HIGH RESOLUTION CRYOEM STRUCTURE AND ASSEMBLY MECHANISM OF A BACTERIAL VIRUS GENOME GATEKEEPER

I. ORLOV [1], S. ROCHE [2], S. BRASILÈS [2], N. LUKOYANOVA [3], Y. CHABAN [4], P. TAVARES [2], E. ORLOVA [3]

[1]Rockfeller University - New York (USA), [2]I2BC - Gif-Sur-Yvette (France), [3]Birkbeck College - London (UK), [4]Diamond Light Source - Oxford (UK)

Viral assembly is a highly coordinated process involving a large number of proteins. This is particularly true for large viruses like the Caudovirales, a family also known as tailed bacteriophages. They comprise two main components: an icosahedral or prolate capsid that contains the viral genome, a double-stranded DNA molecule, and a tail. The tail is bound to the capsid at a functionally and biochemically distinctive vertex via the specialised protein complex named connector.

The connector acts as a gate through which viral genome enters and exits from the capsid. During viral assembly, DNA is translocated to the viral procapsid interior through the portal protein. The channel of the portal complex is subsequently closed by other proteins to build the connector complex, preventing the premature release of the genome. Recognition of the viral receptor by the phage tail triggers the release of the genome through the connector.

In bacteriophage SPP1, the ~900 kDa connector is made of three proteins: the gp6 portal protein, the gp15 adaptor and the gp16 stopper. Structures of the gp6 oligomer (Lebedev et al., 2007) and of the monomeric gp15 and gp16 in solution (Lhuillier et al., 2009) were previously determined. We will present the cryoelectron microscopy structure at 2.7 Å resolution of the entire connector in its closed conformation. The structure reveals major conformational changes in the three components of the complex when compared to their non-assembled forms. These findings combined with inspection of structures of connector proteins from related bacteriophages led to a model of the sequence of conformational changes and folding events engaged in connector assembly and in sealing of the viral genome inside the capsid.