Supplementary Information (SI) for Soft Matter.
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Supplemental Material

A brief introduction to the derivation of lifting force.

The formula for the lifting force induced by polymer solution was derived by Cao et al. in ref [1]. The critical procedure is the calculation of the stress tensor of the flow, modelled as a second-order fluid. The equation is given as follows:

$$\boldsymbol{\sigma} = \underbrace{-p_N\mathbf{I} + \eta_0\dot{\boldsymbol{\gamma}}}_{\text{Newtonian}} + \left(\frac{N_1}{2\eta_0}\frac{D}{D_t}p_N - \left(\frac{N_2}{2} + \frac{N_1}{8}\right)(\dot{\boldsymbol{\gamma}} : \dot{\boldsymbol{\gamma}})\right)\mathbf{I} - \frac{N_1}{2}\overset{\nabla}{\dot{\boldsymbol{\gamma}}} + N_2\dot{\boldsymbol{\gamma}}\cdot\dot{\boldsymbol{\gamma}}$$

where $\dot{\boldsymbol{\gamma}} = \nabla\boldsymbol{u} + \nabla\boldsymbol{u}^T$ and η_0 are the shear rate tensor and dynamic viscosity, respectively, $\boldsymbol{u}$ is the fluid velocity field, $\overset{\nabla}{\dot{\gamma}}$ is the upper-convected derivative of the shear rate tensor, and $\frac{D}{D_t}$ denotes the material derivative, p_N is the pressure, and N_1, N_2 are the first and second normal stress differences, respectively. With the Jeffrey and Onishi solution [2], Cal et al. computed the stress tensor and calculated the normal component on the surface of a rotating cylinder, obtaining the lifting force formula:

$$F_{lift} = \frac{2\pi DeR\omega\eta_0}{\left[\left(\frac{h}{R}\right)^2 - 1\right]^{3/2}}$$

In the calculation of lift force for bacteria, only the contribution of the flagellum bundle is considered, since the force on the cell body is negligible compared to that on the filament [1].

The velocity due to the non-Newtonian lift can be estimated as [1]:

$$u_{lift} = \frac{F_{lift}L}{\eta_0 C_b + \eta_N C_f}$$

This analytical formula is accurate at low *De* numbers compared to numerical simulations, but it still gave quite good results to interpret the data of Cao et al. at high *De* numbers [1]. Thus, we used this formula to characterize the non-Newtonian lift effect in our simulation. The parameters are demonstrated in the following sections.

The rheological properties of CMC solutions.

The solution of CMC is a typical shear-thinning solution that has been widely used in various studies. Its rheological properties depend on the concentration and molecular

weight. We used CMC with a molecular weight of 700k purchased from Sigma-Aldrich in this study and performed our experiments in 500, 1000, and 1700 ppm solutions, which is far below the overlapping concentration (10^4 ppm) for this molecular weight [3]. Within this range, the thixotropic degree of the solutions is very weak, as reported previously [3].

The fluid shear viscosity covering our concentration range has been measured in several studies [4, 5]. In the shear rate range of 1-20 s^{-1}, the solutions exhibit relatively weak shear-thinning behavior, and viscosity decreases more quickly at higher shear rates [4, 5]. The shear-thinning effect is included in our simulation, where we used the low shear-rate viscosity η_0 for the cell body and viscosity of the Newtonian solvent fluid $\eta_N = 10^{-3}$ Pa·s for the filament at high shear rate. As for the first normal stress difference, the stress remains constant at low shear rates (<100 s^{-1}) and increases at high shear rates [4].

Parameters in the simulation

We conducted two sets of simulations in linear gradient with slope at 20 nM/μm and average concentration at 10 μM; the results are shown in Fig. 4. The parameters for the intrinsic swimming behavior of the bacteria in different solutions are based on the data we measured in our experiments, such as run speeds, rotational diffusion coefficients, and the gamma distribution of the tumble angle (Fig. S3). These parameters are shown in Table S1.

For the simulations without hydrodynamic effects, the dipole strength $\alpha = 0$ and rotlet strength $\gamma = 0$ are used. To introduce the hydrodynamic effect, in motility buffer α = 3.05 $\mu m^3/s$ and γ = 2.87 $\mu m^4/s$, and the lifting factor u is set to 0. The value of γ is estimated with the rotlet dipole formula, assuming the angle between the bacteria and the surface is 0 and h = 0.5 μm. Consequently, we can get $R = (32vh^4)/(3|\gamma|(1 - \Gamma))$, and the curvature $1/R$ is measured in our experiment. It should be noted that the value we used for α is searched in parameter space to match the experimental and simulation results in motility medium, which is much smaller than the estimation in previous research [6], probably due to the oversimplification of the far-field theory. In the viscoelastic buffer, i.e., motility buffer with 1700 ppm CMC, α and γ are scaled by a factor $\varepsilon = 0.6$. The lifting factor u is estimated with the following formula [1]:

$$u = \frac{2\pi DeR\omega\eta_0 L}{\eta_0 C_b + \eta_N C_f}, \qquad [1]$$

where the flagellar drag coefficient, denoted as C_f, is defined[1] as:

$$C_f = L\left(f_\perp - \frac{\sin^2(\vartheta)(f_\perp - f_\parallel)}{2}\right), \quad [2]$$

and C_b stands for the viscous drag coefficient along the minor axis of the cell body:

$$C_b = \frac{8\pi a}{\mathrm{In}(2a/b) + 1/2}. \quad [3]$$

In the above equations, $f_\parallel$ and $f_\perp$ represent the geometric resistive coefficients of a slender filament parrel and perpendicular to the axis, respectively [7]:

$$f_\parallel \approx \frac{2\pi}{\mathrm{In}(L/r) - 1/2}, f_\perp \approx \frac{2\pi}{\mathrm{In}(L/r) + 1/2}. \quad [4]$$

Interpretation and value of each parameter in the formulas are listed in the Table S3. Substituting Eqs. [2], [3], and [4] into Eq. [1], we obtain u = 2617 μm/s. All the parameters we used are listed in Table S2.

Supplemental References:

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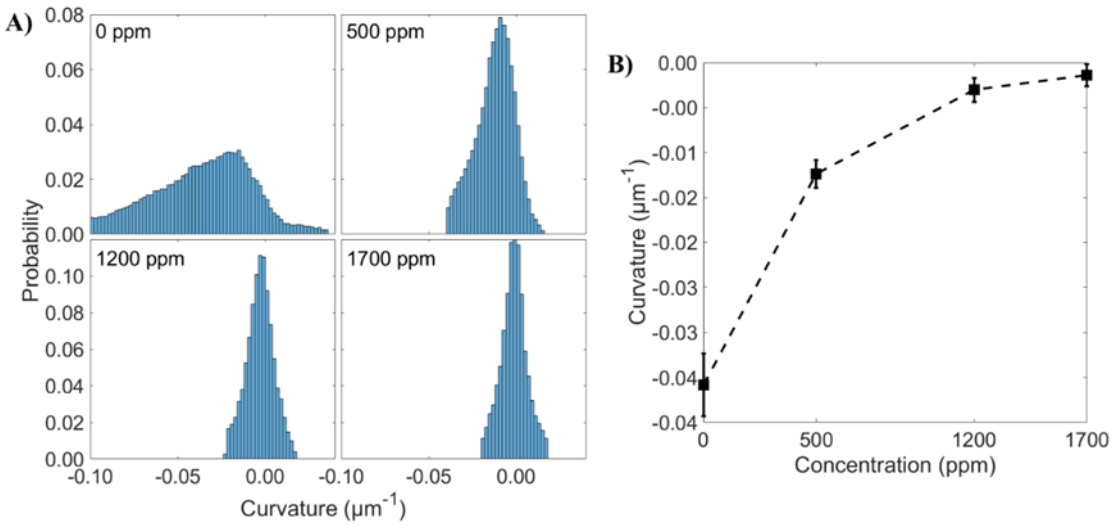

Fig. S1. (A) The probability distribution of the curvature of cell trajectories on a surface under varying concentrations of CMC solutions. (B) The mean curvature in various concentrations of CMC solutions. The presence of a negative (or positive) sign of curvature denotes a clockwise (or counterclockwise) direction of circular motion. The dotted lines function as visual aids, and the error bars indicate the standard errors. The number of videos and tracks was a minimum of 35 and 19,000, respectively.

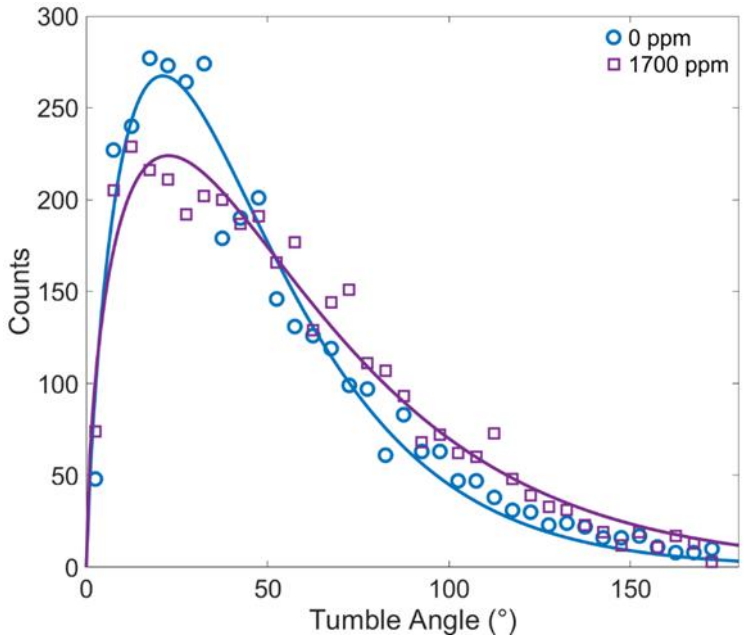

Fig. S2. The distributions of tumble angles were fitted using the Gamma function (solid lines), $\frac{c}{{g_b}^{g_a}\Gamma(g_a)} x^{g_a-1}e^{-x/g_b}$. The fitting parameters are displayed in Table S1. The dataset consisted of a minimum of 91 videos and 1,200 tracks.

Table S1. The parameters used for simulations in different concentrations of CMC solutions.

Buffers (ppm)	Run speed (μm/s)	Rotational diffusion (rad^2/s)	Tumble Angle (°)	Angle distribution[a]	Run length (s)	Tumble length (s)	Curvature (μm^{-1})
0	24.3 ± 0.7	0.025	49.6 ± 4.0	g_a=1.82 g_b=25.87	1.43 ± 0.15	0.21 ± 0.01	-0.0359 ± 0.0035
500	29.5 ± 1.0	0.013	51.8 ± 3.9	g_a=1.68 g_b=31.17	1.46 ± 0.14	0.20 ± 0.01	-0.0124 ± 0.0016
1200	29.0 ± 1.1	0.015	55.9 ± 4.2	g_a=1.72 g_b=34.43	1.23 ± 0.13	0.19 ± 0.01	-0.0030 ± 0.0013
1700	27.1 ± 1.1	0.013	55.6 ± 4.1	g_a=1.60 g_b=37.63	1.22 ± 0.12	0.19 ± 0.01	-0.0014 ± 0.0012

Note: [a]The fitted parameters of the tumble angle distribution obtained by Gamma function fitting, $\frac{c}{g_b{}^{g_a}\Gamma(g_a)} x^{g_a-1} e^{-x/g_b}$. Errors are SEM.

Table S2. The parameters used in simulation

	Without hydrodynamic effects		With hydrodynamic effects	
	Motility buffer	Buffer with 1700 ppm CMC	Motility buffer	Buffer with 1700 ppm CMC
Bacteria intrinsic swimming behaviors	Parameters measured in experiments (Table S1) were used: Run speed, rotational diffusion, angle distribution, run length.			
Dipole strength	α=0 μm^3/s, γ=0 μm^4/s		α=3.05 μm^3/s γ=2.87 μm^4/s	α=0.6*3.05 μm^3/s γ=0.6*2.87 μm^4/s
Lifting factor	u=0	u=0	u=0	u=2617 μm/s

Table S3. The parameters to estimate lifting factor *u*

Parameter	Description	Value
L	Contour length of flagellum	10 μm[8]
r	Radius of flagellum	20 nm[9]
R	Helix radius of flagellum	0.175μm[10]
ω	Rotation speed of flagellum	100 Hz[11]
ϑ	Helical angle of flagellum	25.5°[10]
De=$\lambda\omega$	Deborah number, λ is the relaxation time	λ ~ 0.4 s[12]
a	Semi major length of cell body	1.5 μm
b	Semi minor length of cell body	0.5 μm
η_0	Viscosity at low shear rate	~50 mPa·s[12]
η_N	The viscosity experienced by flagella.	1 mPa·s[13]