




Two Metagenome-Assembled Genome Sequences of Magnetotactic Bacteria in the Order *Magnetococcales*

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ABSTRACT Magnetotactic bacteria represent a valuable model system for the study of microbial biomineralization and magnetotaxis. Here, we report two metagenome-assembled genome sequences of uncultivated magnetotactic bacteria belonging to the order *Magnetococcales*. These genomes contain nearly complete magnetosome gene clusters responsible for magnetosome biomineralization.

Magnetotactic bacteria (MTB) are a diverse group of microorganisms that swim along the geomagnetic field lines, a behavior known as magnetotaxis or microbial magnetoreception (1). MTB affiliated within the order *Magnetococcales* are often the dominant MTB group in nature (2, 3). This group was previously thought to be an order (4) or a subclass (5) near the base of *Alphaproteobacteria* but was recently reclassified as a novel candidate class (“*Candidatus* Etaproteobacteria” [6, 7] or *Magnetococcia* [8]) within the *Proteobacteria* phylum. Genomes of *Magnetococcales* are required to better understand the phylogenetic position, genomic diversity, and evolutionary history of this MTB lineage.

Here, we report two metagenome-assembled *Magnetococcales* genome sequences isolated from freshwater sediments. Surface sediments were collected from East Lake in Hubei Province, China (30.56°N, 114.41°E). MTB cells were magnetically enriched from 300 ml of sediments using a double-ended open magnetic separation apparatus known as the “MTB trap” (9) through 4 h of collection. DNA was directly amplified from magnetically enriched cells using the Genomiphi V2 DNA amplification kit (GE Healthcare, USA) according to the manufacturer’s protocol and purified with the AxyPrep Mag PCR clean-up kit (Axygen, USA). Libraries were prepared with the Nextera XT DNA library preparation kit (Illumina, USA), following the manufacturer’s instructions. DNA sequencing was performed with an Illumina HiSeq 2500 instrument using the paired-end 125-bp by 125-bp library with a 200-bp insert size (BGI-Wuhan, Wuhan, China). Paired-end reads were filtered and trimmed using SOAPnuke (10) and were assembled using metaSPAdes (11) with the following parameters: --only-assembler -k 31, 41, 51, 61, 71, 81, 91, 101, 111. Assembled scaffolds of $\geq 2,500$ bp were binned separately using MetaBAT v0.26.1 (12) and MyCC (13), and the high-scoring, nonredundant set of bins were dereplicated and selected using DASTool (14). QUAST v4.1 (15) was used to assess the quality of acquired genome sequences, and their completeness and contamination were estimated using CheckM (16) (taxonomy_wf domain *Bacteria*). Coverage information was determined using Bowtie 2 v2.3.4.3 (17) and SAMtools v1.6 (18). Genome sequences were annotated using the Prokaryotic Genome Annotation Pipeline (PGAP) (19). Putative magnetosome genes were checked using NCBI PSI-BLAST (20). Average amino acid identity (AAI) values were calculated using enveomics (21). Unless otherwise specified, default parameters were used for all software.

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TABLE 1 Genome statistics of *Magnetococcales* isolates DH2bin6 and DH2bin20

Name	Genome accession no.	Genome size (bp)	No. of scaffolds	N_{50} (bp)	No. of GC genes	GC content (%)	Completeness (%)	Contamination (%)	No. of mapped reads	Coverage (×)
DH2bin6	JAANAU000000000	3,658,807	80	88,744	3,116	56.76	98.28	0.00	2,522,452	105
DH2bin20	JAANAV000000000	5,014,406	525	14,837	4,487	52.96	93.97	8.93	933,940	31

Two distinct (54% of AAI score) genome sequences, designated DH2bin6 and DH2bin20, have been reconstructed here, both of which contain partial 16S rRNA genes (>900 bp). An analysis of the 16S rRNA gene sequence of DH2bin6 using the online NCBI BLASTn nucleotide collection (nonredundant [nr]/nucleotide) database (<https://blast.ncbi.nlm.nih.gov>) shows the best hit to an uncultured magnetotactic coccus, MDA-1 (GenBank accession number [AB537162](https://doi.org/10.1093/nucleotide/AB537162); 99.89% identity) (22), while DH2bin20 has a 95.84% BLASTn identity to uncultivated *Magnetic coccus* CS92 ([X81182](https://doi.org/10.1093/nucleotide/X81182)) (23). Genomes of DH2bin6 and DH2bin20 consist of 80 and 525 scaffolds with average GC contents of 56.76% and 52.96%, respectively (Table 1). Nearly complete magnetosome gene clusters, a group of genes responsible for magnetosome biogenesis and arrangement, have been identified in both genomes, which contain genes homologous to magnetosome genes of *mamD*, *mamH*, *mamI*, *mamE*, *mamK*, *mamF*, *mamL*, *mamM*, *mamN*, *mamO*, *mamP*, *mamA*, *mamQ*, *mamB*, *mamS*, *mamT* and *mmsF*. These two genomes will provide insights into the genome biology and magnetosome biomineralization of MTB within the order *Magnetococcales*.

Data availability. These two genome sequences have been deposited in GenBank under the accession numbers [JAANAU000000000](https://doi.org/10.1093/genbank/JAANAU000000000) and [JAANAV000000000](https://doi.org/10.1093/genbank/JAANAV000000000) (BioProject number [PRJNA400260](https://doi.org/10.1093/bioinformatics/PRJNA400260)). The raw metagenomic read data have been deposited in the NCBI Sequence Read Archive under the accession number [SRR11267947](https://doi.org/10.1093/bioinformatics/SRR11267947).

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REFERENCES

- Blakemore RJS. 1975. Magnetotactic bacteria. *Science* 190:377–379. <https://doi.org/10.1126/science.170679>.
- Flies CB, Peplies J, Schüller Dirk. 2005. Combined approach for characterization of uncultivated magnetotactic bacteria from various aquatic environments. *Appl Environ Microbiol* 71:2723–2731. <https://doi.org/10.1128/AEM.71.5.2723-2731.2005>.
- Lin W, Wang Y, Gorby Y, Nealson K, Pan Y. 2013. Integrating niche-based process and spatial process in biogeography of magnetotactic bacteria. *Sci Rep* 3:1643. <https://doi.org/10.1038/srep01643>.
- Bazylinski DA, Williams TJ, Lefèvre CT, Berg RJ, Zhang CL, Bowser SS, Dean AJ, Beveridge TJ. 2013. *Magnetococcus marinus* gen. nov., sp. nov., a marine, magnetotactic bacterium that represents a novel lineage (*Magnetococcaceae* fam. nov., *Magnetococcales* ord. nov.) at the base of the *Alphaproteobacteria*. *Int J Syst Evol Microbiol* 63:801–808. <https://doi.org/10.1099/ijs.0.038927-0>.
- Ferla MP, Thrash JC, Giovannoni SJ, Patrick WM. 2013. New rRNA gene-based phylogenies of the *Alphaproteobacteria* provide perspective on major groups, mitochondrial ancestry and phylogenetic instability. *PLoS One* 8:e83383. <https://doi.org/10.1371/journal.pone.0083383>.
- Ji B, Zhang S-D, Zhang W-J, Rouy Z, Alberto F, Santini C-L, Mangelot S, Gagnot S, Philippe N, Pradel N, Zhang L, Tempel S, Li Y, Médigue C, Henrissat B, Coutinho PM, Barbe V, Talla E, Wu L-F. 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>.
- Lin W, Zhang W, Zhao X, Roberts AP, Paterson GA, Bazylinski DA, Pan Y. 2018. Genomic expansion of magnetotactic bacteria reveals an early common origin of magnetotaxis with lineage-specific evolution. *ISME J* 12:1508–1519. <https://doi.org/10.1038/s41396-018-0098-9>.
- Parks DH, Chuvochina M, Waite DW, Rinke C, Skarshewski A, Chaumeil P-A, Hugenholtz P. 2018. A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. *Nat Biotechnol* 36:996–1004. <https://doi.org/10.1038/nbt.4229>.
- Jogler C, Lin W, Meyerdierks A, Kube M, Katzmann E, Flies C, Pan Y, Amann R, Reinhardt R, Schüller D. 2009. Toward cloning of the magnetotactic metagenome: identification of magnetosome island gene clusters in uncultivated magnetotactic bacteria from different aquatic sediments. *Appl Environ Microbiol* 75:3972–3979. <https://doi.org/10.1128/AEM.02701-08>.
- Chen Y, Chen Y, Shi C, Huang Z, Zhang Y, Li S, Li Y, Ye J, Yu C, Li Z, Zhang X, Wang J, Yang H, Fang L, Chen Q. 2018. SOAPnuke: a MapReduce acceleration-supported software for integrated quality control and preprocessing of high-throughput sequencing data. *GigaScience* 7:gix120. <https://doi.org/10.1093/gigascience/gix120>.
- Nurk S, Meleshko D, Korobeynikov A, Pevzner PA. 2017. MetaSPAdes: a new versatile metagenomic assembler. *Genome Res* 27:824–834. <https://doi.org/10.1101/gr.213959.116>.
- Kang DD, Froula J, Egan R, Wang Z. 2015. MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. *PeerJ* 3:e1165. <https://doi.org/10.7717/peerj.1165>.
- Lin H-H, Liao Y-C. 2016. Accurate binning of metagenomic contigs via automated clustering sequences using information of genomic signatures and marker genes. *Sci Rep* 6:24175. <https://doi.org/10.1038/srep24175>.
- Sieber CMK, Probst AJ, Sharrar A, Thomas BC, Hess M, Tringe SG, Banfield JF. 2018. Recovery of genomes from metagenomes via a dereplication, aggregation and scoring strategy. *Nat Microbiol* 3:836–843. <https://doi.org/10.1038/s41564-018-0171-1>.
- Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assess-

- ment tool for genome assemblies. *Bioinformatics* 29:1072–1075. <https://doi.org/10.1093/bioinformatics/btt086>.
16. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res* 25:1043–1055. <https://doi.org/10.1101/gr.186072.114>.
 17. Langmead B, Salzberg SL. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods* 9:357–359. <https://doi.org/10.1038/nmeth.1923>.
 18. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup. 2009. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 25:2078–2079. <https://doi.org/10.1093/bioinformatics/btp352>.
 19. Tatusova T, Dicuccio M, Badretdin A, Chetvermin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44: 6614–6624. <https://doi.org/10.1093/nar/gkw569>.
 20. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res* 25:3389–3402. <https://doi.org/10.1093/nar/25.17.3389>.
 21. Rodríguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. *PeerJ Prepr* 4:e1900v1. <https://doi.org/10.7287/peerj.preprints.1900v1>.
 22. Arakaki A, Shibusawa M, Hosokawa M, Matsunaga T. 2010. Preparation of genomic DNA from a single species of uncultured magnetotactic bacterium by multiple-displacement amplification. *Appl Environ Microbiol* 76:1480–1485. <https://doi.org/10.1128/AEM.02124-09>.
 23. Spring S, Amann R, Ludwig W, Schleifer KH, Schüler D, Poralla K, Petersen N. 1995. Phylogenetic analysis of uncultured magnetotactic bacteria from the alpha-subclass of Proteobacteria. *Syst Appl Microbiol* 17: 501–508. [https://doi.org/10.1016/S0723-2020\(11\)80068-8](https://doi.org/10.1016/S0723-2020(11)80068-8).