Fe_3O_4 and Fe_3S_4 in a bacterium

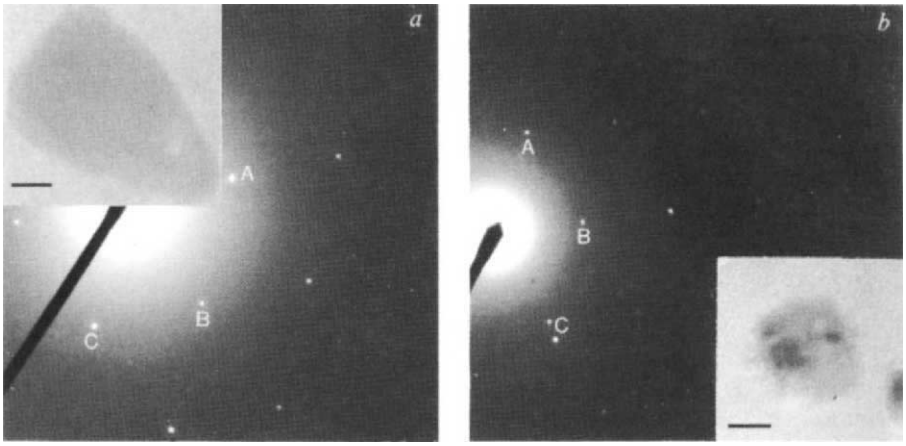

FIG. 2 Single-crystal electron diffraction patterns recorded from the arrowhead-shaped and rectangular particles in the chain shown in Fig. 1. Insets, crystals in the orientation corresponding to the electron diffraction patterns. Scale bar in insets: *a*, 10 nm; *b*, 30 nm. For the electron diffraction patterns, the camera length and wavelength were 1,025 nm and 0.02508 Å, respectively. *a*, The pattern corresponds to the $[1\bar{1}0]$ zone of magnetite, Fe_3O_4. Reflection A (2 2 0) (2.96 Å); reflection B $(1 1 \bar{3})$ (2.53 Å); reflection C $(\bar{1}\bar{1}\bar{3})$ (2.53 Å). Angles $220 \times 11\bar{3} = 64.8°$; $11\bar{3} \times \bar{1}\bar{1}\bar{3} = 50.5°$; $220 \times \bar{1}\bar{1}\bar{3} = 115.2°$. Space group *Fd3m* (cubic); $a = 8.396$ Å. *b*, The pattern corresponds to the [0 1 1] zone of greigite, Fe_3S_4. Reflection A $(\bar{3} 1 1)$ (2.98 Å); reflection B (022) (3.49 Å); reflection C (3 1 1) (2.98 Å). Angles $022 \times \bar{3}11 = 64.8°$; $311 \times \bar{3}11 = 50.5°$; $022 \times 311 = 64.8°$. Space group *Fd3m* (cubic); $a = 9.876$ Å.

SIR — Magnetotactic bacteria, a diverse group of Gram-negative prokaryotes that orient along geomagnetic field lines[1], contain magnetosomes, membrane-bounded intracellular single-magnetic-domain particles of either an iron oxide, magnetite (Fe_3O_4) (ref. 2), or an iron sulphide, greigite (Fe_3S_4) (ref. 3). Particles from any given magnetotactic bacterial species or strain are of a specific mineral type with specific crystallographic parameters[2,3]. Thus, the biomineralization of the magnetosome mineral phase is a highly regulated process[2,3] probably directed and controlled at the gene level.

We are investigating magnetotactic bacteria from the Pettaquamscutt Estuary (Rhode Island), a chemically stratified semi-anaerobic basin[4], where the oxic–anoxic transition zone (OATZ) is in the water column because of the upward diffusion of hydrogen sulphide generated from bacterial sulphate reduction. At least seven different morphologically distinct magnetotactic forms exist in 'plates' together with other bacterial types at or close to the OATZ. Populations of one of these, a morphologically distinct, elliptically shaped organism (about 3.1 × 1.3 μm) were as high as 2×10^5 cells ml^{-1} at the OATZ and also existed in the anoxic zone below the OATZ. Cells of this organism usually contained a double chain of an average of 37 magnetosomes. Particles within the same chain had two different morphologies: arrowhead-shaped (about 76 × 38 nm); and roughly rectangular (about 64 × 49 nm) (*a* and *b* in Fig. 1, respectively).

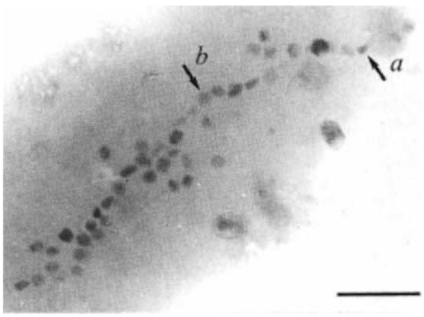

FIG. 1 Electron micrograph of a magnetosome chain within a single magnetotactic bacterial cell containing particles of arrowhead-shaped (*a*) and rectangular (*b*) morphologies. Arrows, particles from which the electron diffraction patterns shown in Fig. 2 were obtained. Scale bar, 500 nm.

We used energy dispersive X-ray analyses to show that arrowhead-shaped and rectangular particles consist of iron and oxygen and iron and sulphur, respectively. Single-crystal electron diffraction patterns of the arrowhead-shaped and rectangular particles (Fig. 2) are consistent with the face-centred-cubic spinel minerals magnetite and greigite, respectively. The magnetite particles were elongated along the <111> crystallographic axis and terminated at one end with a well-defined {111} face, whereas the greigite particles were elongated along the <100> axis and terminated with two well-defined {100} faces.

The organism described here is unique among magnetotactic bacteria in that it contains both magnetite and greigite in the same cell. This finding is important to the understanding of the biomineralization process(es) that occur in magnetotactic bacteria. Both crystal types are positioned within the same chain(s), are mineralized with consistently specific sizes and crystallographic parameters, and have their long axes oriented along the chain direction. Because the two crystal types have different crystallographic parameters that have been observed for particles in other magnetotactic bacteria with single component chains[3,5], and different crystallographic orientations with respect to the chain, it is likely that they are produced by two separate biomineralization processes[6] controlled by separate sets of genes. The organism described here seems to have both sets of genes, whereas other magnetotactic bacteria have only one set.

The large numbers of the bacterium described here could have a significant impact on iron cycling at the OATZ and in the anoxic zone, and could contribute to the deposition of both fine-grained magnetite and greigite that, in turn, contribute to the remanent magnetization of sediments.

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