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I E C B

Describing the tailed bacteriophage virion from a combination of NMR and EM data

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We would like to announce the seminar of **Dr. ()** on **14 April 2017 @ 11am in the IECB** amphitheatre.

Most known bacteriophages are constituted by a capsid (or head) containing their genome and a tail that serve for bacterial target recognition and genome delivery into the infected host cytoplasm. We analyzed the phage protein divergent sequences in order to identify genes coding for the capsid, head-to-tail connection and tail of the phage viral particle (Lopes et al., 2014). We thus classified phages as a function of their head-to-tail connection architecture. We focused on phage SPP1, which is representative of the largest phage class, in order to describe the architecture of its viral particle. We solved the 3D solution structures of four SPP1 proteins before assembly into the viral particle; these structures are characterized by the presence of large flexible loops (Lhuillier et al., 2009; Chagot et al., 2012). We then docked these structures into the EM maps of the head-to-tail connection of the SPP1 virion in two functional states, i.e. before and after DNA ejection (Tavares et al., 2012; Chaban et al., 2015). Loops involved in capsid closure were identified and this was validated by observing disulfide cross-linking between the loops rearranged as b-strands in the assembled particle (Lhuillier et al., 2009; Chaban et al., 2015). In long-tail phages as SPP1, the tail tube results from the assembly of the Major Tail Protein (MTP) gp17.1. We showed that monomeric gp17.1 is partially folded in solution and self-assembles to form native-like fibers. We followed, using solution-state NMR, FTIR, solid-state NMR and EM, the structural changes experienced by gp17.1 during fiber formation, and proposed a 3D model for the gp17.1 fiber (Langlois et al., 2015). Finally, we validated our model by designing a gp17.1 variant with impaired assembly capacities in vitro and in the bacteria. Similarities between virion architectures within tailed bacteriophages will be discussed.

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