MS11 Hot structures in biology

Chairs: Prof. Maria Joao Romao, Prof. Fred Antson

MS11-P10

Structural studies of the five pilin proteins building up the type-V pilus Mfa1 of Porphyromonas gingivalis

Karina Persson[1], Michael Hal[1], Thomas Heidler[1], Yoshiaki Hasegawa[2]

1. Department of Chemistry, Umeå University, Umeå, Sweden
2. Department of Microbiology, Aichi Gakuin University, Aichi, Japan

email: karina.persson@umu.se

Structural and functional information of pili from the Bacteroidetes class of bacteria is sparse. Porphyromonas gingivalis, a periodontal pathogen belonging to the Bacteroidetes class, expresses two forms of pili, FimA and Mfa1. Each pilus consists of five proteins; FimA-E and Mfa1-5 respectively. Both represent the type-V form of pili. While the structure and assembly of type-1 pili from Escherichia coli is well studied, the chaperone-usher pathway, very little is known about the polymerization of type-V pili. In order to obtain an understanding of the structure, function and assembly mechanism of the P. gingivalis pili we have solved the X-ray crystal structures of all five Mfa proteins in recombinant form [1,2]. Despite low sequence similarity the Mfa1-4 proteins are structurally related to each other being built up from two β-sandwich domains. The P. gingivalis pilin proteins start as lipidated precursors before they are transported to the surface and polymerized. The precursor comprises an N-terminal extension, which is cleaved off upon polymerization. Intriguingly, all proteins were crystallized in their precursor forms with their N-terminal extensions still present. Part of this extension forms the first strand of the first β-sheet of the pilin. Maturation of the pilin is the result of cleaving the polypeptide at a conserved arginine downstream of this first β-strand resulting in a new N-terminus and a void in the first β-sheet. In analogy with the strand-displacement mechanism used for polymerization of the type-1 pili we believe that the void is filled by a donor β-strand from another pilin protein. However, despite having the crystal structure of all Mfa1-4 proteins and data from several mutagenesis studies we still do not know if it is the newly formed N-terminus or the long flexible C-terminus present on Mfa1 that constitute the donor strand.

The final protein, Mfa5, differs from the other Mfa proteins; it is much larger and consists of an N-terminal von Willebrand domain followed by a string of Ig-like domains [3]

References:

[1] Kloppsteck, P. et al. (2016). Scientific reports 6, 22945
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MS14 Combined approaches for structure characterization of modulated and complex structures

Chairs: Prof. Joke Hadermann, Dr. Phillipe Boullay

MS14-P05

Structural insights into the membrane-anchored model of FtsQ/FtsB/FtsL complex in divisome

Claire V. Colin[1], Peng Zuo[1], Céline Darie[1], Holger Klein[1]

1. Department of Chemistry, College of Natural Sciences, Seoul Natonal University, Seoul, Korea South

email: yuri93@snu.ac.kr

Bacterial cell division is a fundamental process that is initiated by FtsZ protein into a ring structure at midcell and facilitates a set of essential proteins known as the divisome [1,2]. Among them, the FtsQ/FtsB/FtsL complex was known as a scaffold protein connecting upstream and downstream division proteins. Despite previous intensive studies on the FtsQBL complex, the atomic details of the interface between FtsQ and FtsB were not reported yet. To gain an insight into structural organization of the FtsQBL complex, we have determined the crystal structure of periplasmic domain of FtsQ in complex with C-terminal fragment of FtsB and showed that the C-terminal region of FtsB is a key binding region of FtsQ via mutational analysis in vitro and in vivo. Also, we proposed the model of FtsQ/FtsB/FtsL complex in curved membrane, with opposite N-terminal directions of FtsQ and the FtsB/FtsL complex via small-angle X-ray scattering and analytical gel filtration chromatography. These model suggests that the Y-shaped FtsQ/FtsB/FtsL complex might fit well into the curved membrane for membrane anchoring during cytokinesis.

References:

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