Articles of Significant Interest in This Issue

**EloR and the Lytic Transglycosylase MltG Form a Complex at Midcell in *Streptococcus pneumoniae***

EloR is an RNA-binding protein recently discovered to be involved in regulating cell elongation in *Streptococcus pneumoniae*. It has been found to localize to midcell. Winther et al. (e00691-20) discovered that it is the Jag domain of EloR that determines this localization. Using a bacterial two-hybrid assay and coimmunoprecipitation, they found that EloR acts in complex with the lytic transglycosylase MltG, which is crucial for elongating the pneumococcal cell. They hypothesize that EloR regulates the murelytic activity of MltG, allowing controlled opening of the peripheral cell wall for incorporation of new peptidoglycan in the longitudinal direction.

**Identification of Potential Regulatory Domains within the MreC and MreD Components of the Cell Elongation Machinery**

In most rod-shaped bacteria, the lateral cell wall is built by an essential multiprotein complex called the Rod system. Within this complex, MreC and MreD likely function to activate the peptidoglycan synthesis enzymes. Rohs et al. (e00493-20) developed a genetic selection to identify amino acid residues in MreC and MreD that are critical for cell elongation in *Escherichia coli*. These residues cluster in two regions of MreC and in a putative ligand-binding pocket of MreD. This analysis pinpoints domains in MreC and MreD that influence Rod system function, possibly through conformational changes induced by protein-protein interactions and/or ligand-binding.

**Site-Directed Cross-Linking Identifies the Stator-Rotor Interaction Surfaces in a Bacterial Flagellar Motor**

The bacterial flagellum is a unique organelle that functions as a rotary motor. The motor consists of stator and rotor, and interactions between them are indispensable for function. However, the stator-rotor interface involved in interaction has been defined only by mutational analysis. Terashima et al. (e00016-21) detected the stator-rotor interaction using site-directed photo- and disulfide-cross-linking approaches. They identified several residues in the stator PomA, especially K89, that are in close proximity to the rotor. Furthermore, they identified several pairs of stator and rotor residues that interact. This work provides insights into nature of the stator-rotor interaction in the flagellar motor.