Abstract of Presentation

Presentation Title:

Direct observation of steps in rotation of the bacterial flagellar motor

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Abstract:

The bacterial flagellar motor is a rotary molecular machine driven by an electrochemical potential gradient of H^+ or Na^+ ions across the cytoplasmic membrane. The rotor is a set of rings up to 45 nm in diameter with one ring spanning the cytoplasmic membrane and the others residing in the cytoplasmic space, and the stator contains about 10 torque-generating units anchored to the cell wall at the perimeter of the rotor. The free-energy source for the motor is an inward-directed electrochemical potential gradient of ions across the cytoplasmic membrane, the protonmotive force (pmf) or sodium-motive force (smf) for H^+- and Na^+-driven motors, respectively. Discrete stepping motion characteristic of the ATP-driven molecular motors, such as myosin, kinesin and F1-ATPase, has not previously been observed in the flagellar motor due to its high speed, the presence of multiple torque generating units in a single motor and the small step-size predicted by dividing a small free energy quantum (one ion crossing the membrane) by the relatively large torque that the motor generates. Here we demonstrate stepping motion of a Na^+-driven chimeric flagellar motor in *Escherichia coli* at a low sodium-motive force and with controlled expression of a small number of torque generating units. We observed 26 steps per revolution, consistent with the periodicity of the ring of FliG protein, the proposed site of torque generation on the rotor. Backwards steps despite the absence of the flagellar motor switching protein CheY indicate a small free energy change per step similar to that of a single ion transit. Steps were resolved during intermittent periods of slow rotation, possibly indicating a periodic rotor-stator potential rather than single ion transits.

References:

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