Most of bacterial viruses need an specialised machinery named the tail to deliver its genome inside the bacterial cytoplasm without disrupting cellular integrity. T7 bacteriophage is a well-characterized member of the Podoviridae bacteriophage family infecting E. coli, and it presents a short non-contractile tail that assembles sequentially in the viral head after DNA packaging. T7 tail is a complex of around 2.7 MDa composed by a tubular structure with a central channel that serves as a conduit for DNA ejection surrounded by fibers.

We used cryo-electron microscopy (cryo-EM) and image reconstruction methods together with biochemical interaction essays to determine the precise topology of the 4 proteins that form the tail complex. Further experiments allowed to identify the protein and lipid bacterial compounds used as receptor for the virus, being able to set up an in vitro ejection system for T7. Characterization of the ejection reactions by cryo-EM allowed us to build a three-dimensional model of the tail after DNA ejection. The structural analysis of the three-dimensional models before and after ejection permitted to unravel the conformational changes that take place in the tail complex during DNA delivery and to propose a model for T7 infection.

The similarities found in several components of the tail machinery, comprising the nozzle domain, as well as the gatekeeper and the connector, for different viruses from the podoviridae family suggest that the DNA ejection mechanism is conserved based on common structural arrangements.

Acknowledgement: This work was partly funded by Grant BFU2011-29038