Nucleation of rotating crystals by *Thiovulum majus* bacteria

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Abstract

*Thiovulum majus* self-organize on glass surfaces into active two-dimensional crystals of rotating cells. Unlike classical crystals, these bacterial crystallites continuously rotate and reorganize as the power of rotating cells is dissipated by the surrounding flow. In this article, we describe the earliest stage of crystallization, the attraction of two bacteria into a hydrodynamically-bound dimer. This process occurs in three steps. First a free-swimming cell collides with the wall and becomes hydrodynamically bound to the two-dimensional surface. We present a simple model to understand how viscous forces localize cells near the chamber walls. Next, the cell diffuses over the surface for an average of 63 ± 6 s before escaping to the bulk fluid. The diffusion coefficient $D_{\text{eff}} = 7.98 \pm 0.1 \text{ } \mu \text{m}^2 \text{ } \text{s}^{-1}$ of these 8.5 \( \mu \text{m} \) diameter cells corresponds to a temperature of $4.16 \pm 0.05 \times 10^4 \text{ } \text{K}$, and thus cannot be explained by equilibrium fluctuations. Finally, two cells coalesce into a rotating dimer when the convergent flow created by each cell overwhelms their active Brownian motion. This occurs when cells diffuse to within a distance of $13.3 \pm 0.2 \mu \text{m}$ of each other.

1. Introduction

*Thiovulum majus* [1–3] is one of the fastest-swimming bacteria in the world, reaching speeds of up to 600 \( \mu \text{m} \text{ } \text{s}^{-1} \) [4, 5]. As such, the physical basis of its motion, both individually [6–11] and collectively [12–18], is of interest from both biological and physical perspectives. When these bacteria are confined between a glass slide and cover slip, cells localize on the glass surfaces and self organize into active crystals composed of rotating cells (figure 1(a)), which spin and reorganize [19].

This phenomenon belongs to larger class [20] of active crystals. They form as a result of the flow (figure 1(b)) generated by a force near a no-slip surface [21]. The flow causes cells to aggregate near the surface [22] and pulls nearby cells together [20, 23]. As in other examples of active crystals [24–28] and fluids [29–40], the power of the rotating and swimming cells is dissipated by their large-scale motion [41–45].

We have previously published a paper [19] on the dynamics of bacterial crystals. Here we describe and analyze how 2D bacterial crystals nucleate. This is the only aim of this paper.

As shown in supplementary video 1 available online at stacks.iop.org/NJP/20/015007/mmedia, as cells localize [46, 47] on the glass surfaces they are pulled together to form a co-rotating pair [23], which we call a ‘dimer’. As more cells coalesce around the pair, the dimer grows into a crystallite (supplementary video S2 available online at stacks.iop.org/NJP/20/015007/mmedia), which may grow to hundreds bacteria. The set up of this experiment is identical to that described in our previous report [19].

By observing the dynamics for 15 min, we are able to observe almost 5000 cell trajectories, from which we extract robust statistics.

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2. Methods

Cell tracking and selection. To track the motion of individual cells bound to the surface, we must first identify isolated cells in each frame. We do this by identifying cells as brighter than the background. We only track cells when they are more than 5 cell diameters from any other. Matlab code for this algorithm is available from the authors upon request.

Next, we find the trajectories of cells from the cell positions identified in each frame. Given a mean speed of the cells 65.5 ± 0.1 μm s⁻¹, cells move approximately one quarter of a cell radius between frames. Thus, we track cells simply by identifying the nearest cells in sequential frames. This process identifies two types of behavior. The first (N = 559) are free-swimming cells that swim parallel to the surface and near enough to be partially in focus. A small number of these (N = 55) swim near enough to the surface that interactions with the surface cause them swim in circular paths [48]. The majority (N = 4812) of trajectories are bound cells of the type illustrated in figure 2.

Poincare section. To remove the precession of the cells from their net drift, we strobe the trajectories. We first calculate the cell orientation as θ = Im(log(vx + ivy)), where vx and vy are the instantaneous velocities in the x and y directions. Linear interpolation between measurements of θ provides the times {t₀, t₁, ...} at which θ(tₙ) = 0. We then linearly interpolate between measurements of the cell positions x and y, to find their strobed positions

\[
X_n = x(t_n) \quad \text{and} \quad Y_n = y(t_n)
\]

and velocities \(U_n^x = (X_n - X_{n-1})/(t_n - t_{n-1})\) and \(U_n^y = (Y_n - Y_{n-1})/(t_n - t_{n-1})\). The means of these distributions are slightly different, \(\langle U_n^x \rangle = 0.38 ± 0.16 \mu m s^{-1}\) and \(\langle U_n^y \rangle = 0.24 ± 0.14 \mu m s^{-1}\). Because the average drift velocity 0.45 ± 0.15 μm s⁻¹ is very small compared to the cell speed 65.5 ± 0.1 μm s⁻¹, we neglect this small drift in our analysis.
3. Results

3.1. Cells temporarily localize on chamber walls

We begin our analysis by measuring the rates at which cells become bound \([k_+]=5.1 \times 10^{-4} s^{-1}\) and escape \([k_-]=(1.6 \pm 0.4) \times 10^{-2} s^{-1}\). We conclude that the statistics of binding to and escape from the surface are both determined by Poisson processes with constant rates \(k_+\) and \(k_-\), respectively. Note that, because there are more free-swimming cells than bound cells, binding events occur more frequently than escape events. To find the rates at which a single cell binds or escapes, we first fit the waiting-time distributions (figure 3) to exponentials. We then divide these rates by the number of free-swimming and bound cells to find \(k_+\) and \(k_-\), respectively. We find \(k_+ = (5 \pm 1) \times 10^{-4} s^{-1}\) and \(k_- = (1.6 \pm 0.4) \times 10^{-2} s^{-1}\). Thus we conclude a free-swimming cell localizes near the chamber walls for an average of \(63 \pm 6\) s before escaping.

Let us consider a simplified system. Figure 2 shows a spherical cell of radius \(a = 4.25 \mu m\) swimming towards a surface at a distance \(\epsilon\). As the flagella are misaligned from surface normal by a small angle \(\phi\), there is a force \(F = f_0 \sin \phi\) that pushes the cell along the surface. In the limit of vanishing \(\epsilon\), viscous dissipation in the narrow gap between the cell and the surface is the dominant force. The resulting torque \(L \sim \alpha F = \alpha f_0 \sin \phi\) rolls the cell over the surface. Balancing this torque with the viscous torque [50] required to rotate a sphere parallel to a surface gives the deterministic equation of motion for \(\phi\). Linearizing, we get

![Figure 3. Histograms of waiting times between observations of (blue) free-swimming cells binding to the chamber wall and (red) bound cells escaping from the surface. Both are consistent with exponential distributions. Over the course a total of 15 min of observation, 442 free-swimming cells bound to the surface and 159 cells escaped.](image)

**Table 1. Important physical quantities and their typical values.**

| Variable | Meaning | Value | Reference |
|----------|---------|-------|-----------|
| \(a\)    | Cell radius | 4.25 \(\mu m\) | [4]       |
| \(U_0\)  | Swimming speed | 500 \(\mu m s^{-1}\) | [10]      |
| \(f_0\)  | Flagellar force | 40 \(pN\) | [19]      |
| \(\omega_0\) | Cell angular velocity variability | 5–96 \(s^{-1}\) | [19]      |
| \(n_b\)  | Concentration of bound cells | \(9 \times 10^5\) cells \(cm^{-2}\) |           |
| \(n_f\)  | Concentration of free cells | \(10^6\) cells \(cm^{-3}\) |           |
| \(k_+\)  | Rate cells bind to wall | \((5 \pm 1) \times 10^{-4} s^{-1}\) |           |
| \(k_-\)  | Rate cells escape from wall | \((1.6 \pm 0.4) \times 10^{-2} s^{-1}\) |           |
| \(\epsilon\) | Gap between cell and wall | 4.25–140 \(nm\) |           |
| \(K_0\)  | Rate cells orient normal to a surface | 44 \(\pm 12\) \(s^{-1}\) |           |
| \(\mu\)  | Water viscosity | \(8.8 \times 10^{-4}\) \(Pa s\) | [50]      |
| \(D_{0r}\) | Mean rotational diffusion coefficient | \(0.18 \pm 0.05\) \(rad^2 s^{-1}\) |           |
| \(D_{eff}\) | Mean diffusion coefficient | \(7.98 \pm 0.1\) \(\mu m^2 s^{-1}\) |           |
| \(r_c\)  | Distance at which diffusing cells dimerize | \(13.3 \pm 0.2 \mu m\) |           |
where $\mu$ is the viscosity of water. The dimensionless scale factor $M \approx (2/5) \log(a/\epsilon) + 0.3709$ is the ratio of the viscous torque on a rotating sphere near a wall to the torque in the absence of a wall [51, 52].

There is a single stable fixed point $\phi = 0$, corresponding to a cell swimming directly into the surface. Using the values provided in table 1, cell orientation moves to this fixed point with rate $K = f_0/8\pi M \mu a^2 = 44 \pm 12 \text{ s}^{-1}$.

### 3.2. Cell precession and diffusion

Figure 4 shows the trajectory of a bound cell over the chamber wall. Notice that there are two components to this motion. First, the cell precesses about its axis of rotation (into the page). We interpret this circular motion as arising from counter-rotation of the cell body and flagella near the no-slip boundary, which is known to cause bacteria to swim in circles near surfaces [48]. The second component of cell motion is drift over the chamber wall.

Figure 4(b) shows that cell orientation $\theta$ increases at a constant rate as the cell precesses in the positive sense. The angular velocity $\dot{\theta}$ of each individual cell is approximately constant in time, varying by a factor of only...
0.27 ± 0.19. However, we observe a wide distribution of precession rates between cells, ranging from −6.5 to 95 s−1 (95% confidence interval). This range of values is similar to the variability in the angular velocity of rotating cells 5–96 s−1 [19].

Next, we take a Poincare section [53] of the trajectories to separate the drift from the precession. The red points in figure 4 show the position \( (X_t, Y_t) \) of the cell at a series of times \( \{t_0, t_1, \ldots \} \) such that \( \theta(t_i) = 0 \). To characterize the drift we first measure the distribution of cell velocities. We define \( U^x_t = (X_t - X_{t-1})/(t_i - t_{i-1}) \) and \( U^y_t = (Y_t - Y_{t-1})/(t_i - t_{i-1}) \) as the instantaneous drift velocities. Figure 5(a) shows that the distribution of these velocities are very similar, indicating isotropic motion.

This distribution arises from the rotational diffusion of the cells. As the stochastic firing and misfiring of flagella [49] rotates the cell flagella away from the surface normal, the cell is pushed parallel to the surface (figure 2). We approximate this motion as rolling without slipping. The velocity \( U = 2\pi a\partial_\phi \dot{\phi} = -2\pi aK\phi \) is proportional to \( \phi \). This hypothesis implies that the observed velocity distribution is a simple rescaling of
distribution of \( \phi \),

\[
\langle U^2 \rangle = 4\pi^2 aK^2 \langle \dot{\phi}^2 \rangle.
\]

To find \( \langle \dot{\phi}^2 \rangle \), we return to the the simplified model of a single cell shown in figure 2. Adding random forces to the deterministic equation (1), we assume an Ornstein–Uhlenbeck process [54],

\[
d\phi = -K\dot{\phi}dt + \sqrt{D_\phi}dW,
\]

where \( D_\phi \) is the rotational diffusion coefficient and \( W \) is a Wiener process. The resulting distribution [54] of angles is normal with mean \( \langle \phi \rangle = 0 \) and variance

\[
\langle \dot{\phi}^2 \rangle = \frac{D_\phi}{2K}.
\]

From equation (2), the corresponding distribution of \( U \) is also normal, with variance

\[
\langle U^2 \rangle = 2\pi^2 a^2 KD_\phi.
\]

The measured variance of the velocity \( \langle U^2 \rangle = 2840 ± 10 \text{ \mu m}^2 \text{s}^{-2} \) corresponds to a rotational diffusion coefficient \( D_\phi = 0.18 ± 0.05 \text{ rad}^2 \text{s}^{-1} \). This value is consistent with the measured rotational diffusion coefficients of other microbes [49, 55].

Next, we consider the net effect of these velocity fluctuations on the motion of the cell. Figure 5, shows the fit of the mean square displacement of cells to the prediction of linear diffusion, \( \langle (X_t - X_0)^2 + (Y_t - Y_0)^2 \rangle = 4D_{\text{eff}} t_i \).

Each data point in figure 5(b) represents the average 100 measurements of displacement at a given time calculated from at least 50 different trajectories. Fitting these data to an arbitrary power law, we find the measured exponent \( p = 0.96 ± 0.01 \). The diffusion coefficient \( D_{\text{eff}} = 7.98 ± 0.1 \text{ \mu m}^2 \text{s}^{-1} \), corresponding to a temperature of \( T_{\text{eff}} = 6\pi D_{\text{eff}} \mu a/k_B = (4.16 ± 0.05) \times 10^{-4} \text{ K} \). More quickly spinning cells have lower effective temperatures.

This value of the diffusion coefficient allows us to estimate the critical angle \( \phi_c \) at which a cell escapes from the surface. The escape rate \( k_e = (1.6 ± 0.4) \times 10^{-2} \text{ s}^{-1} \) is necessarily the rate at which random fluctuations push \( \phi \) greater than \( \phi_c \). Thus,

\[
k_e \sim 2 \int_{\phi_c}^{\infty} \frac{K}{\sqrt{\pi D_\phi}} e^{-\frac{K^2}{4D_\phi}} d\phi.
\]

Using the values reported in table 1, the critical angle \( \phi_c = 10^\circ ± 2^\circ \). For reference \( \langle \dot{\phi}^2 \rangle^{1/2} = \sqrt{D_\phi/2K} = 2.7^2 ± 0.6^2 \). This value is similar to the critical angle predicted for \( E. coli \) [49].

### 3.3. Diffusing cells coalesce into dimers

Finally, we consider the fate of cells that are hydrodynamically bound to the chamber wall. Supplementary videos 1 and 3 available online at stacks.iop.org/NJP/20/015007/mmedia show the behaviors of two representative cells. Each shows a free-swimming cell colliding with the chamber wall and diffusing in two dimensions. In video S1, as the cell diffuses close to another, the attractive flow (figure 1(b)) created by each cell pulls them together into a co-rotating pair. We observed 470 cells joining 2D crystals and the formation of 81 dimers. However, in video S3, the cell escapes from the surface and returns to the bulk fluid. As shown in figure 3, cells escape into the bulk fluid at a constant rate.

If one bound cell approaches another, they are pulled into a dimer (supplementary video S1 available online at stacks.iop.org/NJP/20/015007/mmedia) or larger crystallite (supplementary video S2 available online at stacks.iop.org/NJP/20/015007/mmedia). The blue line in figure 6 shows the average distance between

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4 Alternatively, if one takes the distribution measured in figure 5(a) rather than a normal distribution, the estimated critical angle \( \phi_c = 16^\circ ± 4^\circ \) is slightly larger.
dimerizing pairs of cells in the second before they come into contact. Notice that once the cells are approximately \(m_1\) apart, they are rapidly pulled together. Dimerization occurs when cells diffuse within a critical distance of one another.

We begin by estimating this critical distance from the flow created by each cell and the typical velocity fluctuations. Approximating each cell as a point force of magnitude \(f_0 \approx 40\) pN, the radial component of the flow at a height \(a\) above the chamber wall decays asymptotically \([20, 21, 23]\)

\[
u_a(r) = -\frac{3a^3f_0r}{2\pi\mu(4a^2 + r^2)^{3/2}}.
\]

To estimate \(r_c\), we find the distance at which this flow is similar to the cells’ typical velocity fluctuation (figure 5(a)). Taking \(u_a(r_c) \sim \langle U^2 \rangle^{1/2} = 65.5 \pm 0.1\) \(\mu m s^{-1}\) and using the values in table 1, we expect \(r_c \approx 9\) \(\mu m\). Thus, hydrodynamic attraction between cells is only important when cells are separated by approximately one body length.

Let us use a simplified model to measure \(r_c\). Cells are pulled together instantly when they come within a distance \(r_c\), but otherwise diffuse without interacting. This simplification reduces dimer formation to first-passage problem \([56]\). The average distance \(r\) between two random walkers that dimerize at time \(t = t_c\) is

\[
r(t) = \begin{cases} r_c + \frac{16D_{\text{eff}}(t_c - t)}{2a} & \text{if } t < t_c, \\ 2a & \text{if } t > t_c, \end{cases}
\]

where \(D_{\text{eff}} = 7.98 \pm 0.1\) \(\mu m^2 s^{-1}\) is the mean diffusion coefficient of the cells. Fitting this model to the average trajectories of the dimerizing cells, we find \(r_c = 13.3 \pm 0.2\) \(\mu m\).

The average time \(\tau_c = 63 \pm 6\) s that a cell remains localized near a surface and its diffusion coefficient \(D_{\text{eff}}\) define a typical density of cells below which dimer formation is rare. Cells diffuse a typical distance \(\sim \sqrt{D_{\text{eff}}\tau_c} = 22 \pm 1\) \(\mu m\) before they escape to the bulk fluid. Thus, if the density of cells is less than \(n_c \sim (D_{\text{eff}}\tau_c)^{-1} = (2 \pm 0.16) \times 10^{-3}\) cells \(\mu m^{-2}\), cells will typically evaporate before condensing into a dimer.

4. Discussion

We have provided new observations and analysis of the formation of 2D crystals by the fast-swimming bacterium *T. majus*. We characterized the dynamics by which localized cells on the boundary coalesce into dimers. This is the first step in the formation of crystals. As we have not measured the thickness \(\epsilon\) of the gap between the cell and wall, this analysis relies only on the two-dimensional trajectories of cells. Future work should measure \(\epsilon\) directly.

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\(\text{Figure 6.}\) The distance (black points) between cells that dimerize at time \(t_c = 0\) decreases as the cells diffuse towards one another. Their average separation (blue line) is inconsistent with non-interacting diffusing spheres (dashed red line). The solid red line shows a one-parameter fit to equation (8). According to this approximation, cells diffuse together to a distance \(r_c = 13.3 \pm 0.2\) \(\mu m\) without interacting and are then pulled together instantaneously.

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\(5\) Consider two Brownian particles with positions \(r_1\) and \(r_2\) moving in \(d\) dimensions with diffusion coefficient \(D_{\text{eff}}\). The distance \(r = r_1 - r_2\) separating them changes as \(dr = 2\sqrt{D_{\text{eff}}} dw\). Thus \(\langle \|r\|^2 \rangle = 2d(tD_{\text{eff}}) t\).
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