Experimental report

24/05/2022

Proposal: 5-32-887 **Council:** 4/2019

Title: Revealing the configuration of themagnetosome chains within magnetotactic bacteria

Research area: Physics

This proposal is a new proposal

Main proposer: Lourdes MARCANO

Experimental team: Lourdes MARCANO
David GANDIA
Elizabeth MARTIN JEFREMOVAS
Dirk HONECKER

Local contacts: Robert CUBITT

Samples: Bacterial colloid AMB-1 in D2O
Bacterial colloid MV-1 in water
Bacterial colloid MV-1 in D2O
Bacterial colloid AMB-1 in water
Fe3O4 magnetosomes in D2O (AMB-1)
Fe3O4 magnetosomes in D2O (MV-1)

Instrument	Requested days	Allocated days	From	To
D33	7	7	30/09/2019	07/10/2019

Abstract:

Magnetotactic bacteria are microorganisms that can align in and navigate along geomagnetic field lines. This is due to the fact that magnetotactic bacteria biomineralize magnetite nanoparticles, called magnetosomes, arranged in a chain. The chain configuration is strongly affected by the magnetic anisotropy of the magnetosome. In this proposal we will work with two species that synthesize magnetosomes with different morphology: Magnetospirillum magneticum, which synthesize slightly elongated cubooctahedral magnetosomes arrange in 3-5 subchains, and Magnetovibrio blakemorei, which produce hexaoctahedral shaped (35×35×53 nm) magnetosomes arranged in a single chain. Such different morphologies lead to important changes in the vectorial distribution of the magnetic moments. In this experiment we plan to perform spin-resolved small angle neutron scattering at the SANS instrument D33 on isolated magnetosomes and the bacterial colloids of the two different bacterial species. It will allow us to reveal the chain arrangement in these bacterial species, which will help to transfer the knowledge to other magnetotactic strains.

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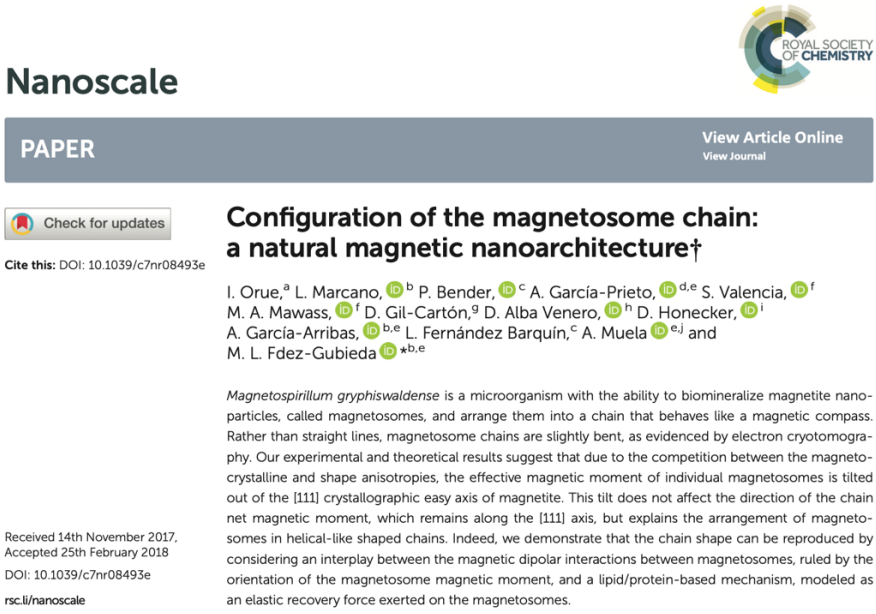
The main outcome of this experiment has been published in [1]. A summary of the information concerning SANS experiments at D33 is summarised briefly in Figures 1, 2 and 3.



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Configuration of the magnetosome chain: a natural magnetic nanoarchitecture†

I. Orue,[a] L. Marcano, [b] P. Bender, [c] A. García-Prieto, [d,e] S. Valencia, [f] M. A. Mawass, [f] D. Gil-Cartón,[g] D. Alba Venero, [h] D. Honecker, [i] A. García-Arribas, [b,e] L. Fernández Barquín,[c] A. Muela [e,j] and M. L. Fdez-Gubieda [*b,e]

Magnetospirillum gryphiswaldense is a microorganism with the ability to biomineralize magnetite nanoparticles, called magnetosomes, and arrange them into a chain that behaves like a magnetic compass. Rather than straight lines, magnetosome chains are slightly bent, as evidenced by electron cryotomography. Our experimental and theoretical results suggest that due to the competition between the magnetocrystalline and shape anisotropies, the effective magnetic moment of individual magnetosomes is tilted out of the [111] crystallographic easy axis of magnetite. This tilt does not affect the direction of the chain net magnetic moment, which remains along the [111] axis, but explains the arrangement of magnetosomes in helical-like shaped chains. Indeed, we demonstrate that the chain shape can be reproduced by considering an interplay between the magnetic dipolar interactions between magnetosomes, ruled by the orientation of the magnetosome magnetic moment, and a lipid/protein-based mechanism, modeled as an elastic recovery force exerted on the magnetosomes.

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Fig. 1. Abstract of results gathered in magnetosome chain of magnetotactic bacteria.

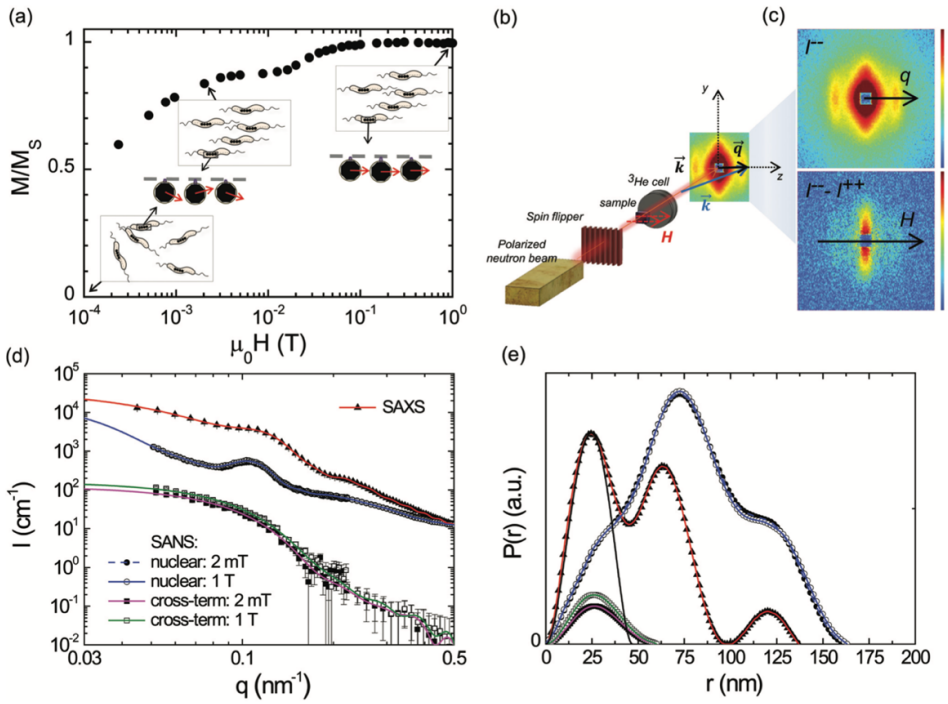

Fig. 2 Magnetic state of the colloidal dispersion of bacteria. (a) Magnetization curve of the colloid. The field axis is in logarithmic scale to magnify the low-field region. The sketches display the two-step magnetization process. The experimental data marked with arrows correspond to the points measured by SANS/SAXS ($\mu_0 H$ = 0 mT;2 mT; and 1 T). (b) Schematic representation of the SANS experiment. The polarized incoming neutron beam can be set to either parallel (+) or antiparallel (–) to the applied field by means of an RF spin flipper. The ^{3}He cell discriminates the polarization of the scattered neutrons (+ or –), hence the recorded intensity is either I^{++} or I^{--}, where superindexes refer to the polarization of the incoming/scattered neutrons. (c) 2D SANS scattering patterns for $\mu_0 H$ = 2 mT. Top: I^{--}; bottom: $I^{--} - I^{++}$. (d) 1D scattering intensities measured by SAXS in zero field (radial average, offset by scale factor 100) and the field dependent nuclear scattering intensities $I_{nuc}(q)$ (offset by scale factor 10) as well as the cross-terms $I_{cross}(q)$ determined by polarized SANS. The lines are the corresponding fits by an indirect Fourier transform. (e) Pair distance distribution functions $P(r)$ determined by an indirect Fourier transform of the 1D scattering intensities from (d). The black line is the $P(r)$ of a homogeneous sphere with diameter D_{SAS} = 48 nm. The distribution function determined by SAXS is offset by arbitrary scaling factors.

Fig. 2. Main SANS results and analysis by IFT.

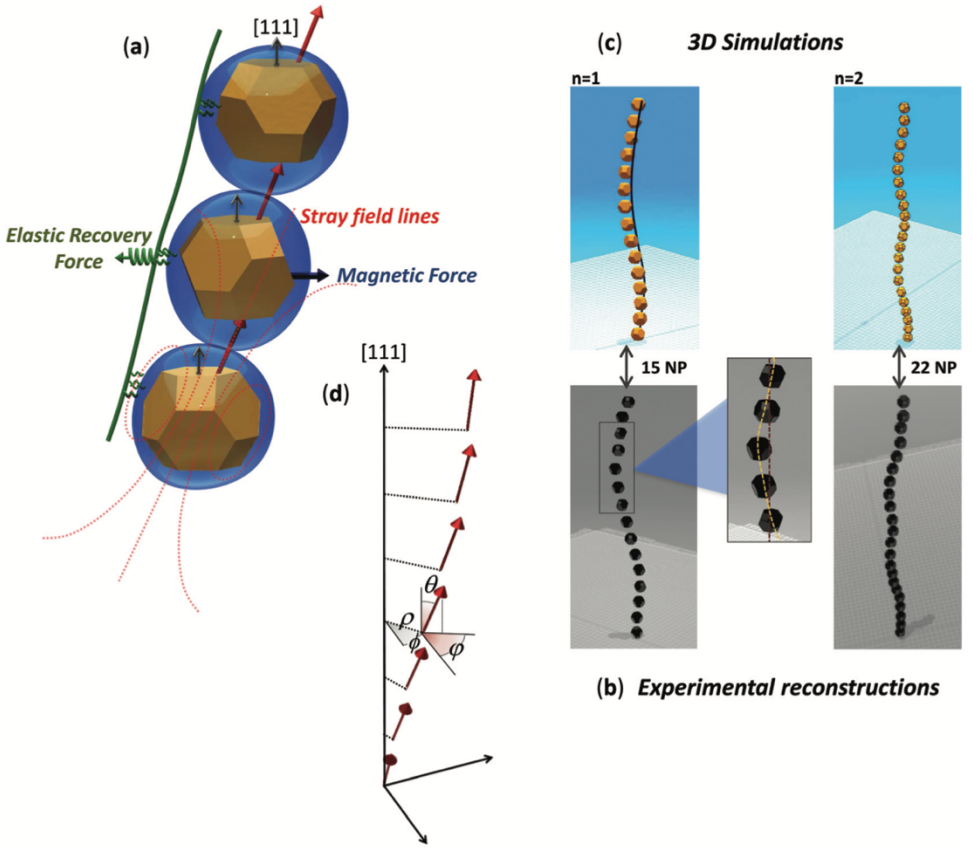

Fig. 5 Equilibrium configuration of the magnetosome chain. (a) Schematic representation of two competing mechanisms: magnetic force pushing to align magnetosome magnetic moments along the stray field lines from neighboring particles, and lipid/protein-based mechanism modeled as an elastic recovery force acting perpendicularly to the chain axis, where the chain axis is the [111] crystallographic direction along which magnetosomes align, as highlighted in the figure. (b) Experimental reconstructions obtained from ECT imaging of the magnetosome chains shown in Fig. 1a and b. A zoom-in of the first magnetosome chain reconstruction highlights the deviation from a straight line. (c) Two stable solutions for the chain patterns obtained as explained in the text. A potential filament has been drawn as a guide for the eye. A video of the experimental reconstruction of the chain on the left (chain (a) in Fig. 1) together with the corresponding simulated chain viewed from different perspectives can be found in the ESI (movie S3†). (d) Schematic representation of the magnetic dipoles and the three independent variables used in the simulation: radial (ρ) and azimuthal (ϕ) coordinates for the magnetosome positions, and azimuthal orientation (φ) of the magnetic dipoles. θ is the polar angle of the magnetic dipoles, fixed to 20°.

Fig. 3. (Labelled in article as Fig. 5). Configuration of magnetosome chain.

References

[1] I. Orue et al., "Configuration of the magnetosome chain: a natural magnetic nanoarchitecture." *Nanoscale* 10, 7407 (2018).