metric to quantify how much information was reflected in the paths. For wild-type bacteria the information in the trajectories is essentially constant across all tumble angles (and several gradients). However, if either the angle variance or the rotational diffusion is set to zero, distinct minima appear in the trajectory information appear at 0, 90, and 180 degrees - and there are broad maxima around 70 and 110 degrees. In simulations where both the angle variance and the rotational diffusion are set to zero, the trajectory information exhibits several more prominent minima, notably at 135, 60, and 45 degrees. We suggest that these minima arise because angles that are small integer fractions of 180 or 540 degrees increase the likelihood of backtracking - thus reducing the new space explored by the bacterium. When a bacterium does tumble, it should do so in a way as to explore as much new space as possible in order to optimize information gathering. Notably that is not 90 degrees, but one maximum is close to the normal tumble angle of 68 degrees for E. coli.

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Antibodies Change the Mechanics of Adhesion Fimbriae - a Case Study of CS20 Fimbriae Expressed by Enterotoxigenic Escherichia Coli

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Enterotoxigenic Escherichia coli (ETEC) express a variety of fimbriae that mediate adhesion to host epithelial cells. It has been shown that the ability of a fimbriated bacterial cell to attach and stay attached to host cells does not merely depend on the adhesin expressed distal of the fimbriae but also the biomechanical properties of the fimbriae are vital for sustained adhesion. Fimbriae can significantly extend under a constant force when exposed to an external force and therefore reduce the load on the adhesin, which is believed to help bacteria to withstand external forces applied by various body defense systems. Thus, it is thought that the fimbrial shaft and adhesin have co-evolved for optimal function when bacteria attach to host cells. To investigate if antibodies, normally found in the intestines, affects the biomechanical properties of fimbriae, we exposed CS20 fimbriae expressed by ETEC to anti-fimbrial antibodies and measured these properties using optical tweezers force spectroscopy. Our data show a change in the force required to extend the fimbriae and that the elasticity is significantly reduced by the presence of antibodies. The reduced elasticity, likely due to cross-linking of fimbrial subunits, could thus be another assignment for antibodies; in addition to their mission in marking bacteria as foreign, our data indicate that antibodies physically compromise fimbrial function. To further confirm interaction of antibodies to their specific target we performed western blot analysis, transmission electron microscopy and immunofluoresence microscopy. In the presence of antibodies, we suggest that our assay and results will be a starting point for further studies aimed at inhibiting bacterial adhesion by antibodies.

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Single Cell Dynamics Drive Turbulent Flow in the Collective Motion of Bacteria

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In most areas of biology, the principal confounding factor is the complexity. Biology from the cellular level to the ecosystem involves the action of a multitude of individuals that come together and achieve specific tasks. For example, at the single cell level, the binding and unbinding of cytoskeletal proteins conspire to allow a cell to move across surfaces or through the extracellular matrix. At the tissue level, these motile cells act together to heal wounds or form cancer metastases. Tissues come together to form organisms, which form societies, and so on. Here we use dense communities of swimming bacteria to understand how collective behavior arises out of the actions of an individual. At high density, rod-shaped bacteria produce complex fluid flows that include vortices and jets. These flows arise partially due to the dipole forces that each bacterium exerts on the surrounding fluid. By confining *Bacillus subtilis* or *Escherichia coli* within Hele-Shaw cells of controllable depth, we probe how individual biophysical parameters, such as shape, speed, external drag, and chemotaxis, affect the resulting collective behavior in this system. We then compare our results to predictions from a two-phase fluid model that is based on the single-cell physics of a swimming bacterium. Comparison of our experimental and simulation results show that the collective behavior in this system is largely determined by the biophysics of the single organism. The physics of these dense communities has many similarities to actomyosin systems, as well as to collective systems of epithelial cells. Therefore, our results are likely broadly applicable to a wide range of problems in cell migration, from the single cell to the collective.

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Coupling Scheme of the Rotary Motor Thermophilic F1

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Thermophilic F_1 (TF_1) is an ATP-driven rotary molecular motor driven by sequential hydrolysis of ATP in three catalytic sites. Rotation occurs in steps of 120° per ATP, and the 120° step is further resolved into 80-90° and 40-30° substeps. In the standard coupling scheme, ATP binding starts rotation from an ATP-waiting angle at 0°, and at ~200° the ATP is cleaved into ADP and Pi, and the ADP is released around 240° after a third ATP is bound. Pi release is at 200° or 320°, yet unsettled. With human mitochondrial F_1 (HF_1), Suzuki (2014) has indicated different angle dependence: cleavage occurs at 210° and Pi release at 305°. A peculiar finding in HF_1 was that supposedly slowly hydrolyzed ATPγS not only lengthened the dwell at 210° but to much greater extent the 305° dwell, implying that the thio-Pi release is much slower than the ATPγS cleavage. We thus re-examined under a microscope how ATPγS affects TF_1. With fluorescently (Cy3) labeled ATPγS we observed a remarkably long dwell at only 200° after its binding. With unlabeled ATPγS mixed in ATP, we observed only one long dwell per ATPγS binding, compared to two consecutive long dwells in HF_1. The long dwell with unlabeled ATPγS, presumably at 200°, comprised two reactions with rates 460 s^{-1} and 30 s^{-1}, compared to 2400 s^{-1} and 820 s^{-1} with regular ATP. We have yet to decide which corresponds to cleavage and (thio-)Pi release, but kinetic difference from HF_1 is obvious: either (thio-)Pi release occurs at 200° in TF_1, or thio-Pi release is not slow in TF_1. Nonhydrolyzable Cy3-AMPPNP halted rotation at 200° after binding, implying that ATP cleavage occurs at 200° or before, a conclusion previously drawn on the assumption of slow cleavage of ATPγS and a mutant.

Energy Transduction, Electron and Proton Transfer, and Light Harvesting

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Exploring the Staphylococcus Epidermidis Respiratory Chain

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Staphylcoccus epidermidis does not invade healthy tissues. However, it has been identified as a major cause of nosocomial infections because of its ability to infect polymer surfaces such as catheters or intra-cardiac valves, forming biofilms and evoking a reaction from the host that eventually leads to removal of prosthesis. S. epidermidis is responsible for 50-70% of catheter-related infections and 30 to 43% of perioperative implant infections. S. epidermidis can survive in a wide range of environments and oxygen concentrations ([O2]). It may grow in atmospheric oxygen levels, in micro-aerobic environments, including normal tissues with [O2]= 3 to 5% and even in pathologically altered tissues where O2 tensions may reach zero. S. epidermidis increases its propensity to form biofilms as [O2] decreases. Bacteria may contain different terminal oxidases that allow them to cope with different [O2]. Also, respiratory chain-branching aids the cell to survive in the presence of toxic substances. Understanding the plasticity of the respiratory chain is necessary to understand the physiology and pathogenicity of S. epidermidis. In this species, we found two terminal oxidases expressed during growth in different [O2]: bo is always present, while aa3 is expressed in aerobic conditions but not in microaerophilic conditions nor in KCN plus a non-fermentable carbon source. In Oxygen consumption experiments, the preference for different substrates varied depending on [O2] exposure during growth.

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New Perspectives on Quinol Binding Motifs at the bc1 Complex Based on MD Simulations

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The bc1 complex is a central player in the conversion of energy into ATP synthesis in photosynthesis and respiration, and its overall mechanism, the Q-cycle, is well known. However, the quinol-protein interaction that initiates Q-cycle at the Qo-binding site have not yet been described. Employing classical MD