



Complete Genome Sequence of *Magnetospirillum* sp. ME-1, a Novel Magnetotactic Bacterium Isolated from East Lake, Wuhan, China

Linfeng Ke,^{a,b} Pengming Liu,^a Shan Liu,^{a,b} Meiying Gao^a

Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, People's Republic of China^a; University of Chinese Academy of Sciences, Beijing, People's Republic of China^b

ABSTRACT A novel spiral magnetotactic bacterium, *Magnetospirillum* sp. ME-1, was isolated from East Lake in China. Here we report the complete genome of ME-1, which contains a 4,551,873-bp circular chromosome and a 5,222-bp circular plasmid. The magnetosome biogenesis-specific genes are located in a 97,664-bp magnetosome genomic island.

Magnetotactic bacteria (MTB) are a group of widely distributed motile prokaryotes that produce magnetosomes, which consist of magnetic nanoparticles (1). Magnetosomes are attractive materials for applications in nanotechnology, biomedicine, and other fields (2). The formation of magnetosomes is strictly controlled by the magnetosome island (MAI) (3). To date, complete MTB genome sequences have been reported for just seven strains: *Magnetospirillum magneticum* AMB-1, *Magnetospirillum gryphiswaldense* MSR-1, *Magnetospira* sp. QH-2, *Magnetospirillum* sp. XM-1, *Magneto-coccus marinus* MC-1, "*Candidatus Magnetococcus massalia*" MO-1, and *Desulfovibrio magneticus* RS-1 (4–10). Furthermore, the molecular mechanisms of magnetosome formation are far from fully understood. To further understand and advance the application of MTB, we present here the complete genome sequence of *Magnetospirillum* sp. ME-1.

Strain ME-1, a novel spiral MTB strain, was isolated from East Lake in Wuhan, People's Republic of China. The genome of ME-1 was sequenced using the Illumina HiSeq 2500 platform by the paired-end method (2 × 150 bp) with a coverage of 400×. A complete genome was obtained by *de novo* assembly (11) combined with genome walking with a total length of 4,551,873 bp and a G+C content of 65.63%. In addition, a 5,222-bp circular plasmid with a 60.67% G+C content was found.

Phylogenetic 16S rRNA analysis revealed that ME-1 is closely related to *M. magneticum* AMB-1. Furthermore, genome annotation was performed using the Prokaryotic Genome Automatic Annotation Pipeline (12). The ME-1 genome contains 4,086 protein-coding genes, 36 pseudogenes, 6 rRNAs (5S, 23S, and 16S), 50 aminoacyl-tRNA synthetases, and 4 noncoding RNAs (ncRNAs). Functional classifications of these predicted genes were performed using the Integrated Microbial Genomes system (13).

In particular, the MAI of ME-1 was located at nucleotide (nt) position 422080 to 519743 in the genome. The MAI was 97,664 bp in length with a G+C content of 61.18%, lower than that of the genome. In total, 96 genes were predicted in the MAI region of ME-1 and 37 magnetosome-specific genes were clustered into five operons, including *mamCDFG*, *mms*, *mamAB*, *mamXY*, and an *mamAB*-like operon. The gene sequences of the *mamAB*-like operon (*mamEJOPAQRB*) are highly similar to those in the *mamAB* operon. In addition, an *mamW* and another *mamF* were deviated from these operons.

A cobalt-zinc-cadmium resistance system (*WV31_01800-01815*) and a ferrous iron transport system (*feo*) (*WV31_01745-01750*) were also found in the MAI. Additionally,

Received 18 April 2017 Accepted 28 April 2017 Published 24 August 2017

Citation Ke L, Liu P, Liu S, Gao M. 2017. Complete genome sequence of *Magnetospirillum* sp. ME-1, a novel magnetotactic bacterium isolated from East Lake, Wuhan, China. *Genome Announcements* 5:e00485-17. <https://doi.org/10.1128/genomeA.00485-17>.

Copyright © 2017 Ke et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Meiying Gao, mygao@wh.iov.cn.

another *feo* system and three ferric uptake regulator-like genes were identified in the genome. These genes may play roles in the biomineralization of magnetosomes.

Further investigations into the genome of ME-1 may enhance the understanding of the formation of magnetosomes and facilitate the applications of MTB in a broad range of fields.

Accession number(s). The genome sequence of strain ME-1 has been deposited in NCBI GenBank under the accession number [CP015848](https://doi.org/10.1093/genomeA/00171-14).

ACKNOWLEDGMENTS

This study was supported by the National Natural Science Foundation of China (grant no. 31170123 and 31500155). We declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as potential conflicts of interest.

REFERENCES

- Lefevre CT, Bazylinski DA. 2013. Ecology, diversity, and evolution of magnetotactic bacteria. *Microbiol Mol Biol* 77:497–526. <https://doi.org/10.1128/MMBR.00021-13>.
- Jacob JJ, Suthindhiran K. 2016. Magnetotactic bacteria and magnetosomes—scope and challenges. *Mater Sci Eng C Mater Biol Appl* 68: 919–928. <https://doi.org/10.1016/j.msec.2016.07.049>.
- Komeili A. 2012. Molecular mechanisms of compartmentalization and biomineralization in magnetotactic bacteria. *FEMS Microbiol Rev* 36: 232–255. <https://doi.org/10.1111/j.1574-6976.2011.00315.x>.
- Schübbe S, Williams TJ, Xie G, Kiss HE, Brettin TS, Martinez D, Ross CA, Schüler D, Cox BL, Nealson KH, Bazylinski DA. 2009. Complete genome sequence of the chemolithoautotrophic marine magnetotactic coccus strain MC-1. *Appl Environ Microbiol* 75:4835–4852. <https://doi.org/10.1128/AEM.02874-08>.
- Matsunaga T, Okamura Y, Fukuda Y, Wahyudi AT, Murase Y, Takeyama H. 2005. Complete genome sequence of the facultative anaerobic magnetotactic bacterium *Magnetospirillum* sp. strain AMB-1. *DNA Res* 12: 157–166. <https://doi.org/10.1093/dnares/dsi002>.
- Wang X, Wang Q, Zhang W, Wang Y, Li L, Wen T, Zhang T, Zhang Y, Xu J, Hu J, Li S, Liu L, Liu J, Jiang W, Tian J, Li Y, Schüler D, Wang L, Li J. 2014. Complete genome sequence of *Magnetospirillum gryphiswaldense* MSR-1. *Genome Announc* 2(2):e00171-14. <https://doi.org/10.1128/genomeA.00171-14>.
- Zhu K, Pan H, Li J, Yu-Zhang K, Zhang SD, Zhang WY, Zhou K, Yue H, Pan Y, Xiao T, Wu LF. 2010. Isolation and characterization of a marine magnetotactic spirillum axenic culture QH-2 from an intertidal zone of the China Sea. *Res Microbiol* 161:276–283. <https://doi.org/10.1016/j.resmic.2010.02.003>.
- Wang Y, Lin W, Li J, Zhang T, Li Y, Tian J, Gu L, Heyden YV, Pan Y. 2015. Characterizing and optimizing magnetosome production of *Magnetospirillum* sp. XM-1 isolated from Xi'an-City-Moat, China. *FEMS Microbiol Lett* 362:fnv167. <https://doi.org/10.1093/femsle/fnv167>.
- Nakazawa H, Arakaki A, Narita-Yamada S, Yashiro I, Jinno K, Aoki N, Tsuruyama A, Okamura Y, Tanikawa S, Fujita N, Takeyama H, Matsunaga T. 2009. Whole genome sequence of *Desulfovibrio magneticus* strain RS-1 revealed common gene clusters in magnetotactic bacteria. *Genome Res* 19:1801–1808. <https://doi.org/10.1101/gr.088906.108>.
- Ji B, Zhang SD, Zhang WJ, Rouy Z, Alberto F, Santini CL, Mangenot S, Gagnot S, Philippe N, Pradel N, Zhang L, Tempel S, Li Y, Médigue C, Henrissat B, Coutinho PM, Barbe V, Talla E, Wu LF. 2017. The chimeric nature of the genomes of marine magnetotactic coccoid-ovoid bacteria defines a novel group of *Proteobacteria*. *Environ Microbiol* 19: 1103–1119. <https://doi.org/10.1111/1462-2920.13637>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. *Omics* 12:137–141. <https://doi.org/10.1089/omi.2008.0017>.
- Markowitz VM, Chen IM, Palaniappan K, Chu K, Szeto E, Grechkin Y, Ratner A, Jacob B, Huang J, Williams P, Huntemann M, Anderson I, Mavromatis K, Ivanova NN, Kyrpides NC. 2012. IMG: the integrated microbial genomes database and comparative analysis system. *Nucleic Acids Res* 40:D115–D122. <https://doi.org/10.1093/nar/gkr1044>.