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**Pinning and hydrodynamic coupling determine the motility pattern of interfacially trapped bacteria**[1] JIAYI DENG, MEHDI MOLAEI, NICHOLAS CHISHOLM, KATHLEEN STEBE, University of Pennsylvania —

Fluid interfaces are unique environments for swimming bacteria, which display complex motility patterns influenced by concomitant capillary forces and hydrodynamic interactions. In 3-d suspension, *P aeruginosa* swims along symmetric straight paths in run and reverse motions by altering the rotation direction of its flagellum to switch between pusher and puller modes. Near solid walls, the straight trajectories become circular paths due to the well understood hydrodynamic interactions. Trajectories of *P. aeruginosa* trapped at an oil-water interface, however, display a diverse set of trajectory types: fast and straight visitors, Brownian diffusive cells, stable curly paths, and pirouettes. Which of these patterns occurs depends on the trapping state of the cell and its orientation with respect to the interface. An analysis of the curly paths reveals that highly asymmetric trajectories occur with higher angular velocity and curvature for pullers and higher linear velocity and lower curvature for pushers. Our hydrodynamic analysis suggests that this motion is regulated by the re-orientation of the bacterial flagellum, which pivots normal to the interface in the puller mode and parallel to the interface in the pusher mode.

[1] GomRI

Mehdi Molaei
University of Pennsylvania

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