

Title: Ultrastructure and motility in the magnetotactic bacterium *Magnetofaba australis* strain IT-1

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Abstract:

Magnetotactic bacteria (MTB) are aquatic prokaryotes capable of producing chains of nano-sized, membrane-bound magnetic crystals named magnetosomes. Magnetosome chains impart the bacterial cell a magnetic moment that allow MTB to orient themselves in relation to the geomagnetic field while swimming propelled by flagella, in a phenomenon called magnetotaxis. In most MTB, the chains of magnetosomes are positioned along the major axis of the cell allowing the flagella to propel the cell body in a parallel or antiparallel trajectory in relation to the geomagnetic field lines. *Magnetofaba australis* strain IT-1 consists of coccoid to ovoid MTB capable of producing a single chain of magnetosomes. The cell morphology is similar to a "bean" with a concave region where two flagellar bundles emerge and a convex region without flagella. This strain swims at speeds up to 300 $\mu\text{m}\cdot\text{s}^{-1}$ along an apparently helical trajectory. To better understand the swimming trajectories and their relation to magnetotaxis in this strain, transmission electron microscopy (TEM) was used to observe the position of the chain in relation to the cell body and flagella. Cells were high pressure frozen, freeze-substituted with osmium tetroxide and embedded in epoxide resin for serial section ultramicrotomy. Ultra-thin sections (60 nm) were imaged on a Morgagni transmission electron microscope and used for 3D reconstruction. Preliminary results indicate that the magnetosome chain is oriented to an axis not parallel to the major axis of the cell and consequently misaligned in relation to the flagella. Thus, the flagellar movement itself would lead to a disorientation of the cell body in relation to magnetic field. However, when observing the cell movement with light microscopy using a high speed camera, we observed that all cell trajectories are, in fact, linear and each bacterium moves along the applied magnetic field in a straight line. New serial sections, together with TEM 3D computer modelling, may provide the structural framework for the correct interpretation of the mechanisms underlying the magnetotactic behavior in *M. australis* strain IT-1.

Key words: magnetotactic bacteria, magnetosomes, transmission electron microscopy

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