Helicobacter pylori Couples Motility and Diffusion to Actively Create a Heterogeneous Complex Medium in Gastric Mucus

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Helicobacter pylori couples motility and diffusion to actively create a heterogeneous complex medium in gastric mucus

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Helicobacter pylori swims through mucus gel by generating ammonia that locally neutralizes the acidic gastric environment, turning nearby gel into a fluid pocket. The size of the fluid zone is important for determining the physics of motility: in a large zone swimming occurs as in a fluid through hydrodynamic principles, while in a very small zone motility could be strongly influenced by nonhydrodynamic cell-mucus interactions including chemistry and adhesion. Here we calculate the size of the fluid pocket. We model how swimming depends on the de-gelation range using a Taylor sheet swimming through a layer of Newtonian fluid bounded by a Brinkman fluid. Then we model how de-gelation range depends on swimming speed by considering advection-diffusion of ammonia exuded from a translating sphere. Self-consistency between both models determines the values of swimming speed and de-gelation range. We find that *H. pylori* swims through mucus as if unconfined, in a large pocket of Newtonian fluid.

Microorganisms often navigate complex media and geometries, including during infection and mammalian fertilization [1]. The effect of non-Newtonian environments [2–24] and geometrical confinement [25–34] have both been the subject of much research, including situations combining the two [35–37]. Usually, medium rheology and geometrical configuration are considered a background environment that microorganisms do not change during swimming [38]. Here, we address the active creation of heterogeneous geometries in complex environments by swimming microorganisms, during which geometry, medium response, diffusion, and motility couple to mutually influence each other. For example, *E. coli* can mechanically deplete polymer concentration near their fast-rotating flagella, decreasing the local viscosity [39]. In this paper we concentrate on another such example, the local chemical alteration of gastric mucus from gel to sol by *Helicobacter pylori* [40].

A $\sim$200μm gastric mucus layer forms a barrier between the acidic (pH 2) environment inside the stomach and the epithelial cells lining the stomach (Fig. 1) [41, 42]. At biological concentrations, the mucus is a gel at acidic pH, and a viscoelastic solution with little elasticity [43, 44] for pH > 4. *H. pylori* survives in the acidic stomach by using urease to convert ambient urea into basic ammonia, neutralizing the acid in its vicinity [42]. The same mechanism allows it to traverse the mucus: the neutralization elevates the pH, locally de-gelling the mucus into a solution that the bacterium can move through [40, 45]. We examine the dynamics of swimming through this mucus layer when a bacterium ($\sim$3μm cell body) is far away from the epithelial boundary.

Although Celli et al. [40] showed that *H. pylori* can de-gel surrounding mucus into a navigable viscous solution, their study left unresolved the correct physical picture of motility *in vivo*. In their *in vitro* experiments bacteria raised pH and induced de-gelling globally, but *in vivo*, global neutralization is unlikely and hence de-gelling must be localized. In this paper we address the size of this de-gelled region, which is important since it affects the physical mechanism of motility: if the de-gelled region is large, then the bacterium swims as in a viscous fluid using the principles of low-Reynolds number hydrodynamics, while if the de-gelled region is small, then motility may be controlled by contact interactions with the mucus and chemical kinetics of neutralization and de-gelation.

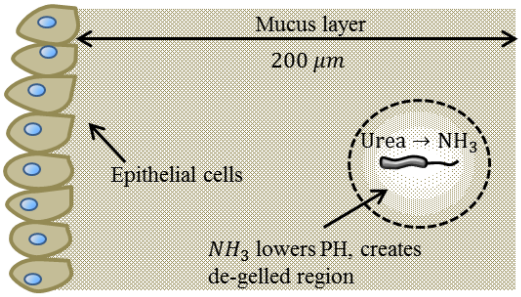

FIG. 1. *H. pylori* swims through the gastic mucus layer lining the stomach by locally neutralizing the acidic environment with ammonia, which de-gels the mucus into a fluid.

This scenario couples swimming hydrodynamics and chemical diffusion. First, we model how the swimming speed depends on the de-gelation range using an analytic hydrodynamic model of a Taylor sheet swimming by deformations through a layer of Newtonian fluid bounded by a Brinkman fluid. Second, we model how the de-gelation range depends on swimming speed by using an advection-diffusion model of ammonia exuded from a translating sphere. The coupled problem demands that both speed and neutralization range are in agreement for both models. We show that swimming occurs in a relatively large zone of Newtonian fluid, and that the assumptions within our approach are consistent with the result. We discuss whether recent artificial swimmers

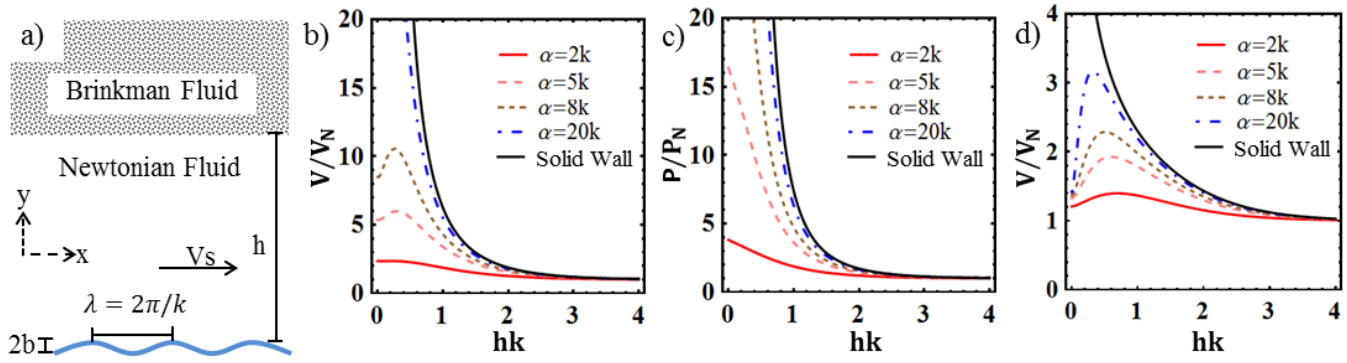

FIG. 2. a) Taylor swimming sheet in layer of Newtonian fluid of thickness h confined by Brinkman medium representing mucus gel. b) Swimming speed normalized by unconfined speed versus layer thickness h for constant stroke, porosity $\epsilon = 0.95$, and various values of resistance α. Solid black line is the result for a solid no-slip boundary at distance h. c) Power dissipated normalized by power dissipated by unconfined swimmer for cases plotted in (b). d) Swimming speed normalized by unconfined speed versus layer thickness h for constant power dissipation, porosity $\epsilon = 0.95$, and various values of resistance α.

mimicking *H. pylori's* neutralization strategy [46] may be in the same swimming regime as the bacteria.

Effect of local confinement by mucus on swimming. We consider a waving two-dimensional sheet in the frame of the sheet, so material points can be labeled by x (Fig. 2). Material points are displaced in the y-direction from $y = 0$ by the deformation $b\sin(kx - \omega t)$. The half-space above the sheet is a Newtonian fluid for $y < h$, and a Brinkman medium for $y > h$. Brinkman media are appropriate representations of dilute gels [5] (gastric mucus is $3 - 5\%$ w/v [45]) when the swimmer does not directly contact the gel, as in our case, and the gel network is not deformed by the swimmer [7].

The velocity field satisfies incompressibility ($\nabla \cdot \mathbf{v} = 0$) everywhere, Stokes equations in the Newtonian fluid, and

$$-\nabla p + \frac{\mu}{\epsilon}\nabla^2 \mathbf{v} - \frac{\mu\alpha^2}{\epsilon}(\mathbf{v} + \mathbf{V}_s) = 0 \qquad (1)$$

in the Brinkman fluid, where $\alpha = \sqrt{\epsilon/K}$ is the resistance, K is the permeability, and ϵ is the porosity (volume fraction of liquid) of the gel. We work in the frame of the sheet swimming with velocity $\mathbf{V}_s$, so $(\mathbf{v} + \mathbf{V}_s)$ is the velocity of the fluid relative to the gel network, which is stationary in the lab frame.

At the sheet surface we use no-slip boundary conditions, $\mathbf{v}(x, b\sin(kx - \omega t)) = -b\omega\cos(kx - \omega t)$. At the interface between the fluid and Brinkman medium, we use boundary conditions maintaining continuous velocity, $\mathbf{v}^-(x) = \mathbf{v}^+(x)$, where $\pm$ corresponds to the limit $y \to h$ from below $(-)$ or above $(+)$; and continuous traction, $[-\boldsymbol{I}(p^+ - p^-) + \mu(\epsilon^{-1}\nabla\mathbf{v}^+ - \nabla\mathbf{v}^-)] \cdot \hat{\mathbf{y}} = 0$, where $\boldsymbol{I}$ is the identity [47]. The full velocity field can be obtained from a boundary perturbation expansion in bk as in Taylor [48]. The swimming velocity is obtained by imposing the force-free condition on the swimmer [49].

In Fig. 2b, the swimming speed normalized by the unconfined (Newtonian) swimming speed V_N is plotted as a function of layer height h for various values of resistance α, constant values of porosity $\epsilon = 0.95$, and constant swimming stroke (ω, b, k constant). The effect of confinement by gel is only large when $hk < 1$, and is very small for $hk > 3$. We examine various limits to check the result. As $\alpha \to 0$, the Newtonian swimming speed is recovered. As $\alpha \to \infty$, the swimming speed confined by a solid boundary at distance h [50] is recovered (solid black line). Finally, as $h \to 0$, we recover the swimming speed of a sheet in a Brinkman medium [5], $V_s = \frac{1}{2}\omega k b^2\sqrt{1 + (\alpha/k)^2}$.

It is also interesting to examine the results for constant power. The expended power can be calculated by integrating the power per unit area at the swimmer surface [$\int \mathbf{v} \cdot \boldsymbol{\tau} \cdot \hat{\mathbf{n}}\, dA$ with $\boldsymbol{\tau}$ the stress tensor], or by the sum of power lost by viscous dissipation and the action of Darcy resistance on the fluid [$-\int \boldsymbol{\tau} \cdot \nabla\mathbf{v}\, dV + \frac{\mu\alpha^2}{\epsilon}\int(\mathbf{v} + \mathbf{V}_s) \cdot (\mathbf{v} + \mathbf{V}_s)\, dV$]. Agreement between the two methods provides an internal check on our results. The lowest order contribution to the power comes from the $\mathcal{O}(bk)$ velocity field and is shown in Fig. 2c. Power increases as the gap size h decreases. In the limit $h \to 0$, we obtain the power expended in a Brinkman medium, $\frac{1}{2}b^2\omega^2 k(1 + (\alpha/k)^2 + \sqrt{1 + (\alpha/k)^2})$, which agrees with a direct calculation of power expended by Taylor sheet in a Brinkman medium with no Newtonian layer [51]. The resulting swimming speed at constant power is plotted in Fig. 2d. In contrast to the constant stroke case, the swimming speed remains finite as $h \to 0$. However, in both cases the effect of confinement by gel is only large when $hk < 1$, and is very small for $hk > 3$.

Effect of swimming on size of local confinement. We examine the range of neutralization and de-gelling using a simplified model that treats the bacterium as a spherical body. Neutralization is controlled by a reaction-diffusion process involving urease, urea, ammo-

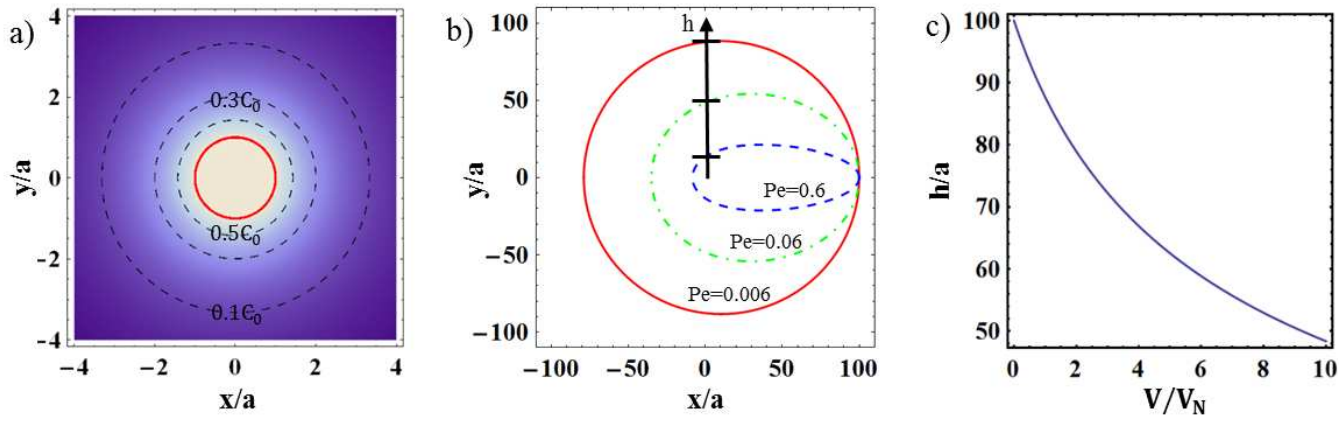

FIG. 3. a) Concentration profile due to diffusion near sphere in a uniform background flow in $+x$ direction for Pe = 0.006. C_0 is the concentration at the sphere surface. b) Contours of concentration $0.01C_0$ corresponding to de-gelation boundary for various Pe. We take the layer thickness for the confined sheet model from the distance in the y-direction (h) to the de-gelation boundary. c) De-gelation range h as a function of velocity, for the cell-parameters specified in the text.

nia, (bi)carbonate, and H^+. Urease may act within or be bound to the cell [42], and in any case urease and urea diffuse more slowly than protons or ammonia hence have less effect on the neutralization range. Thus we assume that the pH is controlled by the diffusion of ammonia through the aqueous de-gelled solution surrounding the cell, with the same diffusion constant as in water. We consider the diffusion of ammonia rather than H^+ since H^+ is supplied through the mucus and diffuses in mucus gel 4-10 times slower than in water [41]; however, using reasonably faster or slower diffusion constants does not change our conclusions [52]. Since *H. pylori* regulates the pH near its cell wall [42] (we assume a near-neutral pH 6), and the critical de-gelation pH is near 4 [40], we model the concentration of ammonia at the cell surface as a constant and at the boundary of the de-gelled region as decreased by a factor of 100.

The diffusion of ammonia is affected by the swimming flow of *H. pylori*, which we approximate as advection-diffusion from a stationary sphere in the presence of a uniform background flow at the swimming velocity. Although this flow captures the dominant effect of advection due to swimming translation, it differs from that of a force-free bacterium since it results in a net force on the sphere, but as discussed later, the difference does not affect our conclusions. Advection-diffusion is controlled by the Peclet number, $\mathrm{Pe} = 2aV_s/D$, which weighs the relative importance of advection to diffusion. We estimate a typical Peclet number of 0.006 from the thickness of *H. pylori* ($a = 0.5\mu$m), the Newtonian swimming speed ($V_s = 10\mu$m/s [53]), and the diffusion constant of ammonia in water ($D = 1.64 \times 10^{-9}$ m^2/s [54]); hence the concentration profile is dominated by diffusion. If the bacterium swims faster due to the effects of confinement, the Peclet number may increase. For small Peclet numbers (Pe < 1), the solution to this advection-diffusion problem was found via singular perturbation theory by Acrivos and Taylor [55], and we use their solution here.

In Fig. 3a we show contours of equal concentration near the sphere (surface concentration c_0) obtained from the Acrivos and Taylor solution for Pe = 0.006. In Fig. 3b we show the concentration contour $c_0/100$, which represents the boundary of the de-gelled region, for various Pe. As Pe increases (i.e., swimming velocity increases) the de-gelled region is swept into a narrower shape. The gap size h in our 2D swimming model is perpendicular to the traveling wave, so corresponds to the vertical distance from the sphere to de-gelled boundary. By varying the Peclet number, we deduce a de-gelation range $h^{A-D}(V_s)$ as a function of V_s (Fig. 3c).

Self-consistent estimate of range of de-gelation. Finally, we estimate the range of de-gelation for swimming *H. pylori* by demanding that the swimming speed and de-gelation range are consistent with both the hydrodynamical swimming calculation and the diffusion-advection calculation. Graphically, the swimming speed and gap size are determined by finding the intersection of plots of the hydrodynamic swiming speed $V_s^H(h)$ and $h^{A-D}(V_s)$ from diffusion-advection (Fig. 4). The unconfined speed of the swimming sheet is set to the observed swimming speed (10μm/s [53]) of *H. pylori* in buffer solution, and we assume the effect of confinement is the same as for a sheet. Since the pitch (P) of *H. pylori* flagella has not been measured we obtain the wavenumber $k = 2\pi/P$ from the value $P = 1.58\,\mu$m for *V. alginolyticus* [53]. The resulting de-gelation size is $h^* \approx 175/k$, or 44μm, much larger than the pitch or cell body. Therefore swimming occurs in the unconfined regime and is largely unaffected by the mucus gel surrounding the de-gelled region.

The result is also self-consistent with our assumptions. The bacterium is in a large region of dissolved mucin, so treating diffusion as in aqueous solution is appropri-

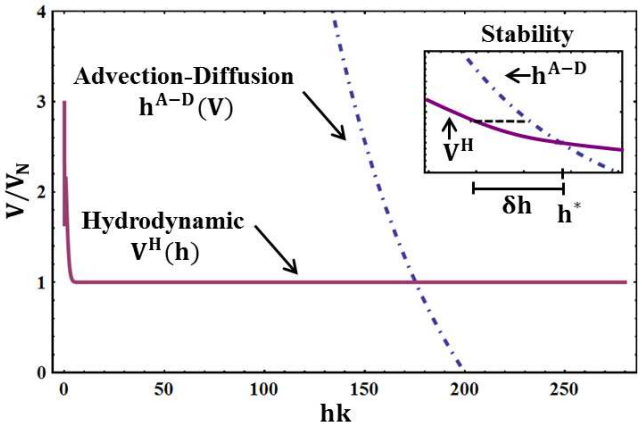

FIG. 4. Estimate of de-gelation range by simultaneous solution of hydrodynamic swimming and advection-diffusion models. The solution ($h^* = 175/k$, or 44 μm for parameters in text) is deep in the unconfined regime for all values of α at constant stroke or power. Inset: the solution is stable to perturbations; a fluctuation to $h = h^* - \delta h$ leads to velocity $V^H(h)$ with $h^{A-D}(V^H(h))$ closer to h^* (horizontal line).

ate. Since h^* is large, the swimming speed is close to the Newtonian speed and the Peclet number is small. Since the Peclet number is so small, the concentration profile is diffusion-dominated and the details of the velocity field (e.g., due to a force-free swimmer or non-spherical geometry) will not significantly affect the result. The effect of confinement on swimming speed was calculated for a 2D sheet rather than a 3D bacterium (although the observed speed of a 3D bacterium was used for the unconfined speed), but based on the effect of confinement by solid boundaries, we expect that taking into account helical flagellar geometry and finite length effects should make the swimming speed even closer to the unconfined speed (see supplemental materials for details [58]). Finally, since we are in the unconfined regime, the results are the same for constant stroke or constant power, and if one calculated the swimming speed by matching the torque exerted in the presence of confinement to the rotation-torque curve of a bacterial motor, one would find a swimming speed very close to the unconfined speed as well.

The self-consistent solution found in Fig. 4 is stable. Consider a fluctuation in size of the de-gelled region to $h = h^* - \delta h$. Then the resulting swimming velocity $V^H(h)$ is slightly larger than the self-consistent velocity (intersection of horizontal line in inset of Fig. 4 with hydrodynamic curve). Consequently the gap size $h^{A-D}(V^H(h))$ at the new swimming velocity is closer to h^* than the original fluctuation (intersection of horizontal line in inset of Fig. 4 with advection-diffusion curve). Repeating the process brings the swimming velocity and gap size back to the self-consistent point. In contrast, if near h^* the diffusive curve were less sloped in magnitude than the hydrodynamic curve, the self-consistent solution would be unstable by similar reasoning.

Discussion. Our calculation makes clear predictions: the size of the de-gelled region should be large compared to the size of the cell, the swimming speed of *H. pylori* through mucus gel should be close to that in Newtonian buffer, and the swimming should occur by the mechanisms of low-Reynolds number hydrodynamics. Future experiments may be able to measure the range of de-gelation and neutralization using microrheological bead tracking and pH-sensitive dyes, respectively, perhaps simultaneously observing swimming speeds and behavior in locally (rather than globally) de-gelled mucus.

We assumed that once the pH is raised above 4, the mucus is de-gelled, i.e., that de-gelation occurs on a fast time-scale relative to changes in pH. So far, experiments have not measured the de-gelation timescale of gastric mucus; in Celli *et al.* [40], experiments measuring the time-course of de-gelation were likely dominated by the kinetics of ammonia production rather than de-gelation. Experiments probing de-gelation timescales could be useful. For our assumption to be valid, de-gelation of a 10 μm layer of mucus should take much less than a second.

Recently, Walker *et al.* [46] have fabricated artificial magnetic propellers with surface-bound urease to mimic the motility strategy of *H. pylori* through mucus. In our calculation, the main difference between the artificial propeller and the bacterium is that in the advection-diffusion model the propeller generates a constant flux instead of a constant concentration at its surface. Based on the information provided in Ref. [46] we cannot quantitatively estimate the neutralization zone, but since they emphasize that swimming is only successful for very small acid concentrations, it is possible that the generated flux of ammonia is barely enough to locally neutralize the acid, implying a small neutralization zone. If the neutralization zone is small enough, propeller motility may be controlled by different physics (close-range mucus contact and chemistry) than *H. pylori* motility.

Here we considered the motility of a single bacterium rather than a group of bacteria. If multiple bacteria swim through mucus very close together, they may be effectively treated as a larger sphere in our advection-diffusion model, but if they are separated by intermediate distances richer phenomena may occur due to interaction effects from coupled advection and swimming.

The effects of confinement by mucus on a swimmer may also have application to bacteria or sperm swimming near, but not within, mucus in respiratory or reproductive tracts as well as the digestive tract. Our self-consistent approach could be applicable to other cases of motility with local alteration of the environment. For example, for flagella that mechanically deplete polymer solutions, the torque on the flagella is dependent on the depletion range and magnitude, while depletion is dependent on the torque via the rotation rate and geometry.

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