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.

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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

complexes share a common evolutionary origin, *PNAS*, **106(11):**4154-4159.

4. S. Pukatzki et al. (2007) Type VI secretion system translocates a phage tail spike-like protein into target cells where it cross-links actin, *PNAS*, **104(39):**15508-15513.