Singly-flagellated bacteria chemotax efficiently by unbiased motor regulation VERNITA GORDON, University of Texas at Austin, QIUXIAN CAI, Beijing University, University of Texas at Austin, QI OUYANG, CHUNXIONG LUO, ZHAOJUN LI, Beijing University — *Pseudomonas aeruginosa* is a widespread bacterial pathogen that can chemotax. Genes that allow *P. aeruginosa* to chemotax are homologous with genes in the paradigmatic model organism for chemotaxis, *Escherichia coli*. However, *P. aeruginosa* is singly-flagellated and *E. coli* has multiple flagella. Therefore, the regulation of counter-clockwise/clockwise flagellar motor bias that allows *E. coli* to efficiently chemotax by runs and tumbles would lead to inefficient chemotaxis by *P. aeruginosa*, as half of a randomly-oriented population would respond to a chemoattractant gradient in the wrong sense. How *P. aeruginosa* regulates flagellar rotation to achieve chemotaxis is not known. Here, we analyze the swimming trajectories of single cells in microfluidic channels and the rotations of cells tethered by their flagella to the surface of a flow cell with variable environment. We show that *P. aeruginosa* chemotaxes by symmetrically increasing the durations of both counterclockwise and clockwise flagellar rotations when swimming up the chemoattractant gradient, and symmetrically decreasing rotation durations when swimming down the chemoattractant gradient. Unlike the case for *E. coli*, the counter-clockwise/clockwise bias stays constant for *P. aeruginosa*. Using analytical modeling and simulation, we show that, given *P. aeruginosa*'s physiological constraints on motility, their symmetric regulation of motor switching optimizes chemotaxis.

Vernita Gordon
University of Texas at Austin