SCHOOL OF LIFE SCIENCES / FACULTE DES SCIENCES DE LA VIE

Global Health Institute / Institut de recherche en infectiologie

ÉCOLE POLYTECHNIQUE FÉDÉRALE DE LAUSANNE

GHI Floor Seminars

Special seminar by invited speaker

Prof. Tracy Palmer

Division of Molecular Microbiology, College of Life Sciences,
University of Dundee, UK

Protein transport by the bacterial Tat pathway

The Tat protein transport system functions to export folded proteins across the bacterial cytoplasmic membrane. Many Tat substrate proteins bind complex metal cofactors and the Tat pathway is required for important bacterial cellular processes including respiration and photosynthesis, cell division, motility and iron and phosphate acquisition. The Tat system is found in many animal and plant bacterial pathogens where in most cases it is required for virulence.

Proteins are targeted to the Tat system by N-terminal signal peptides that contain a conserved twin arginine motif. Our studies with the model organism *Escherichia coli* have shown that the integral membranes proteins TatA, TatB, and TatC form essential components of the transport machinery. Multiple copies of TatB and TatC associate to form a large TatBC complex that recognises twin-arginine signal peptides and binds substrate proteins. Binding of substrate proteins to TatBC triggers polymerization of TatA to form the transmembrane translocation pathway.

Recently the crystal structure of the TatC component from *Aquifex aeolicus* has been determined. TatC contains six closely-packed transmembrane helices forming a central cavity on one face of the protein overhung by an extensive periplasmic cap [1]. This structure forms a framework for understanding the location and dynamic nature of the binding sites for the TatA and TatB partner proteins and the twin-arginine signal peptide. We have been using a combination of molecular biology, suppression genetics and cross-linking studies to explore the molecular interactions between the Tat components at different stages of the Tat translocation cycle. Our latest findings will be presented.

1. Rollauer, S.E., *et al. Nature* **2012**, *492*, 210-214.

Host : Stewart Cole

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12:15, SV 1717a

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