Structure of the central spike complex from the Type VI Secretion System

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The Type VI Secretion System (T6SS) is used by many Gram negative bacteria (Pseudomonas, Vibrio, Acinetobacter etc.) to deliver virulence-associated protein effectors to the external milieu and sometimes directly into the cytoplasm of target cells in a contact-dependent manner [1]. The system comprises 15-20 proteins which form a large structure orthologous to a contractile phage tail [2]. The valine-glycine repeat protein G (VgrG) is homologous to the tail's central spike protein complex and is responsible for piercing the target host cell during infection [3]. We have solved the structure of the PA0091 VgrG1 protein from Pseudomonas aeruginosa PAO1 using X-ray crystallography and used this structure as a template for modelling other VgrG proteins from P. aeruginosa and V. cholerae. Employing this strategy, we have obtained the model of the complete VgrG1 spike from V. cholerae V52, which carries a C-terminal actin-cross-linking domain specifying the virulence towards eukaryotic cells [4]. The crystal structure of PA0091 VgrG1 from P. aeruginosa and the model of VgrG1 from V. cholerae advance our understanding of the mechanism of effector delivery by T6SS and make it possible to describe many characteristic features of the VgrG proteins family.

1. M. Basler et al. (2013) Tit-for-Tat: Type VI secretion system counterattack during bacterial cell-cell interaction, Cell, 152:884–894.

2. F. Boyer et al. (2009) Dissecting the bacterial type VI secretion system by a genome wide in silico analysis: What can be learned from available microbial genomic resources? BMC Genomics, 10:104.

3. P.G. Leiman et al. (2009) Type VI secretion apparatus and phage tail-associated protein