IN BRIEF

BACTERIAL PHYSIOLOGY

Distinct roles of the FliI ATPase and proton motive force in bacterial flagellar protein export

Minamino, T. & Namba, N. *Nature* **451**, 485–488 (2008)

Energy source of flagellar type III secretion

Paul, N. *et al*. *Nature* **451**, 489–492 (2008)

Motile bacteria are able to move in their environment by virtue of their flagellum. The flagellum contains a protein-export apparatus that is related to the type III secretion system and which allows the protein components of the flagellum to be secreted across the bacterial cell membrane for flagellar assembly. Previously, it had been assumed that the energy for this transport was provided by the ATPase FliI, but two reports in a recent issue of *Nature* now argue against this view. Both groups investigated flagellar secretion in *Salmonella enterica* serovar Typhimurium and found that flagellar proteins were secreted in the absence of FliI and that the energy that is required for secretion is derived from the proton motive force.

BACTERIAL SECRETION

Membrane localization and topology of the *Yersinia pestis* YscJ lipoprotein

Silva-Herzog, E. *et al. Microbiology* **154**, 593–607 (2008)

The lipoprotein YscJ is an essential component of the type III secretion apparatus in *Yersinia pestis*, yet little is known about its topology or precise localization. Previous work had indicated that YscJ and related proteins (the YscJ/PrgK family) form a ring-like structure that is located in the inner membrane. Bacterial lipoproteins that are destined for the inner membrane typically contain a canonical inner membrane lipoprotein sorting signal. Eugenia Silva-Herzog *et al*. confirm that despite lacking this canonical signal, YscJ is located in the inner membrane, and that this localization is determined by the amino-terminal domain, which comprises residues 1–61. YscJ/PrgK proteins therefore seem to use a unique mechanism for localization to the inner membrane.

TECHNIQUES & APPLICATIONS

A functional genomic yeast screen to identify pathogenic bacterial proteins

Slagowski, N. L. *et al. PLoS Pathogens* **4**, e9 (2008)

Bacterial effectors are poorly conserved and not essential for growth, and so they can be difficult to identify. In a recent issue of *PLoS Pathogens*, Naomi Slagowski and colleagues report on the development of a new semi-automated screening system in *Saccharomyces cerevisiae* that can be used to identify bacterial effectors. The system is based on yeast growth inhibition, and Slagowski *et al*. developed a quantitative yeast liquid growth assay in 96-well plates. The bacterial genes of interest were cloned as GFP fusion proteins in both high and low copy number plasmids under the control of an inducible promoter. Using this system, the authors identified a novel *Shigella flexneri* type III-secreted effector, IpaJ.