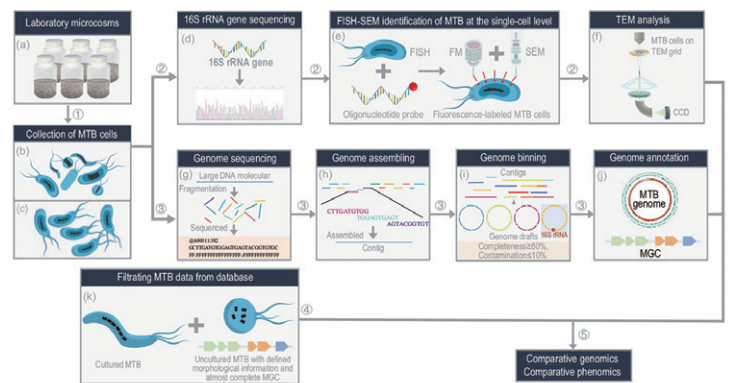
In a study, published online in *National Science Review* on October 28, researchers led by Dr. LI Jinhua at the Institute of Geology and Geophysics (IGG) of the Chinese Academy of Sciences have used an integrative genomic and phenomic analysis to explore the genetic basis of magnetosome biomineralization in magnetotactic bacteria (MTB).

Magnetotactic bacteria (MTB) are abundant, mobile, and varied single-celled organisms capable of creating a distinctive organelle known as the magnetosome. Comprised of a nanoscale magnetic iron mineral crystal enveloped by a lipid bilayer membrane, magnetosomes are typically arranged in a highly ordered chain within the cell. The chain of magnetosomes enables the cell to act like a mobile, tiny compass needle, allowing it to align and move in accordance with magnetic field lines.

Understanding the biogenesis and assembly of magnetosomes in MTB is crucial for deciphering the mechanisms behind biologically controlled mineralization of magnetic iron minerals and the evolution of magnetoreception in organisms.

The researchers devised a five-step process to study uncultured MTB, which involved collecting living MTB cells, characterizing them using gene sequencing and microscopy techniques, analyzing their genomes, and integrating the findings to gain insights into magnetic particle biogenesis and chain organization in various MTB species.

By combining 15 data sets of uncultured MTB strains with 32 other data sets of previously reported

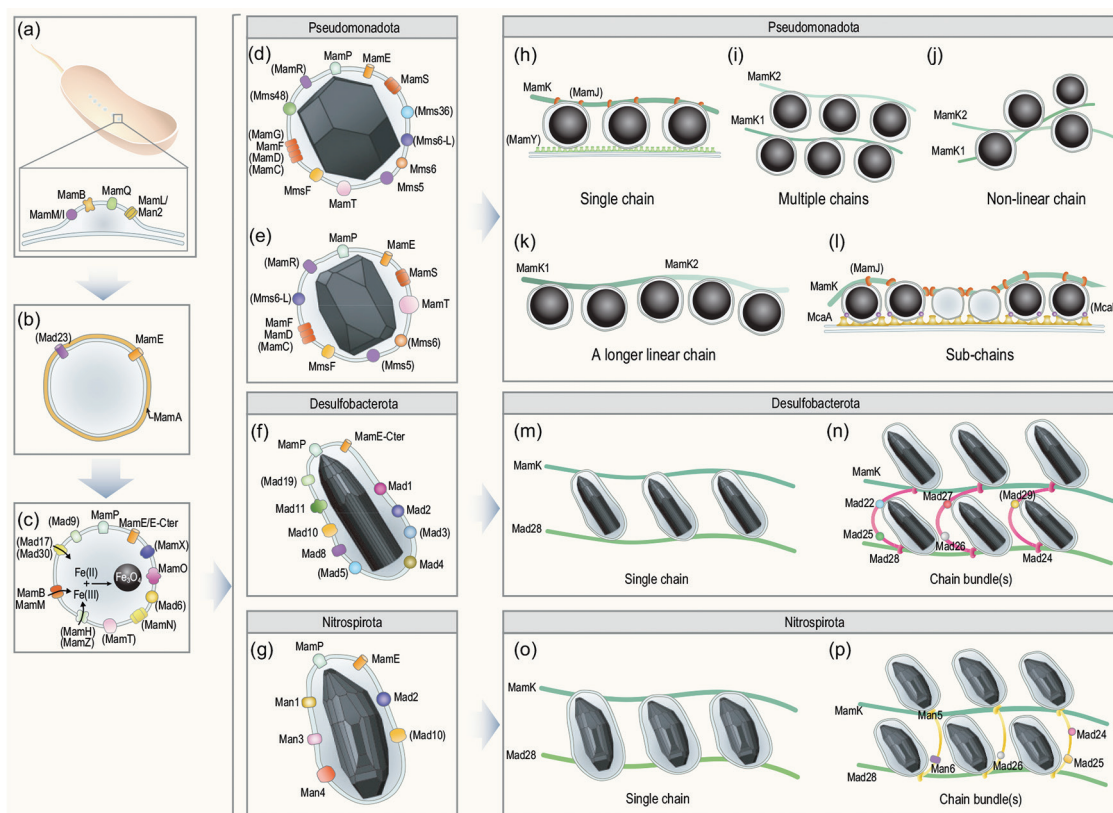


Five-step workflow for genomic and phenomic study of uncultured MTB. (Image by Dr. LI Jinhua's Group)

cultured and uncultured MTB strains, the researchers were able to identify genes controlling magnetosome crystal morphology in the *Pseudomonadota*, *Desulfobacterota*, and *Nitrospirota* phyla. They also found genetic evidence supporting phylum-specific morphology of magnetosome magnetite, which could be useful for understanding the taxonomic lineage and paleoecology of ancient MTB.

They also introduced a workflow for comparative analysis of cultured and uncultured MTB and a tentative general model for the gene networks controlling magnetosome biogenesis and chain assembly. While the model is still incomplete, it offers new insights into magnetosome gene function and chain assembly, especially for MTB species.

The researchers also presented a conceptual model for the gene network involved in magnetosome



Conceptual model for the gene network responsible for magnetosome biomineralization. (Image by Dr. Li Jinhua's group)

biomineralization. The model outlines five steps, including magnetosome membrane formation, protein recruitment, iron transportation and magnetite nucleation, magnetite growth in various shapes, and chain assembly of magnetite in different MTB phyla.

In conclusion, the study revealed the presence of core magnetosome genes and phylum-specific magnetosome genes, providing genetic evidence for the phylum-specific morphology of magnetosome magnetite. The researchers suggest that this gene network could

be used for *in vivo* site-directed mutagenesis of cultured strains or heterologous magnetosome gene expression to better understand the molecular mechanisms of biogenesis and chain assembly of magnetite.

Finally, these findings could have practical applications in nanomedicine and nanotechnology. Certain proteins identified in the study could provide targets for biomimetic synthesis of highly elongated magnetite nanoparticles with higher magnetic coercivity, which could prove valuable in these fields.

## Reference

Liu, P., Zheng, Y., Zhang, R., Bai, J., Zhu, K., Benzerara, K., . . . Li, J. (2023). Key gene networks that control magnetosome biomineralization in magnetotactic bacteria. *National Science Review*, 10(1), nwac238. doi:10.1093/nsr/nwac238