Bacterial Flagellar Switching: Hidden Markov Steps Revealed

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Here we describe a Markov chain that accounts for hidden steps in the switching mechanism of bacterial flagellar rotation. The bacterial flagellar motor apparatus switches between counterclockwise rotation (CCW) and clockwise rotation (CW) in response to interactions between ligands bound to subunits of the rotor and motor units of the stator. If the ligand, CheY, binding elicits the elasticotaxis response, we are investigating whether compression of stresses in compressed substrates with experimental data showing the correlation between the mechanical stress in the substrate and the degree of the extensional aggregation of bacterial cells by depletion attraction and generates phase separation patterns in a nonequilibrium growing colony. This generic mechanism powers the way biologists explore the living cell at a molecular resolution. Atomic Force Microscope (AFM) and force spectroscopy analysis have been used to directly measure reversible physicochemical and specific binding interactions between cells. Stickiness is important biofilm formation stage that could also be measured at nM level. A significant source of foodborne illness results from biofilms. These are caused by microorganisms that attach to surfaces and grow as highly organized multicellular communities. This study examines the impact of silver resistance on bacterial adhesion and its viscoelastic formation. We present the first set of data that evaluates the elastic deformation of a bacterial cell surface upon evolution of silver resistance in E. coli MG1655 using AFM compared to controls in different generations. The adhesion stiffness and stickiness mean of the treated (evolved Ag resistant) and non-treated samples were tested at nM level. The evolved samples had a significantly (P < 0.05) higher stickiness ratio and value (from 0.01 ± 0.04 nM to 0.06 ± 0.02 nM) compared to the controls (non-resistant) strains (from 0.01 ± 0.02 nM to 0.04 ± 0.02 nM). The highest difference of adhesion force happened on Generation 100. According to images of the bacteria in different generations, we can see some major phenotype changes on the appearance at generation 100. The MIC data for the non-evolved strains of E. coli MG 1655 through 200 generations were also significantly lower 38.58 ± 10.9 mg/l compared to evolved strains 272.25 ± 153.9 mg/l (p < 0.01). The experiment demonstrates important features of phenotype modulation resulting from the evolution of Ag resistance that will be further studied by this group.

Depletion-Mediated Pattern Formation in a Growing Bacterial Colony Pushpita Ghosh, \textsuperscript{1} Jagannath Mondal, \textsuperscript{1} Estel Ben-Jacob, \textsuperscript{1} Herbert Levine \textsuperscript{2}

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Secretion of extracellular polymeric substances into growth medium of bacteria is the hallmark of forming biofilm-like structures. The morphological property of such systems might depend upon the physical interactions of cells with extracellular polymeric substances (EPS). We have studied self-organization of nonmotile rod-shaped bacterial cells growing on solid substrate in presence of self-producing EPS, secreted into the growth medium in expanding colony. In our individual-based simulation model of bacterial cells and EPS, all the particles interact mechanically via repulsive forces by pushing each other away as bacterial cells grow and divide consuming diusing nutrient and produce EPS. We show that mechanical interactions control the collective behavior of the system, particularly, we show that the presence of nonadhering EPS leads spontaneous aggregation of bacterial cells by depletion attraction and generates phase separated patterns in a nonequilibrium growing colony. This generic mechanism powered by entropic forces could explain one of the possible ways to spontaneous aggregated structure formation and spatial heterogeneity in a biofilm.

Bacterial Chemotactic Tumble Angles Reduce Backtracking and Maximize Information Gathering

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Chemotaxing bacteria gather information from the environment and use that to control the balance between runs and tumbles in order achieve a biased motion toward the source of a chemotactant. We have examined the role of the tumble angle on how effectively gradients are coupled into a bacterium’s trajectory. Chemotaxis was simulated using the ZBP program, and the average tumble angle varied from 0 to 180 degrees in the presence and absence of the normal angle variance and/or rotational diffusion. 100,000 step (0.1 μm/step) trajectories from these simulations where analyzed using the k-space information