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Magnetization processes in magnetotactic bacteria systems

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Abstract

In low fields, the magnetization of magnetotactic bacteria (MTB) culture is affected by chemotaxis and can be described by the Langevin function which depends on magnetic field strength and chemotaxis energy. In moderate fields, bacteria magnetization switching occurs as the second-order phase transition induced by increasing the field applied opposite the MTB magnetic moments. For bacteria containing one or two chains of magnetosomes we calculated the switching field as a function of the gap between magnetic particles.

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Magnetic properties of magnetotactic bacteria (bacteria containing intercellular magnetite or iron sulfide greigite particles) have been a subject of growing interest in recent years [1–4]. These types of micro-organisms are promising for practical use, such as in the process of continuous radionuclide recovery or heavy metal adsorption. The study of chemotaxis-exhibiting magnetic bacteria is also quite important because (i) they represent a new example of magnetic system which is also affected by non-magnetic interaction. The bacteria's orientation is also governed by their chemical environment; (ii) it is possible to predict MTB motion by applying magnetic fields of different orientation and combining it with a proper chemotactic gradient. Chemotaxis is present in many other biological processes, such as embryonic development, migration of white blood cells to the sites of infection, and formation of new blood vessels [5]. We assume that chemotaxis in bacteria leads to their orientation relative to a chemotactic gradient by a series of motions for example exerted by means of flagella rotation. The alternating flagella's modes of "run" and "tumble" enable the cell to recognize different chemical environments and allow bacteria to turn and move towards the direction of a chemotactic gradient. A theory on this phenomenon was recently suggested [6].

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In view of the both important potential applications and theoretical interest, we have developed a model to describe magnetization processes in magnetotactic bacteria (MTB) culture with regard to chemotactic effects. This paper is also aimed at the description of magnetic chain switching in magnetic fields directed opposite to the chain magnetization. To calculate the switching field for a bacterium consisting of one or two magnetic particle chains we apply the chain-of-sphere model suggested in Ref. [7].

Firstly, let us describe the low field region in which magnetization of MTB culture could be influenced by chemotaxis. So, here considering magnetization processes in the MTB system we take into account chemotaxis—the response of cells to chemical stimuli by orientation and movement in the direction of chemotactic gradient. Thus, in the presence of the stimuli gradient the preferable direction in the bacteria's orientation appears. Since the interbacteria interaction is insignificant for any real interbacteria spacing [3], one can neglect this interaction and consider a MTB system as ideal gas of magnetic moments affected by unidirectional chemotaxis anisotropy. It was suggested in Ref. [8] to describe the chemotaxis anisotropy energy as $E_{an} = c_{ch} W_{ch} \cos\varphi$, where c_{ch} is a numerical coefficient which is proportional to the gradient of chemotactans concentration, W_{ch} is the chemotaxis energy defined in Ref. [8] and φ is the angle between the bacterial magnetic moment and the chemotactic gradient. Using the above definition of the chemotaxis energy it is possible to quantitatively describe the bacteria's ability to orient themselves along the gradient of chemotactans concentration.

If the applied magnetic field is parallel to the chemotactic gradient the normalized MTB culture magnetization is

$$m = \frac{\langle M \rangle}{M_{S0}} = \mathrm{cth}\left(\frac{\mu_0 p_{mb} H - W_{ch}}{k_B T}\right) - \frac{k_B T}{\mu_0 p_{mb} H - W_{ch}}, \quad (1)$$

where p_{mb} is the bacterium magnetic moment, H is the applied magnetic field strength, k_B is the Boltzman constant, M_{S0} is the saturation magnetization of the MTB culture, T is the temperature, μ_0 is the free-space permeability. Depending on the type of microorganisms the magnetic moment varies in the range of 10^{-16}–10^{-14} Am^2 [2,9–13]. For different values of the ratio between the chemotaxis and thermal fluctuations energies, $w = W_{ch}/k_B T$ and $p_{mb} = 2.7 \times 10^{-16}$ Am^2 we calculated the magnetization curves of the MTB system (see Fig. 1).

The shown magnetization curves are equilibrium curves without any hysteresis. In Fig. 1 in the low field region, magnetization processes of MTB are characterized by the following distinctive features: (i) magnetization curves are shifted due to the chemotaxis energy contribution; (ii) the shift value is $H_0 = W_{ch}/\mu_0 p_{mbb}$; (iii) at $H \approx H_0$ the magnetic susceptibility of the MTB culture reaches its maximum; (iv) appearance of polarization by chemotaxis—non-zero magnetization at $H = 0$. The value of polarization by chemotaxis, $m(0)$ grows as the chemotaxis energy increases. On the basis of the obtained results by measurements of the magnetic susceptibility and remnant magnetization one can extract the chemotaxis energy and MTB concentration.

In moderate fields magnetization goes through the reversal of bacterial magnetic chains. In this section we describe the magnetization reversal processes in MTB culture consisting of elongated bacteria, each of them contains several magnetic

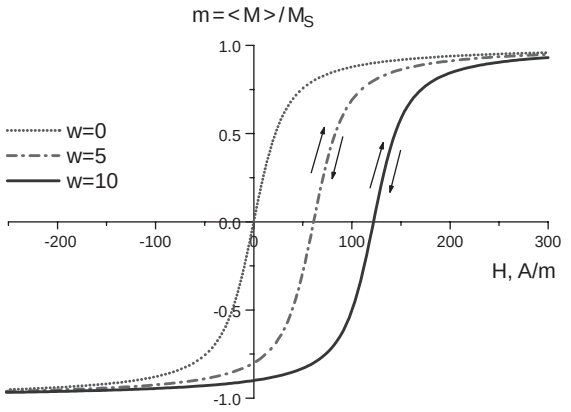

Fig. 1. Magnetization curves of MTB for different values of the chemotaxis energy.

nanoparticles inside. Our goal is to calculate the switching magnetic field. We apply the approach [7] to find the explicit dependence of the switching field on the gap value between bacteria magnetic particles.

Let us consider a chain of spherical magnetosomes in which magnetic particles of radius R are separated by a short distance δ, i.e. the period of the magnetosomes in the chain is $D = 2R + 2\delta$. The magnetosomes are connected by magnetic dipole–dipole interactions. We assume that the spherical uniformly magnetized particles have no crystal anisotropy. The external magnetic field is applied opposite to the direction of the chain's magnetic moment. For one chain it was shown in Ref. [7] that fanning in a plane is favored over any other arrangements of fanning with respect to the chain axis. So, it will be enough to treat a flat configuration of magnetic moments.

Firstly we consider a bacterium with one chain of magnetic particles inside. The total energy of a chain consisting of N dipoles is

$$W = \mu_0 p_m H \sum_{i=1}^{N} \cos\,\theta_i + \frac{\mu_0 p_m^2}{8\pi} \sum_{i\neq j}^{N} \frac{\cos\,\theta_{ij} - 3\,\cos\,\theta_i\,\cos\,\theta_j}{r_{ij}^3}, \quad (2)$$

where θ_i and θ_j are the angles between the applied magnetic film and a dipole, θ_{ij} and $r_{ij} = D(i-j)$ are the angle and distance between the i and j—dipoles in the chain, respectively; p_m is the magnetic moment of a magnetic particle, $p_m = 4\pi R^3 M_s/3$, M_s is the saturation magnetization of a nanoparticle. The normalized to $8\pi D^3/\mu_0 p_m^2$ total system energy is

$$\tilde{W} = 6\pi h\left(\frac{D}{R}\right)^3 \sum_{i=1}^{N} \cos\,\theta_i + \sum_{i\neq j}^{N} \frac{\cos(\theta_i - \theta_j) - 3\,\cos\,\theta_i\,\cos\,\theta_j}{(i-j)^3}, \quad (3)$$

where $h = H/M_s$. Now we assume the fanning mechanism [7,14] of the chain reorientation under the influence of the increasing opposite magnetic field. As it will be shown below the fanning magnetosomes reorientation is a more favorable reversal process than the coherent rotation of the particle magnetic moments. Also this mechanism could be relevant to describe the switching of the tree-like bundle of magnetosomes suggested in Ref. [4]. So, in this case depending on the dipole positions the angles varies as $\theta_i = (-1)^i\theta$ and $\theta_j = (-1)^j\theta$ (see Fig. 2). The dipole sum S can then be calculated as the second term in Eq. (3) for arbitrary numbers of N. The direct calculation gives

$$S = -c_1 - c_2\,\cos\,2\theta, \quad (4)$$

where c_1, and c_2 are numerical coefficients which depend on the total number of magnetosomes N. We calculated these coefficients for several particular cases (see Table 1). By inserting S into

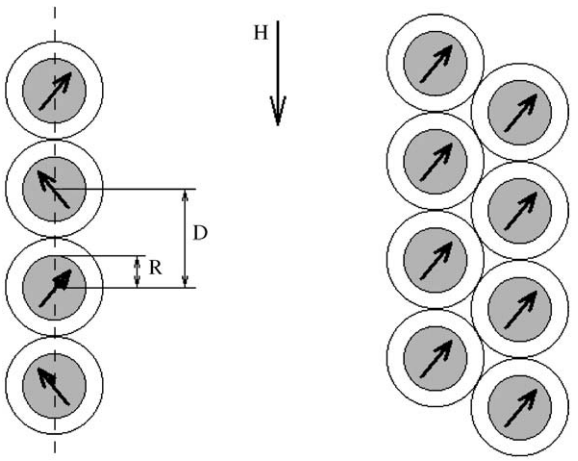

Fig. 2. Sketch of chains of magnetosomes in a rod-shaped magnetotactic bacteria.

Table 1
Numerical coefficients c_1 and c_2 for different numbers of magnetosomes, N

N	c_1	c_2
5	12.6128	5.2460
10	29.0443	12.6579
20	62.0508	27.6340
30	95.0907	42.6431
40	128.139	57.6604
50	161.19	72.6812

Eq. (3) one can arrive at

$$\tilde{W} = 6\pi h\left(\frac{D}{R}\right)^3 N\ \cos\ \theta - c_1 - c_2\ \cos\ 2\theta. \qquad (5)$$

Let us analyze the angular dependence of the dipolar and total energies in this equation. It is obvious that the dipolar term (S) has the two minimums at $\theta = 0$ and $\theta = \pi$ which correspond two opposite magnetic dipole orientations in the chain. These minimums are separated by the barrier which corresponds to $\theta = \pm\pi/2$. Note, if one considers the coherent rotation of the chain's moments the barrier value will be much higher because, for perpendicular orientation ($\theta = +\pi/2$ for the all moments), the magnetostatic poles energy is larger than for the opposite oriented neighboring dipoles. For non-zero magnetic field the total energy shows the two minimums separated by the barrier, too. However, increasing field leads to a decrease in the value barrier and its shifting towards the minimum at $\theta = 0$. Note, there are no equilibrium states if $\theta \neq 0$ or $\theta \neq \pi/2$. Thus, as the external magnetic field increases from $h = 0$ the system becomes metastable. The chain switches to the field direction when the barrier (maximum) disappears. The conditions for such instability are $dW/d\theta = 0$ and $d^2W/d\theta^2 = 0$. To calculate the switching field we utilized both conditions and Eq. (5). By solution of the proper system of equations we obtain:

$$h_{sw} = \frac{c_2}{12\pi(1+\delta/R)^3 N} \qquad (6)$$

and $\theta = 0$. Thus, reaching $h = h_{sww}$ at $\theta = 0$ the chain suddenly loses its stability and switches to the field direction. This reorientation occurs like the second-order phase transition, similar to the instability of a loaded elastic rod [15]. Remarkably, the normalized switching field does not depend on the magnetic dipole moment of bacteria.

In Fig. 3 we show the normalized effective switching field as a function of δ/R (the gap between magnetic particles in a cell). In the frameworks of the chain-of-sphere model similar dependencies were numerically calculated in Refs. [4,16]. It is seen from Eq. (6) and Fig. 3 that if the gap is small enough, the switching field weakly

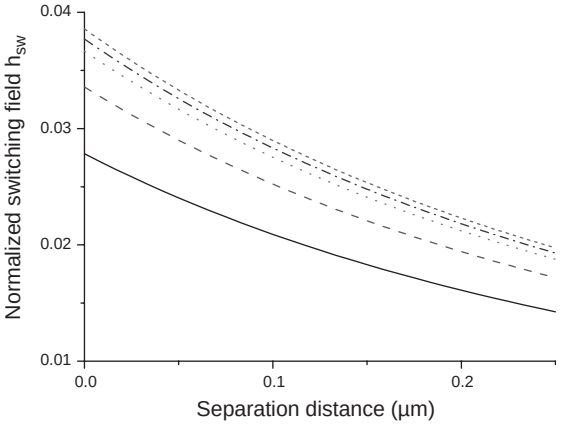

Fig. 3. Normalized switching field (H/M_s) as a function of the separation distance, $x = \delta/R$ calculated from Eq. (6). The curves from bottom to top correspond to $N = 5$, 10, 20, 30 and 50.

depends on the radius of the nanoparticle. For $\delta = 0$ the switching field does not depend on R, and this agrees with the results presented in Ref. [7]. Increasing the number of magnetic particles above $N = 50$ does not significantly change the switching field.

Now we consider the double chain of magnetosomes and calculate the switching field for such a system. It should be noted here: (i) the half period shifted chain (see Fig. 2) will minimize the dipole–dipole interaction energy; (ii) in such a double chain the coherent rotation of magnetic moments is a more favorable process than the symmetrical fanning reorientation. Assuming the coherent switching one can insert $\theta_i = \theta_j = \theta$ and $\theta_{ij} = 0$ into Eq. (2). Applying the above described method we calculated the swathing field as a function the separation distance for double chains of $N = 3$, 5 and 10. The results are shown in Fig. 4. From Fig. 4 one can see that for the double chain the switching field is sufficiently larger than that for a single chain of magnetosomes. However, for a triple chain one can expect lower values of the switching fields because in this case the symmetric fanning rotation is again a more energetically favorable process than the coherent rotation.

It should be noted that the above calculated switching field plays the role of the coercive force in ideal experimental conditions—initially, all

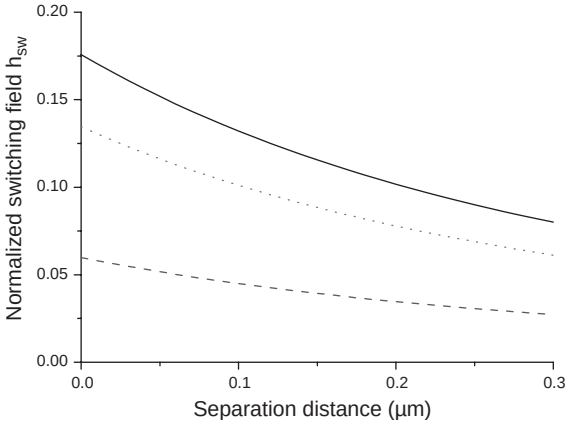

Fig. 4. Normalized switching field (H/M_s) as a function of the separation distance, $x = \delta/R$ calculated for double-chains. The curves from bottom to top correspond to $N = 2 \times 3$, 2×5, and 2×10.

MTBs are almost perfectly aligned parallel to the applied field and the field increases from $H = 0$ in the direction opposite to the chain magnetization. In a real case bacteria may somehow be distributed in their orientations with respect to the field. For an infinite chain of spheres the influence of uniaxial magnetocrystalline anisotropy of magnetic particles on the switching field and its dependence on the field angle was calculated in Ref. [14].

One of the new aspects of MTB behavior in magnetic fields is connected with the ability of magnetic chains to follow the direction of a rotating magnetic field. It was recently shown [17] that magnetic chains are able to synchronously rotate with the applied rotating magnetic field of low frequency. Following the rotating field the flexible magnetic chain has a bent shape below the critical frequency. On the basis of this phenomenon one can suggest a biomagnetic nano-motor—a rotating magnetotactic bacterium governed by rotating magnetic field of a proper frequency. In a capillary the rotating magnetic bacteria may act as propeller and create a stream to transport something small along the capillary. Of course, the shape of the rotating bacterium should be properly modified to be an effective propeller. The maximal power of such a motor is given by $BP\omega$ (where ω is the frequency of the rotating magnetic field, B is the magnetic field induction and P is the total magnetic moment of MTB which depends on its shape, e.g. for a straight bacteria $P \approx p_m N$, for a semicircle shaped bacteria $P = 2p_m N/\pi$. The maximal stream velocity which the motor can produce can then be calculated as

$$v \approx 2(PB\omega/\pi\rho l^2)^{1/3},$$

where l is the bacteria length, and ρ is the liquid density. It may also find applications in microfluid-dynamic devices.

In conclusion, a model allowing calculations of the MTB culture magnetization curves with regards to the effect of chemotaxis was proposed. In low-field magnetization processes chemotaxis manifests itself in the shift of the magnetization curves and appearance of MTB zero-field magnetization. Thus, in MTB systems one can detect magnetic polarization by chemotaxis. For elongated bacteria containing one chain of magnetosomes the explicit dependence of the switching field on the particles separation distance was deduced. Unified dependencies allowing estimations of the switching fields for bacteria with different number of magnetosomes (see Figs. 3 and 4) are given. It was shown that the switching field for a bacterium with a double chain of magnetosomes is sufficiently larger than that for a single chain bacterium.

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