

Fan Bai^{1,2}, Tohru Minamino², Zhanghan Wu³, Keiichi Namba², **Jianhua Xing**³

1 Biodynamic Optical Imaging Centre, Peking University, Beijing 100871, People's Republic of China

2 Graduate School of Frontier Biosciences, Osaka University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan

3 Department of Biological Sciences, Virginia Tech, Blacksburg, Virginia, 24061-0406, USA

Coupling between switching regulation and torque generation in bacterial flagellar motor

The bacterial flagellar motor plays a crucial role in both bacterial locomotion and chemotaxis. Recent experiments reveal that the switching dynamics of the motor depend on the rotation speed of the motor, and thus the motor torque, non-monotonically. Here we present a unified mathematical model which treats motor torque generation based on experimental torque-speed curves and the torque-dependent switching based on the conformational spread model. The model successfully reproduces the observed switching rate as a function of the rotation speed, and provides a generic physical explanation independent of most details. A stator affects the switching dynamics through two mechanisms: accelerating the conformational flipping rate of individual rotor-switching units, which contributes most when the stator works at a high torque and thus a low speed; and influencing a larger number of rotor-switching units within unit time, whose contribution is the greatest when the motor rotates at a high speed. Consequently, the switching rate shows a maximum at intermediate speed, where the above two mechanisms find an optimal output. The load-switching relation may serve as a mechanism for sensing the physical environment, similar to the chemotaxis mechanism for sensing the chemical environment. It may also coordinate the switch dynamics of motors within the same cell.