

Supporting Information for

Chain organization of dimple-ended magnetite magnetosomes supports field-dependent cell linking in unicellular magnetotactic bacteria

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Movies S1 to S7

Supporting Text

1 Microbiology and molecular ecology experiments

1.1 Swimming behavior and magnetic collection of WYHV-1

Surface sediments (~10 cm in thickness) were collected from water depths of ~1-2 m in Weiyang (WYH) Lake (34°24'16.3" N, 108°59'16.0" E), a freshwater lake located north of Xi'an, Shaanxi province, northwest China (1). At the time of sampling (April 2015), the site had a salinity of 0.58‰, a pH of 8.38, and a temperature of ~18°C, as measured using an HQ40d portable multi-parameter meter (Hach, USA). The sediment-water mixture was transferred into 500-ml wide-mouth reagent bottles with sludge:water ratio of 2:1 and stored in the dark at ambient temperature (~20°C) to establish laboratory microcosms for incubation of magnetotactic bacteria (MTB) (2).

Living MTB in the microcosms were examined periodically using the hanging-drop method (3); their swimming behaviors were observed under an externally applied magnetic field generated by a pair of Helmholtz coils using an Olympus BX51 microscope equipped with phase-contrast and fluorescence optics and a DP70 digital camera system (Olympus Corp., Tokyo, Japan). The magnetic field intensity produced by the Helmholtz coils at the water droplet center ranges from ~0.1 to ~1 mT.

As expected, living MTB swam toward the S-pole and accumulated at the droplet edge, indicating that they are north-seeking MTB (4). In contrast to other MTB types detected in Weiyang sediments, which consistently behave as individual cells (1, 5, 6), living WYHV-1 cells can connect head-to-tail to form long chains, reaching ~20-50 µm or more in length, resembling multicellular filaments (Movies S1-S3). This self-assembly of many individual cells makes WYHV-1 readily distinguishable from other MTB types. Stronger external magnetic fields appear to promote formation of longer cell chains (Movie S3).

Swimming observations indicate that once assembled, long WYHV-1 cell chains can reorient with an external field but do not swim actively along it. Instead, they appear to perform a larger U-turn as a unit to realign with the field (Movie S2). By contrast, individual WYHV-1 cells behave similarly to other MTB types, swimming along the applied field, reversing direction via a U-turn, and then swimming in the opposite direction (Movie S2). When a magnetic field direction is maintained, individual cells accumulate at the droplet edge and can swim in both directions along field lines (Movies S1-S3), consistent with an axial magneto-aerotactic response (7).

To our knowledge, this type of self-assembly accompanied by field alignment but lacking collective motility has not been described in MTB, except possibly in uncultured strain NMV-1, which has a remotely similar behavior (8). However, no further study of NMV-1 has been reported since its description nearly 20 years ago. Attempts to obtain WYHV-1 in pure culture were unsuccessful. We, therefore, performed culture-independent analyses on magnetically enriched WYHV-1 cells. Approximately 200 ml of sediment enriched in WYHV-1 was subjected to magnetic extraction using a homemade separation apparatus under an external magnetic field of ~1 mT for ~2 h (9). Harvested WYHV-1 cells (~10⁹ cells) were washed three times with Milli-Q water and were then used for microscopic and molecular experiments.

1.2 16S rRNA gene sequencing

The 16S ribosomal RNA (rRNA) genes of magnetically extracted MTB were amplified by polymerase chain reaction (PCR) using the universal bacterial primer pair 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and 1492R (5'-GGTTACCTTGTTACGACTT-3') (10), following the protocol of Li et al. (9). PCR products were purified using a QIAquick gel extraction kit (Qiagen, Germany), ligated with the pMD19-T vector (TaKaRa, Japan), and transformed into *Escherichia coli* DH5α competent cells (Huada Genome Center, China). Thirty clones were selected randomly and sequenced using the pMD19-T vector primers M13-47 (5'-CGCCAGGGTTTTCCCAGTCACGAC-3') and RV-M (5'-GAGCGGATAACAATTTTCACACAGG-3') (Huada Genome Center, China).

All 30 sequences were clustered into a single operational taxonomic unit (OTU1) using the cd-hit software (11) at the 98.7% sequence identity threshold, corresponding to the species-level cutoff (12), and erroneous bases were corrected using the Gblocks 0.91b online algorithm with default parameters (13). Further analyses indicate that OTU1 shares ~95.73% and ~95.56% 16S rRNA gene sequence identity with uncultured MTB strains XQGS-1 (GenBank accession: MZ268120) (14) and YQV-1 (GenBank accession: ON340537) (15), respectively. These data indicate that WYHV-1 represents a novel species affiliated with the class *Alphaproteobacteria* within the phylum *Pseudomonadota* (formerly *Proteobacteria*).

1.3 Correlative fluorescence *in situ* hybridization and scanning electron microscopy (FISH-SEM) experiments

To confirm whether the derived 16S rRNA gene sequence (clone OTU1) originates from WYHV-1, a WYHV-1-specific oligonucleotide probe, WYHV1-166 (5'-CTAAAGCGACCGAAGTCTTTGCCC-3'), with a melting temperature (T_m) of ~64°C, was designed. Probe specificity was assessed using the online ProbeMatch tool (16); no 16S rDNA sequence in the RDP database matches WYHV1-166. The universal bacterial probe EUB338 (5'-GCTGCCTCCCGTAGGAGT-3') was used as a positive-control probe for fluorescence *in situ* hybridization (FISH) experiments (9, 17).

Probe EUB338 was synthesized and labelled fluorescently with fluorescein phosphoramidite (FAM) at the 5' end, whereas the probe WYHV1-166 was synthesized and labeled with the hydrophilic sulfoindocyanine dye (Cy3) at the 5' end. A suitable amount of *Magnetospirillum magneticum* AMB-1 cells were added as an inner control for FISH (9). Epifluorescence microscopy was performed using an Olympus BX51 microscope. After fluorescence imaging, the same sample was carbon-coated using a Leica ACE200 Low-vacuum sputter coater (Leica Microsystems, Wetzlar, Germany) and then examined with a Zeiss Ultra-55 field-emission scanning electron microscope (SEM) at 5 kV at the Electron Microscope Laboratory, Institute of Geology and Geophysics, Chinese Academy of Sciences (EML-IGGCAS), Beijing, China.

Correlative FISH-SEM experiments indicate that all observed bacterial cells hybridized with the EUB338 probe (green) (Fig. S2A), whereas only some vibrio- or spiral-shaped cells, corresponding to WYHV-1, hybridized with both the EUB338 and WYHV1-166 probes (red) (Fig. S2B). Correlated SEM observations clearly distinguish WYHV-1 cells from AMB-1 cells. WYHV-1 cells are vibrio- or spiral-shaped and contain large magnetosomal magnetite particles tightly arranged into a long chain, whereas AMB-1 cells are spirillum-shaped and contain relatively smaller magnetosomes forming a single fragmented chain (Fig. S2C-G). These results demonstrate that OTU1 is recovered from WYHV-1 cells.

1.4 Phylogenetic analysis of WYHV-1 and other dimple-forming MTB

Phylogenetic analysis of WYHV-1 was performed based on 16S rRNA gene sequences. A maximum-likelihood tree was then inferred with IQ-TREE (18) under the best-fit evolutionary model selected by ModelFinder (19), using 1,000 ultrafast bootstrap replicates. The resulting tree was visualized using FigTree v1.4.2. 16S rRNA gene sequences of MTB and representative *Alphaproteobacteria* from the NCBI database were used to construct a phylogenetic tree using the same procedure described above. WYHV-1 forms a distinct monophyletic clade with MTB strains YQV-1 and XQGS-1, representing a putative novel genus within the *Alphaproteobacteria* (Fig. S1). A survey of known MTB morphologies further shows that both YQV-1 and XQGS-1 can form octahedral magnetic particles with a dimple at one terminal face of the crystal (14, 15), whereas strain NS-1 forms elongated prismatic magnetic particles with dimples at both ends (20). NS-1 was identified from a brackish lagoon in Brazil (Southern Hemisphere) and belongs phylogenetically to the class *Gammaproteobacteria*. These observations indicate that dimple-ended magnetite crystals can form in several MTB lineages distinct from WYHV-1, although they are clearly not universal among MTB.

2 Micromagnetic simulation

2.1 Setup of crystal and chain models for micromagnetic simulations

Based on transmission electron microscope (TEM) analyses of crystal morphology and average particle sizes for WYHV-1 (Fig. 2, Fig. S3, Movies S4, S5), we first built a standard crystal model of a magnetite particle with 105 nm length and 81 nm width for micromagnetic simulations. The particle was modeled as a truncated hexagonal prism with dimples at both ends (hereafter referred to as a dimple-ended particle). For comparison, we constructed a second particle model with the same particle size and overall morphology but with flat ends (referred to as a non-dimpled particle). To investigate the magnetic behavior of WYHV-1 magnetic particles over their observed size range, two sets of magnetite particle models, with and without dimples, were generated. Each set contains a series of single particles with 5-nm size increments and lengths ranging from 40 to 150 nm, spanning more than 90% of the observed WYHV-1 magnetosome size distribution (Fig. S3).

To simulate the magnetic behavior of WYHV-1 magnetosome chains, we analyzed the size distribution of magnetic particles in 120 cells. On average, each cell contains 14 ± 3 particles with approximate bilateral symmetry. Most particles in the middle of a chain are relatively larger and more uniform in size, whereas a few particles, generally two at each end, are smaller and decrease progressively in size toward chain termini (Figs. 2, S3). To simplify calculations, we constructed a representative chain model containing 14 magnetite crystals divided into three size-based parts. The middle part (Part 1) contains 10 particles 116.1 nm long and 90.7 nm wide. The transition (Part 2) contains two particles, each 95.7 nm long and 71.1 nm wide, positioned adjacent to the middle. The terminal part (Part 3) contains two particles, each 68.7 nm long and 50.2 nm wide, located at the chain ends (Fig. S8). For comparison, we also constructed a single-chain model with 14 identical magnetite crystals, each 60 nm long and 46 nm wide. Each chain model was generated using either dimple-ended or non-dimpled particles. The dimple-ended model provides a more realistic representation of the WYHV-1 magnetosome chain, whereas the non-dimpled model serves as a comparative control. The gap between adjacent particles was set to 2 nm, corresponding closely to the spacing observed between adjacent magnetosomes in WYHV-1.

To investigate intracellular magnetic interactions between two head-to-tail aligned WYHV-1 cells, we constructed a double-chain model by placing two identical single chains in a head-to-tail arrangement. The single-chain models used are described above. The interparticle distance within each chain was fixed at 2 nm. The spacing between the two chains was set to 200 nm, 400 nm, 600 nm, 800 nm, 1000 nm, and 2000 nm. Based on TEM observations and statistical analyses, ~400 nm corresponds approximately to the distance between two chains when two WYHV-1 cells are connected head-to-tail, whereas 2,000 nm is approximately equivalent to the length of one WYHV-1 cell (Fig. S10).

2.2. Micromagnetic simulations

For individual-particle simulations, the magnetic domain state of each particle size was calculated 50 times at room temperature (293 K) under zero external field to sample possible magnetic domain states. The resulting domain states were then compiled for statistical analysis (Fig. S7).

For chain simulations, the influence of the demagnetizing field on both the entire chain and individual particles within a chain must be considered. Accordingly, micromagnetic simulations were performed to calculate the magnetic induction magnitude $\mathbf{B}$ of magnetosome chains at room temperature under zero external field, to compare models with different particle sizes, particle arrangements, and dimple structure on chain micromagnetic behavior, through the function $\mathbf{B} = \mu_0(\mathbf{M} + \mathbf{H}_d)$, where μ_0 is the vacuum permeability, $\mathbf{M}$ is the magnetization vector, and $\mathbf{H}_d$ is the demagnetizing field.

To evaluate interchain magnetic coupling, magnetostatic (stray) fields were calculated for both single- and double-chain models by embedding modeled chains in nonmagnetic mesh regions (Figs. S9 and S10). Magnetic coupling between two head-to-tail aligned chains was quantified from the maximum magnetic induction magnitude, $\mathbf{B}$, extracted from slices through the models as a function of D_d , where D_d is the distance from the chain end to the slice position in the single-chain

model and half of the interchain spacing in the double-chain model. For the double-chain models, two chains with fixed 2 nm interparticle spacing were arranged in a head-to-tail configuration within a nonmagnetic cylinder, and the magnetic induction distribution inside and outside the chains was calculated. The corresponding single-chain model was simulated in the same nonmagnetic cylinder geometry for comparison. The difference in magnetostatic interaction energy between the double- and single-chain models at the same D_d was taken as a measure of the magnetic coupling enhancement associated with addition of the second chain. Magnetostatic energy gain was further calculated as a function of D_d to assess whether interchain coupling could exceed thermal energy at room temperature (Fig. S10).

Figures

Fig. S1. Phylogenetic position of strain WYHV-1 and other MTB that form dimpled magnetosomal magnetite particles. (A) Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences of representative MTB (yellow nodes) and non-MTB bacteria (blue nodes). **(B)** TEM image of a strain YQV-1 cell. Bottom, enlarged view of dimpled magnetite particles in YQV-1. **(C)** HAADF-STEM image of an XQGS-1 cell. Right, enlarged view of dimpled magnetite particles in XQGS-1. **(D)** TEM image of an NS-1 cell. Right, HAADF-STEM image of dimpled magnetite particles in NS-1. **(E and F)** Three-dimensional HAADF-STEM reconstruction of magnetosomal magnetite in XQGS-1. Solid yellow arrows in B–F indicate terminal dimple structures in the magnetite. Images in D are reprinted with permission from the American Society for Microbiology, *Applied and Environmental Microbiology* (20).

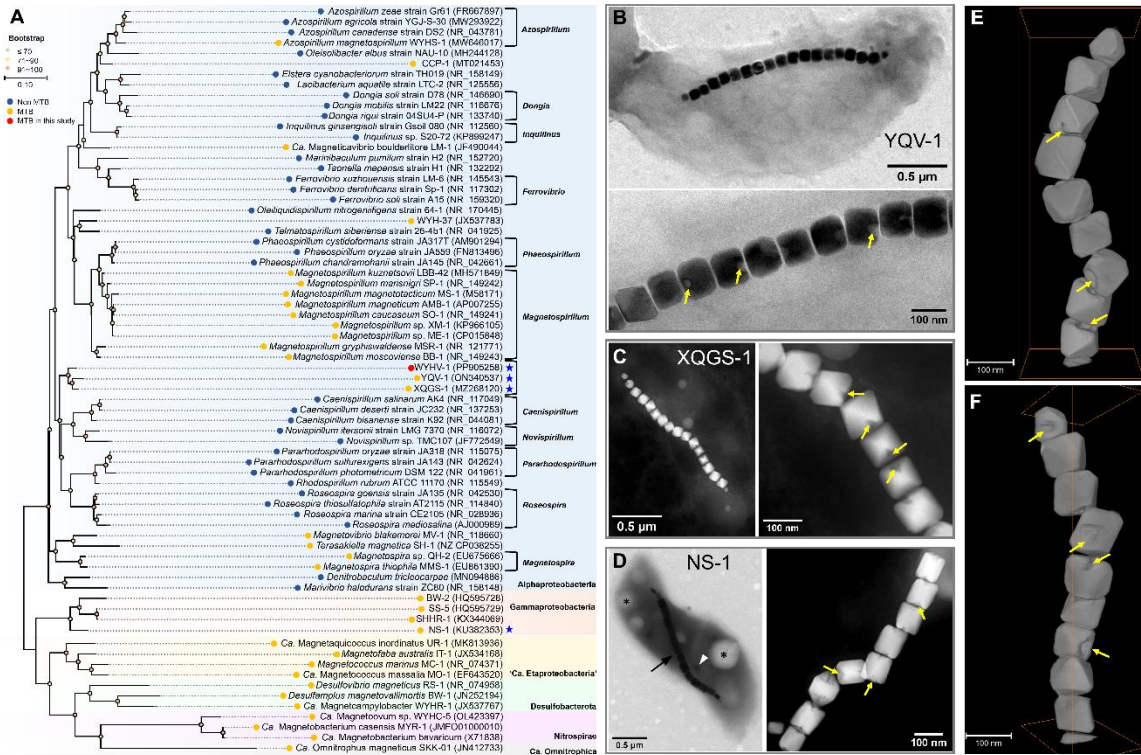


Fig. S2. Single-cell phylogenetic and structural identification of WYHV-1 by correlative fluorescence *in situ* hybridization and scanning electron microscopy (FISH-SEM). (A and B) False-color fluorescence microscopy images of bacteria hybridized *in situ* with **(A)** the 5'-FAM-labelled universal bacterial probe EUB338 and **(B)** the 5'-Cy3-labelled probe WYHV1-166 specific for strain WYHV-1. **(C)** Overlay of the fluorescence microscopy images shown in **A** and **B**. **(D)** Low-magnification SEM image of the region outlined by the lower right-hand dashed box in **C**. **(E)** High-magnification SEM image of two WYHV-1 cells outlined by the lower right-hand dashed box in **D**. **(F)** Low-magnification SEM image of the region outlined by the upper left-hand dashed box in **C**. **(G)** High-magnification SEM image of two WYHV-1 cells and one AMB-1 cell (internal control) outlined by the lower right-hand dashed box in **F**.

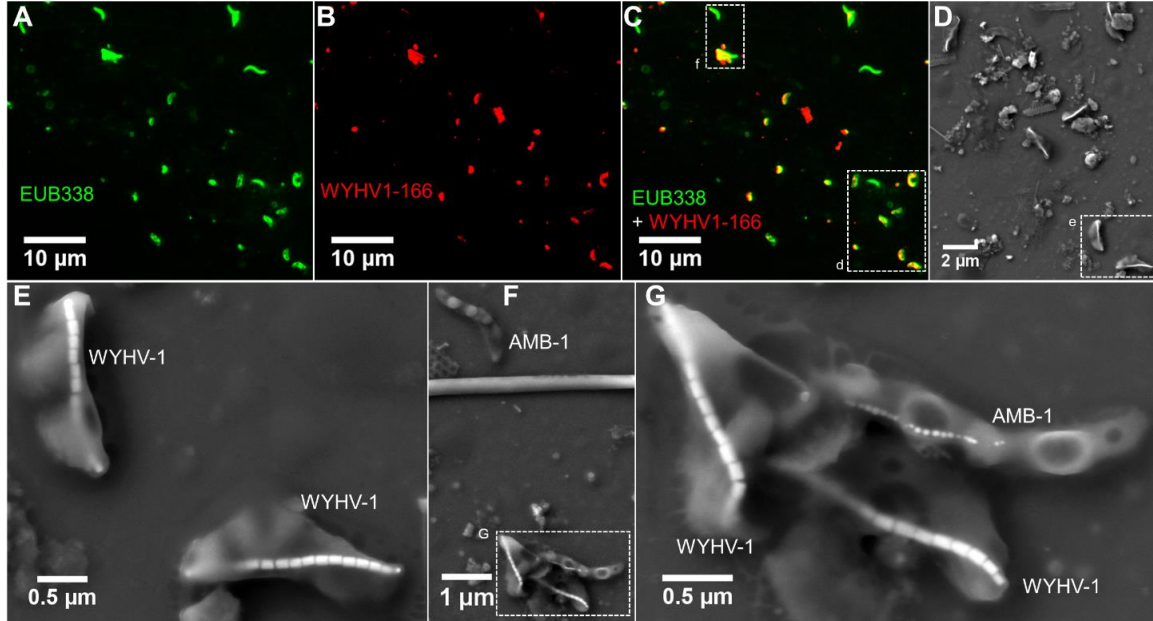


Fig. S3. Morphological features of WYHV-1. (A) HAADF-STEM illustration of cell morphology and intracellular magnetosome chains for multiple WYHV-1 cells. Note that magnetosome chains in some cells appear disordered or collapsed, likely resulting from cell shrinkage during sample preparation. (B-E) High-magnification images of WYHV-1 magnetite particles with key morphological features: (B) tight packing, (C) smaller particles at the chain end, (D) dimple structures from a collapsed chain, and (E) a small terminal particle lacking visible dimples. (F-L) Histograms of (F) cell length, (G) cell width, (H) magnetosome number per cell, (I) dimple depth, (J) crystal length, (K) crystal width, and (L) shape factor (width/length). Crystal length and width distributions are skewed negatively, whereas other parameters are approximately distributed normally. More than 75% of WYHV-1 magnetite particles have 90-150 nm lengths and 75-120 nm widths. (M) Plot of magnetosomal magnetite crystal length versus width. The four blue stars indicate particles for which no dimple structure is observed.

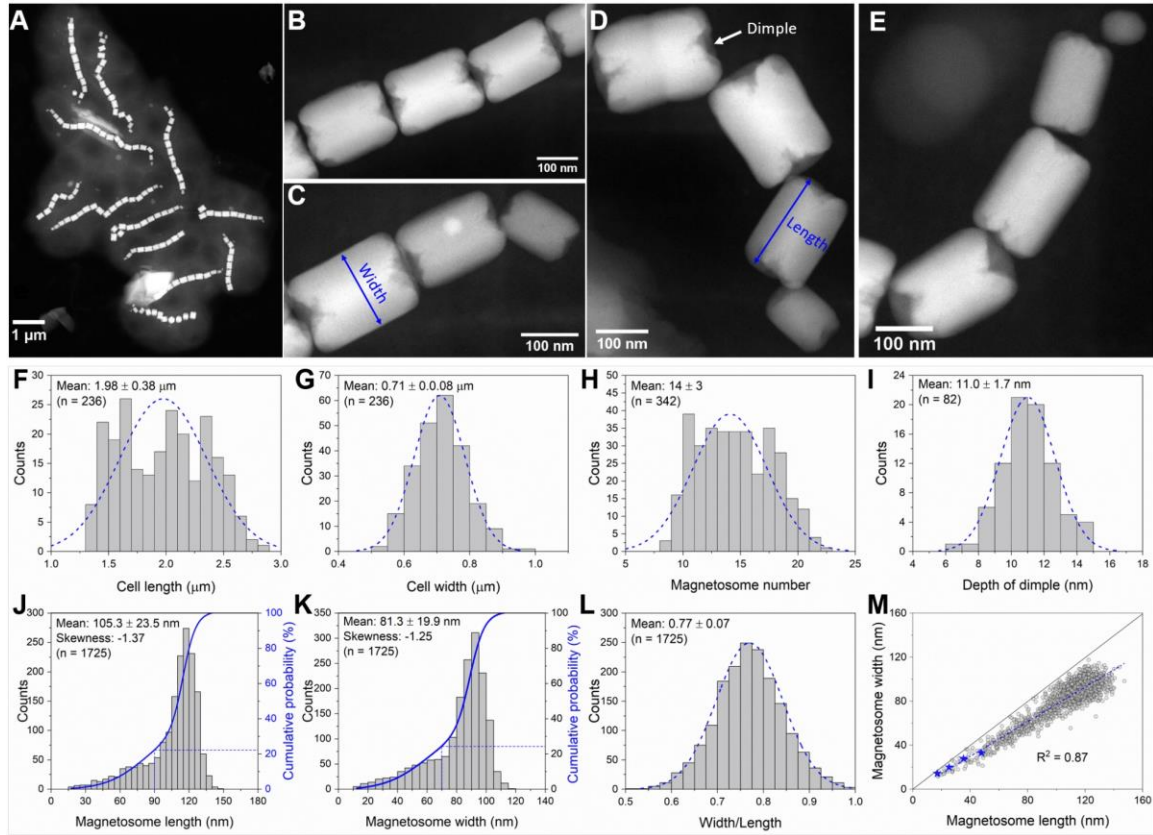


Fig. S4. WYHV-1 magnetosomal magnetite dimensions plotted on a theoretical magnetic domain-state phase diagram (21). (A) Length and width/length distributions of individual magnetite particles produced by WYHV-1. (B) Comparison of the mean length and width/length ratio of magnetosomal magnetite particles in WYHV-1 with those of representative magnetotactic bacteria (MTB); source data are provided in Table S1. The boundaries separating the superparamagnetic (SP), single-domain (SD), and multidomain (MD) regions for noninteracting and interacting magnetite particles are from the micromagnetic calculations of Muxworthy and Williams (21).

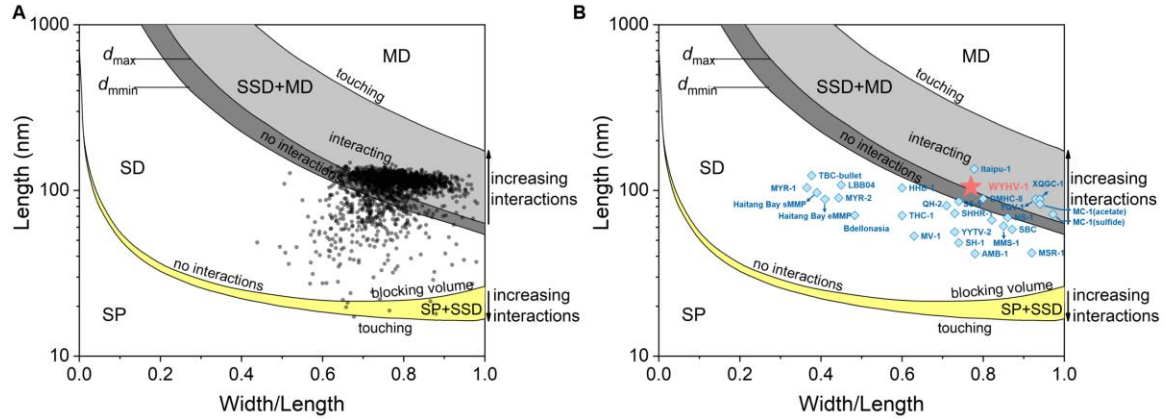


Fig. S6. Chemical features of WYHV-1 revealed by STEM-EDXS elemental mapping and synchrotron-based STXM analysis. (A) HAADF-STEM image of two representative WYHV-1 cells containing magnetosome chains and S-rich granules. (B-E) STEM-EDXS elemental maps of (B) C (C K α), (C) O (O K α), (D) S (S K α), and (E) Fe (Fe K α). (F) RGB composite map with C in blue, S in green, and Fe in red. (G) EDXS spectra acquired from selected ~100-nm-diameter regions of the carbon film on the TEM grid, cytoplasm, S-rich granule, and magnetite (Mag) in WYHV-1 cells. (H) Average STXM image of a S L-edge stack (158-180 eV). (I-K) STXM absorption images of a WYHV-1 cell at (I) 160 eV, (J) 163.5 eV, and (K) the difference between J and I, highlighting the sulfur granule within the cell. The sulfur granule is clearly visible because of its distinct sulfur absorption at 160 eV and 163.5 eV. (L) S L-edge XANES spectrum of the S granule (white arrow), consistent with zero-valent sulfur. STXM absorption images were converted to optical density (OD) images before subtraction.

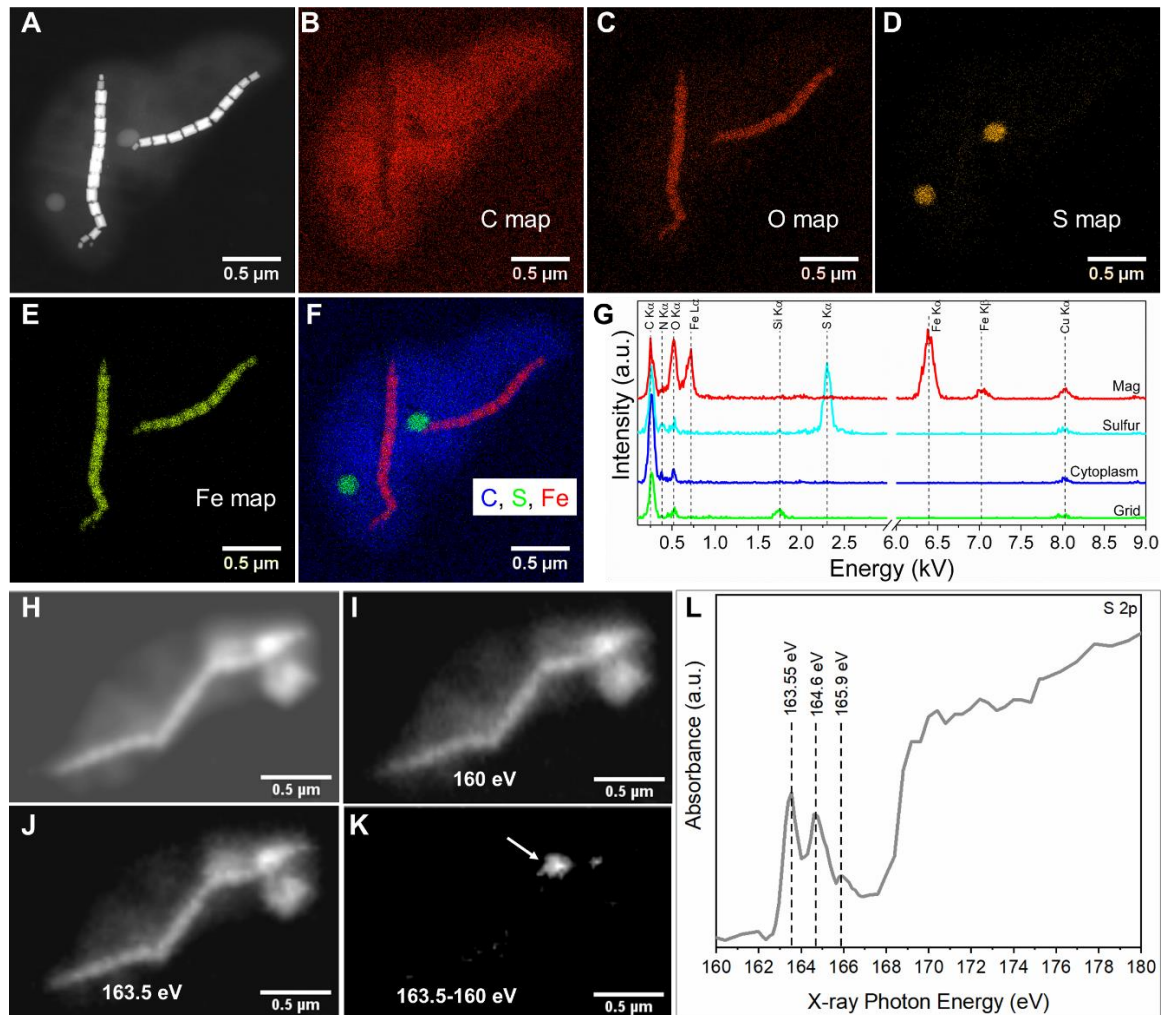


Fig. S7. Magnetic field distributions of WYHV-1 magnetosome chains revealed by off-axis electron holography. Magnetic fields associated with magnetosome chains in two parallel and magnetically attached cells (**A–C**), and six aggregated cells (**D–F**) were analyzed by off-axis electron holography. The first column is mean inner potential, the second column is magnetic phase, and the third column is corresponding magnetic phase contours in the remanent state. Colors, derived from the gradient of each phase image, indicate the local projected magnetic induction direction according to the color wheel (lower right), whereas contour density represents the magnetic field magnitude. Magnetic phase contour spacing is $\pi/5$ radians; a phase difference of 2π corresponds to an enclosed magnetic flux of $4.14 \times 10^{-15} \text{ T} \cdot \text{m}^2$. In the two-cell (**A–C**) and six-cell (**D–F**) examples, adjacent magnetosome chains are magnetically coupled. Regardless of the spatial cell arrangement, once cells are sufficiently close or in contact, their chains interact magnetostatically, and each intracellular chain behaves approximately as a single elongated uniaxial magnetic unit with strong dipole moment.

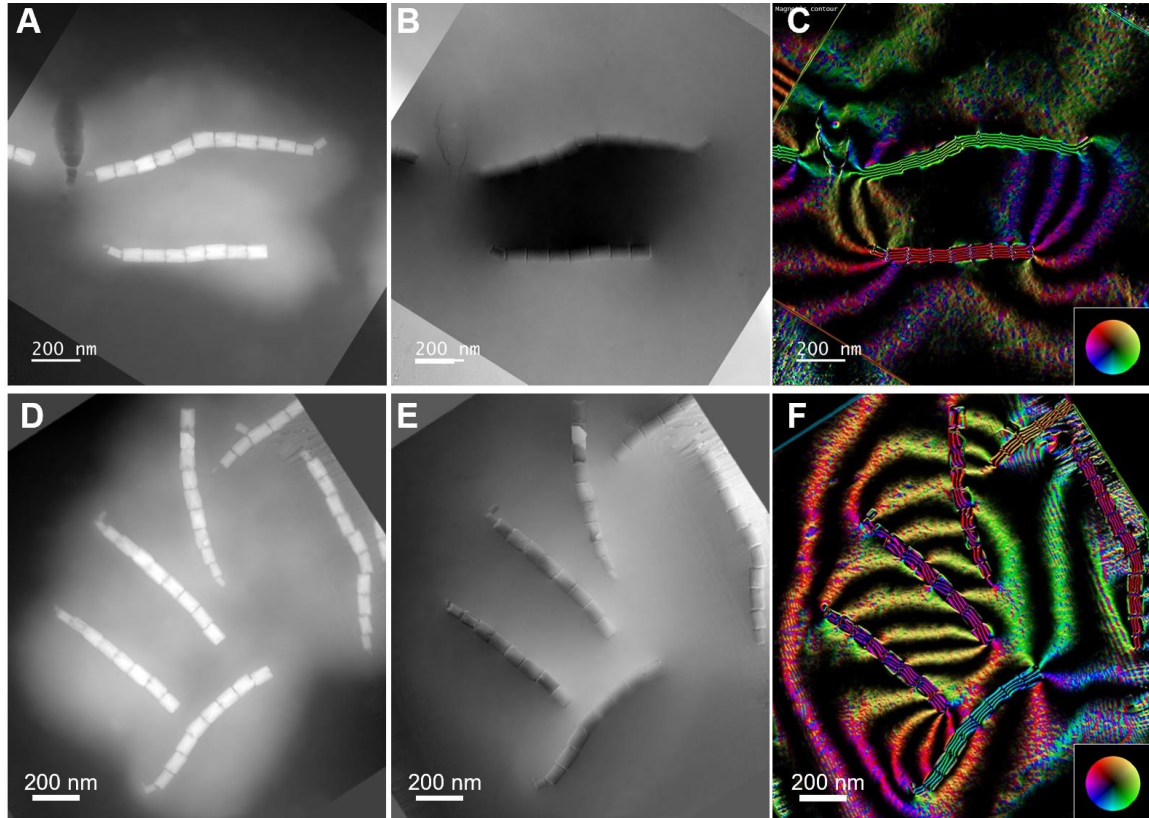


Fig. S8. Micromagnetic simulation of individual WYHV-1 magnetosome particles. (A) Micromagnetic structures of dimple-ended particles with different lengths. The leftmost panel show the corresponding three-dimensional finite-element model. The resulting magnetic configurations are classified as single-domain (SD), single-vortex with the vortex core parallel to the particle long axis (LSV), or single-vortex with vortex core parallel to the particle short axis (SSV). The color scale indicates magnetic helicity. **(B)** Relative frequencies of magnetic states obtained for dimple-ended particles of different sizes. Fifty independent simulations were performed for each particle size. A value of 1 indicates that all simulations converged to the corresponding state, whereas 0 indicates that the state was not observed.

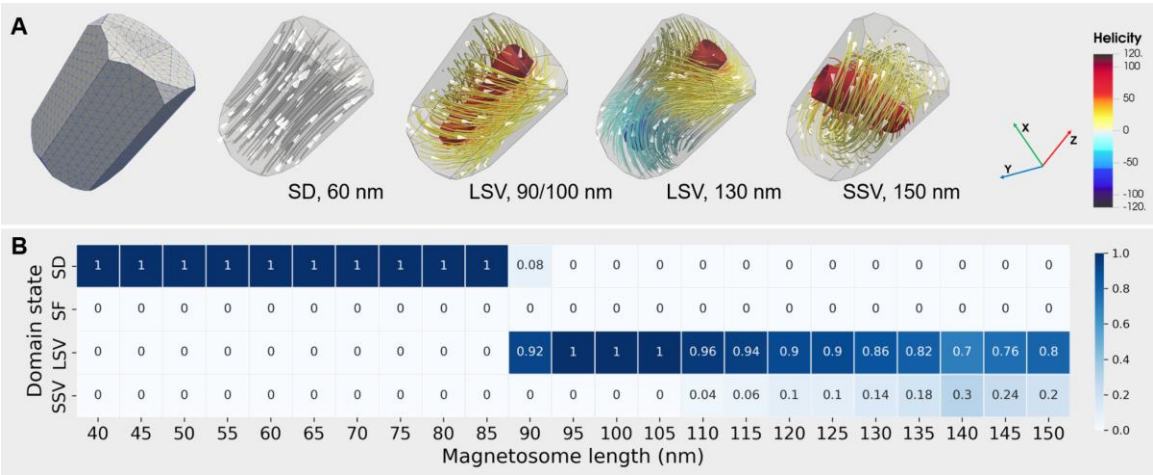


Fig. S9. Micromagnetic simulations of non-dimpled prismatic magnetite magnetosomes. (A) Simulated magnetic structures of non-dimpled particles with different lengths. The leftmost panel is the corresponding three-dimensional finite-element model. Resulting magnetic configurations are classified as SD, single-flower (SF), LSV, or SSV states. The color scale indicates magnetic helicity. **(B)** Relative frequencies of magnetic states obtained for non-dimpled particles of different sizes. Fifty independent simulations were performed for each particle size. A value of 1 indicates that all simulations converged to the corresponding state, whereas a value of 0 indicates that the state was not observed. **(C)** Remanent magnetic state of a non-dimpled magnetosome chain. Insets are enlarged views of selected particles within the chain and at the chain end; the lower central inset is the micromagnetic structure of an individual particle within the chain. Individual particles remain nearly uniformly magnetized, and the intact chain retains a strong, nearly uniaxial remanent magnetization parallel to the chain axis. The color bar B (T) denotes magnetic induction, where $\mathbf{B} = \mu_0(\mathbf{M} + \mathbf{H}_d)$, μ_0 is the vacuum permeability, $\mathbf{M}$ is the magnetization vector, and $\mathbf{H}_d$ is the demagnetizing field. Terminal dimples promote LSV-state formation and shift vortex-state formation to smaller particle sizes.

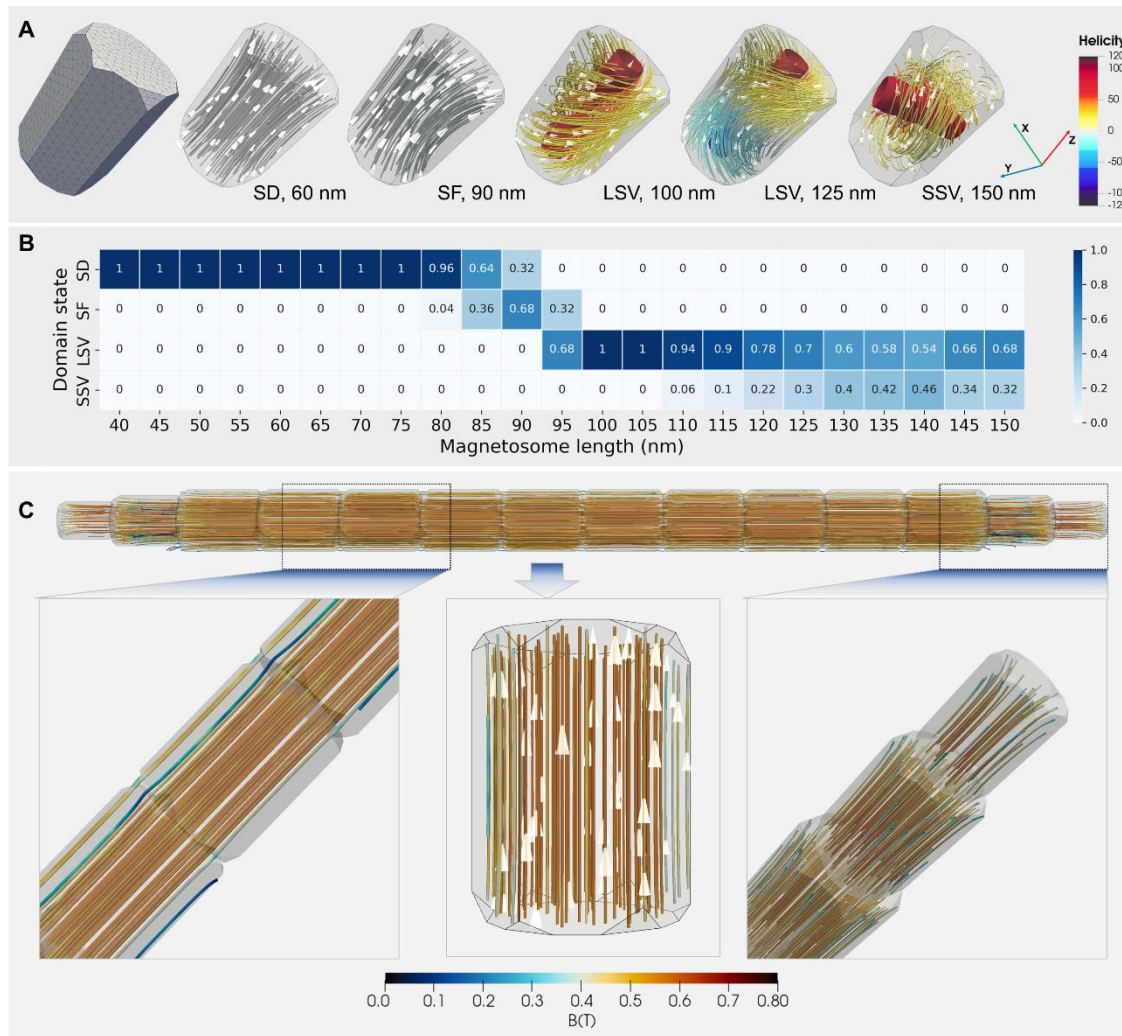


Fig. S10. Model of a WYHV-1 magnetosome chain for micromagnetic simulation. (A and B) Histograms of magnetosomal (A) crystal length and (B) width at different positions within a WYHV-1 chain. For each chain, the center particle is defined as the chain midpoint. Top, probability distribution of magnetite particles at different chain positions. Right, position-specific probability distributions of crystal length (A) and width (B). Based on TEM observations and statistical analyses of 120 WYHV-1 cells, individual chains can be divided into either three or two size-defined parts. Most chains (~87.5%) can be divided into three parts, whereas a smaller fraction (~12.5%) contains only two size-defined parts. (C-H) Histograms of WYHV-1 magnetite crystal size for **Part 1** (C, F; mean length = 116.1 ± 10.9 nm, mean width = 90.7 ± 9.2 nm), **Part 2** (D, G; mean length = 95.7 ± 13.4 nm, mean width = 71.1 ± 13.9 nm), and **Part 3** (E, H; mean length = 68.7 ± 22.6 nm, mean width = 50.2 ± 18.3 nm). (I) Schematic magnetosome chain model used for micromagnetic simulations.

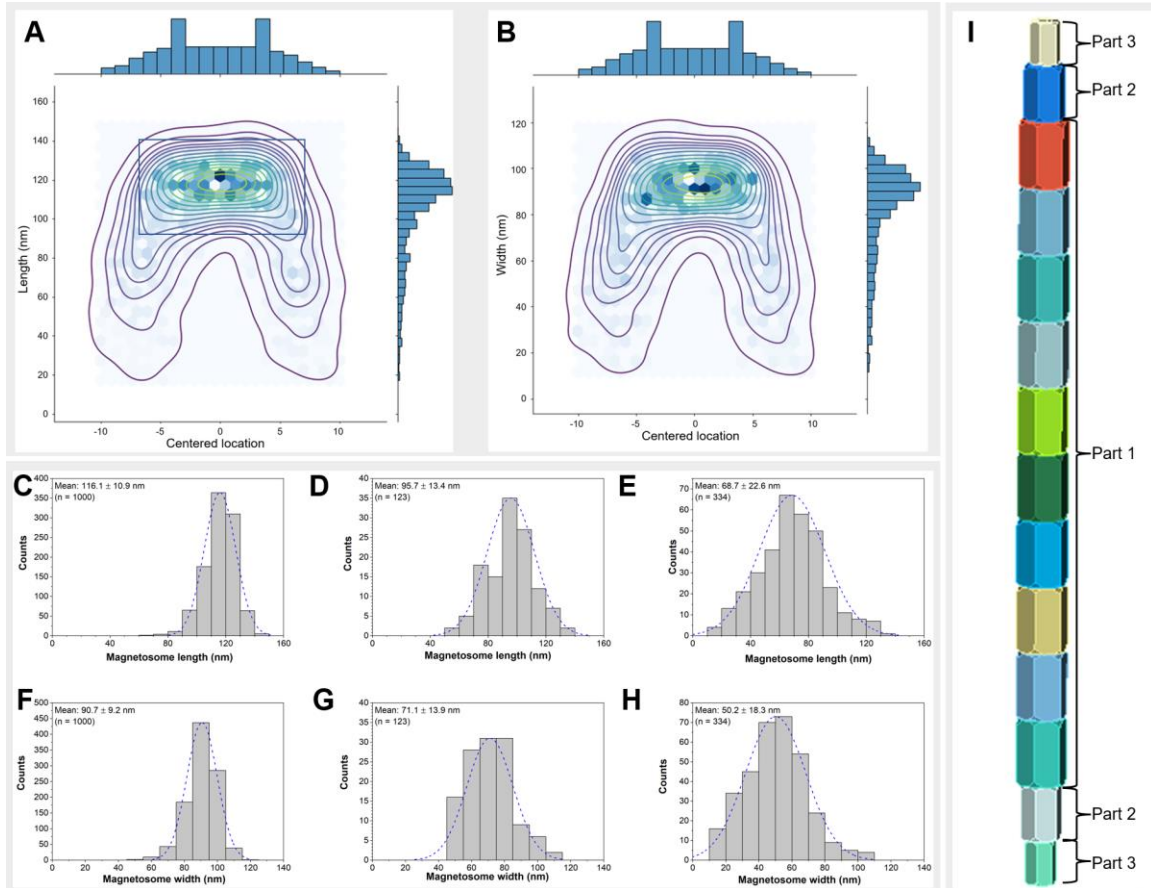


Fig. S11. Micromagnetic models of magnetosome chains. (A) Single-chain models with a fixed interparticle spacing of 2 nm. Two representative chains are shown: the upper SD-particle chain, composed of 14 identical particles, each 60 nm long and 46 nm wide, with a total chain length of 866 nm; and the lower SV-particle chain, with a total chain length of 1580 nm (see Fig. S10 for detailed parameters). **(B)** Double-chain models in which the inter-particle spacing within each chain is fixed at 2 nm, whereas the inter-chain distance varies from 200 nm to 2000 nm. Representative inter-chain distances of 200, 1000, and 2000 nm are illustrated.

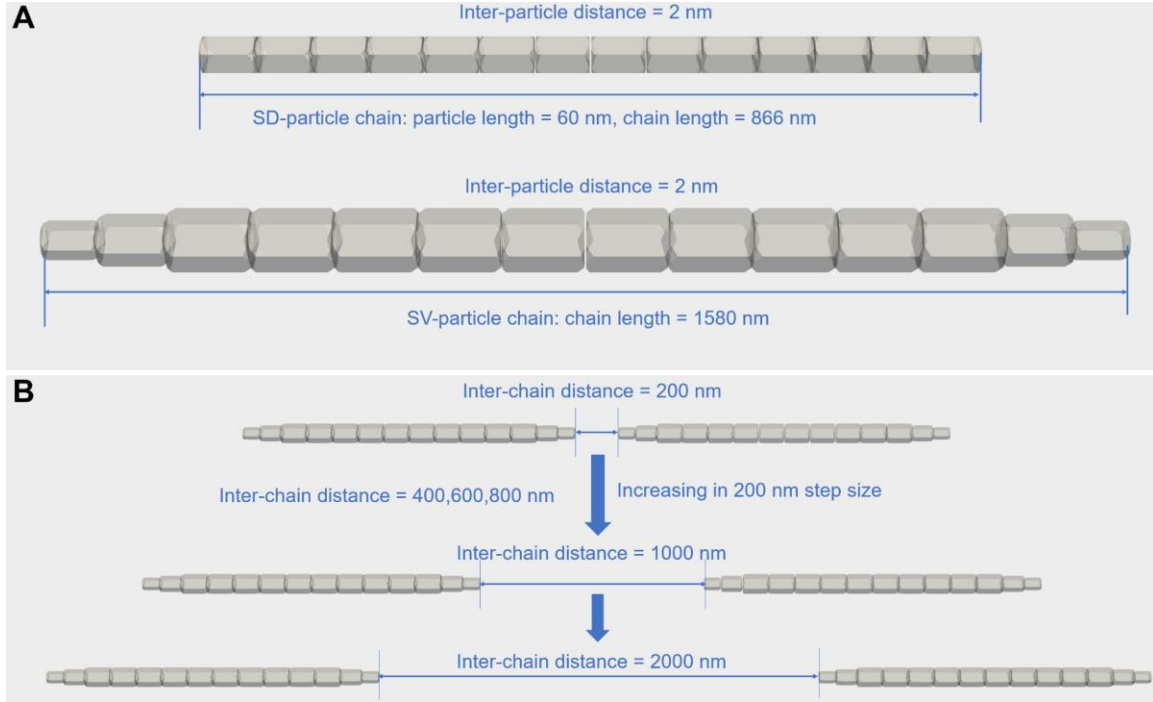


Fig. S12. Distance-dependent magnetic induction intensity and magnetostatic energy gain in magnetosome chains. (A) SV-particle single-chain model. (B) SV-particle double-chain model. (C) SD-particle single-chain model. (D) SD-particle double-chain model. In A–D, the red dashed lines indicate slice positions. D_d represents the distance from the chain end to the slice position in the single-chain models, and half of the inter-chain spacing in the double-chain models. The color scale labeled B (T) indicates magnetic induction magnitude, where $B = \mu_0(M + H_d)$, μ_0 is the vacuum permeability, M is the magnetic vector, and H_d is the demagnetization field. (E, F) Central-slice views as a function of D_d for SV-particle chains (E) and SD-particle chains (F). In each panel, the left-hand and right-hand sides are single and double chains, respectively; slices of dimple-ended chains are shown above the arrows and those of non-dimpled chains below. The color scale is $\lg B = \log_{10} B$. (G, H) Magnetic induction intensity at the central slice as a function of D_d for dimple-ended (G) and non-dimpled (H) particle chains. The horizontal dashed line marks the present-day local geomagnetic field in the Beijing region (4.5×10^{-5} T). (I) Magnetostatic energy gain as a function of D_d for different magnetosome chain models; the horizontal dashed line indicates thermal energy at room temperature. Magnetic induction outside the chains decreases with increasing distance from the chain end but remains appreciable at the submicron scale. At sufficiently small separations, the magnetostatic energy gain of the double-chain configuration exceeds thermal energy, which indicates the potential for magnetic coupling between chains.

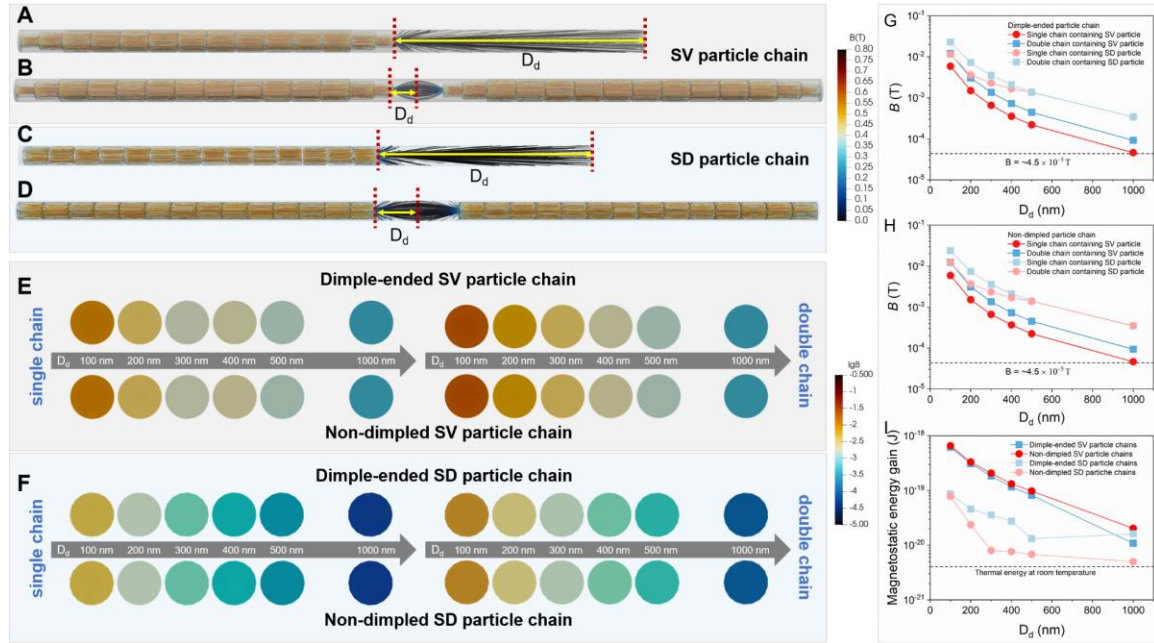


Table S1. Comparison of magnetosomal magnetite dimensions, morphologies, and chain organization among representative magnetotactic bacteria and selected magnetofossil assemblages.

Strain, morphotype, or assemblage	Phylogeny or sample identity	Magnetosome morphology (original wording)	Mean length, <i>L</i> (nm)	Mean width, <i>W</i> (nm)	Size range or directly reported statistics	Chain organization	Dimpled crystal ends	Reference
WYHV-1	Pseudomonadota; Alphaproteobacteria; <i>Azospirillum</i> -related lineage	Elongated prismatic, with dimples at both ends	105.3 ± 23.5	81.3 ± 19.9	More than 75% of particles: <i>L</i> , 90–150; <i>W</i> , 75–120; <i>W/L</i> = 0.77 ± 0.07	Single chain; 14 ± 3 particles per cell	Yes; dimples at both crystal ends; dimple depth, 11.0 ± 1.7 nm	This study
YQV-1	Pseudomonadota; Alphaproteobacteria; <i>Azospirillum</i> -related lineage	Cubo-octahedral	88.6 ± 13.0	82.0 ± 11.0	<i>W/L</i> = 0.93	Single chain; 19 ± 2 particles per cell	Not explicitly reported	(15)
XQGS-1	Pseudomonadota; Alphaproteobacteria	truncated octahedral	88.3 ± 11.7	83.3 ± 11.0	<i>W/L</i> = 0.94 ± 0.04; most <i>L</i> ≈ 80–105 nm	Single chain; 17 ± 3 particles per cell	Not explicitly reported	(14)
NS-1	Pseudomonadota; Gammaproteobacteria	Elongated prismatic	NR	NR	Size = (<i>L</i> + <i>W</i>)/2: 68.8 ± 16.2 nm (range, 26.8–87.8 nm); <i>W/L</i> = 0.86 ± 0.20 (range, 0.56–0.91)	Single chain	Not explicitly reported	(20, 22)
Itaipu-1	Uncultured large spherical MTB (Itaipu Lagoon morphotype; no formally established cultivated taxon)	Elongated prismatic	135 (standard deviation not reported)	105 (standard deviation not reported)	Maximum <i>L</i> ≈ 250 nm; <i>W/L</i> ≈ 0.9	Double chain	Not explicitly reported	(23, 24)
MV-1	Pseudomonadota; Alphaproteobacteria; <i>Magnetovibrio</i>	Truncated hexaoctahedral	53 ± 10.86	35 ± 7.86	<i>L</i> , 21–74 nm; <i>W</i> , 12–54 nm; <i>W/L</i> ≈ 0.63	Subchains; approximately 10 ± 4 particles per cell	Not explicitly reported	(25, 26)
MSR-1	Pseudomonadota; Alphaproteobacteria; <i>Magnetospirillum</i>	Cubo-octahedral	~42	NR	Mean diameter ≈ 42 nm; a later TEM study reported a mean diameter of 40–45 nm and <i>W/L</i> = 0.92	Single chain; ~ 20 particles per cell	Not explicitly reported	(27, 28)
AMB-1	Pseudomonadota; Alphaproteobacteria; <i>Magnetospirillum</i>	Cubo-octahedral	41.5 ± 15	NR	<i>W/L</i> = 0.78 ± 0.12	Subchains; 12 ± 5 particles per cell (anaerobic conditions)	Not explicitly reported	(29)
MC-1	Pseudomonadota; Magnetococcia; <i>Magnetococcus</i>	Acetate-grown: rectangular, slightly truncated; sulfide-grown: truncated prismatic	83 ± 14 (acetate); 72 ± 11 (sulfide)	78 ± 11 (acetate); 70 ± 13 (sulfide)	Acetate: <i>L</i> , 30–110 nm; <i>W</i> , 15–107 nm; sulfide: <i>L</i> , 33–95 nm; <i>W</i> , 29–87 nm	Single chain; 14 ± 3 (acetate) and 10 ± 2 (sulfide) particles per cell	Not explicitly reported	(30)
WYHR-1	Desulfobacterota; Deltaproteobacteria	Elongated bullet-shaped	88.6 ± 39.3	31.0 ± 5.5	<i>W/L</i> = 0.41 ± 0.11 (range, 0.13–1.0)	Chain bundle	Not explicitly reported	(6, 31)

Strain, morphotype, or assemblage	Phylogeny or sample identity	Magnetosome morphology (original wording)	Mean length, <i>L</i> (nm)	Mean width, <i>W</i> (nm)	Size range or directly reported statistics	Chain organization	Dimpled crystal ends	Reference
MYR-1	Nitrospirota; Ca. <i>Magnetobacterium casensis</i>	Bullet-shaped	104 ± 31	38 ± 6	<i>L</i> , 10–180 nm; <i>W</i> , 10–56 nm	Chain bundles; hundreds of particles per cell	Not explicitly reported	(32)
THC-1	Pseudomonadota; Candidatus Etaproteobacteria	Hexagonal prismatic	70.6 ± 8.6	42.3 ± 5.2	<i>W/L</i> = 0.60	Nonlinear chain; 35 ± 15 particles per cell	Not explicitly reported	(33)
QH-2	Pseudomonadota; Alphaproteobacteria; <i>Magnetospira</i>	Prismatic	81 ± 23	58 ± 20	<i>W/L</i> = 0.71	Single chain; 16 ± 5 particles per cell	Not explicitly reported	(34)
MMS-1	Pseudomonadota; Alphaproteobacteria; <i>Magnetospira</i>	Elongate cuboctahedra	61 ± 12	52 ± 11	<i>W/L</i> = 0.85	Single chain; 17 ± 5 particles per cell	Not explicitly reported	(35, 36)
SH-1	Pseudomonadota; Alphaproteobacteria; <i>Terasakiella</i> -related lineage	Elongated prismatic	48.3 ± 8.9	35.7 ± 5.2	<i>W/L</i> = 0.74	Single chain	Not explicitly reported	(37)
SHHR-1	Pseudomonadota; Gammaproteobacteria	Elongated prismatic	72.9 ± 15.7	52.6 ± 11.0	<i>W/L</i> = 0.73 ± 0.07	Single chain; 15 ± 4 particles per cell	Not explicitly reported	(9)
SS-5	Pseudomonadota; Gammaproteobacteria	Elongated octahedral	86 ± 27	63 ± 19	<i>W/L</i> = 0.74 ± 0.07	Long linear chain; 20 ± 7 particles per cell	Not explicitly reported	(38)
DMHC-8	Pseudomonadota; Candidatus Etaproteobacteria	Prismatic	89.1 ± 22.6	71.5 ± 20.6	<i>W/L</i> = 0.80	Two double chains; 42 ± 8 particles per cell	Not explicitly reported	(39)
YYTV-2	Pseudomonadota; Alphaproteobacteria; Rhodospirillales; Ca. <i>Magneticavibrio</i>	Elongated cubo-octahedral	56.2 ± 12.3	41.2 ± 11.3	<i>W/L</i> = 0.73 ± 0.11	Single chain; 22 ± 3 particles per cell	Not explicitly reported	(40, 41)
HHB-1	Pseudomonadota; Candidatus Magnetococcia; Magnetococcales	Prismatic magnetite	103.70 ± 28.33	62.15 ± 18.09	<i>W/L</i> = 0.60 ± 0.10	Multiple chains; 91 ± 17 particles per cell	Not explicitly reported	(42)
LBB04	Thermodesulfobacteriota; Syntrophales	Elongated bullet-shaped	108 ± 21.1	45 ± 8.1	<i>W/L</i> = 0.45	Chain bundle; 33 ± 9 particles per cell	Not explicitly reported	(43)
MYR-2	Nitrospirota	Curved bullet-shaped	90.2 ± 24.3	40 ± 3.6	Mean <i>W/L</i> not directly reported	Single chain; 56 ± 13 particles per cell	Not explicitly reported	(41)
Bdellonasia morphotype	Bdellovibrionota; Bdellonasia class nov.	Bullet-shaped	70.8 ± 12.1	34.2 ± 4.2	Mean <i>W/L</i> not directly reported	Single chain; 5 ± 2 particles per cell	Not explicitly reported	(44)

Strain, morphotype, or assemblage	Phylogeny or sample identity	Magnetosome morphology (original wording)	Mean length, <i>L</i> (nm)	Mean width, <i>W</i> (nm)	Size range or directly reported statistics	Chain organization	Dimpled crystal ends	Reference
Haitang Bay eMMP	Thermodesulfobacteriota/D esulfobacterota group; pooled ellipsoidal MMP morphotypes from multiple OTUs, not a single strain	Bullet-shaped	90.1 ± 22.8	34.0 ± 4.9	<i>W/L</i> = 0.39 ± 0.08	Relatively regular arrangement, with chain formation and irregular clusters; >2,000 particles per eMMP	Not explicitly reported	(45)
Haitang Bay sMMP	Thermodesulfobacteriota/D esulfobacterota group; pooled spherical MMP morphotypes from multiple OTUs, not a single strain	Bullet-shaped	97.2 ± 21.4	36.3 ± 3.4	<i>W/L</i> = 0.39 ± 0.10	Mostly clustered; not a regular single chain; approximately 928 particles per sMMP	Not explicitly reported	(45)
TBC cubo and prism	Sedimentary magnetofossil assemblage; IODP Hole 1409A; not a bacterial strain	Cubo and prism (pooled)	66.30 ± 33.89	52.53 ± 23.65	<i>W/L</i> = 0.821 ± 0.153	Not directly observed	Not explicitly reported	(46)
SBC cubo and prism	Sedimentary magnetofossil assemblage; IODP Hole 1409A; not a bacterial strain	Cubo and prism (pooled)	58.23 ± 18.06	50.43 ± 15.06	<i>W/L</i> = 0.872 ± 0.107	Not directly observed	Not explicitly reported	(46)

Notes. Values are means ± SD unless otherwise indicated. NR, not reported in the cited source; *L*, crystal length; *W*, crystal width; MTB, magnetotactic bacteria; MMP, multicellular magnetotactic prokaryote; eMMP, ellipsoidal MMP; sMMP, spherical MMP; OTU, operational taxonomic unit. Mean *L* or *W* was not back-calculated from *W/L*. eMMP and sMMP are morphotype-level summaries rather than single strains. TBC and SBC are sedimentary magnetofossil assemblages from IODP Hole 1409A, not bacterial strains. For Xue et al. (2024), pooled cubo-and-prism means and sample SDs were calculated from the supplied particle-level data (TBC, *n* = 1,364; SBC, *n* = 959).

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Movie S1 (separate file). Behavior of WYHV-1 cells under a fixed external magnetic field. Under an applied field of ~ 0.1 mT, WYHV-1 cells swim along the field direction and accumulate near the droplet edge. Some cells form elongated head-to-tail chains aligned with the external field.

Movie S2 (separate file). Response of WYHV-1 cells to magnetic-field reversal. Under an applied field of ~ 0.1 mT, individual cells perform U-turns and reverse their swimming direction after field reversal. Head-to-tail cell chains undergo larger collective rotations to realign with the new field direction.

Movie S3 (separate file). Behavior of WYHV-1 cells under a stronger fixed external magnetic field. Under an applied field of ~ 1 mT, individual cells exhibit axial magneto-aerotaxis, aligning with and swimming along the field in both directions. Head-to-tail cell chains align with the field but show no clear active swimming along it.

Movie S4 (separate file). Three-dimensional HAADF-STEM tomography of WYHV-1 cells. The movie shows the reconstruction and visualization of magnetosome chains within five WYHV-1 cells.

Movie S5 (separate file). Three-dimensional HAADF-STEM tomography of WYHV-1 magnetosome chains. The movie shows the reconstruction and visualization of several magnetosome particles within two WYHV-1 cells.

Movie S6 (separate file). Three-dimensional FIB-SEM tomography of a WYHV-1 magnetosome chain. The movie shows the reconstruction and visualization of magnetosome chain within a single WYHV-1 cell.

Movie S7 (separate file). Three-dimensional HAADF-STEM tomography of XQGS-1 magnetosome chain. The movie shows the reconstruction and visualization of magnetosome chain within a single XQGS-1 cell.