

Structure of bacteriophage T5 tail tube: revisiting the trigger for DNA ejection

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The vast majority (96%) of bacteriophages possess a tail that allows host cell recognition, cell wall perforation and safe viral DNA channelling from the capsid to the cytoplasm of the bacterium. 60% of all tailed phages, the *Siphoviridae*, bear a long flexible tail, which tube is formed of the tail tube protein (TTP) that polymerises in stacks of hexamers around the tape measure protein (TMP). At the distal end of the tail, the tail tip complex harbours the receptor binding proteins (RBP). For these phages, little is known on the mechanism that triggers DNA ejection after binding to the host. We report the crystal structure at 2.2 Å resolution of pb6, an unusual trimeric TTP, of siphophage T5. Structure analysis however confirms the homology of pb6 with all TTPs and related tube proteins of bacterial puncturing devices (type VI secretion system and R-pyocin). We fit this structure into the cryo-electron microscopy map of the tail tube determined at 6 Å resolution. Comparing the structure of the tail tube before and after interaction with the host receptor, we show that unlike previously proposed, the host binding information is not propagated to the capsid by the tail tube, as the two structures, at that resolution, are identical (Figure 1). Rather, we suggest a role of the TMP that would be folded in a metastable state in the tail tip. It would be destabilised by the RBP-host receptor interaction, leading to its own ejection and ultimately to DNA release.

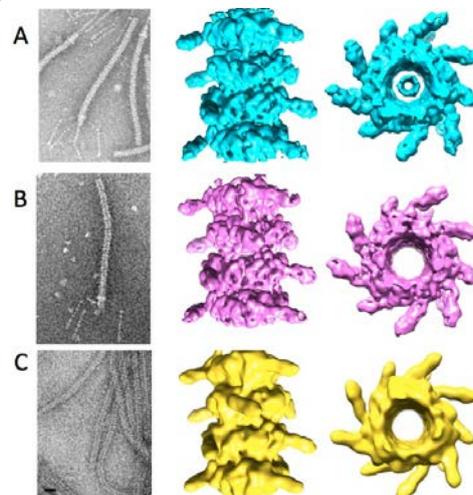


Figure 1: Negative stain micrographs (Left) of full (A) and empty tails (B), and of pb6 tubes (C). Cryo-EM reconstruction of T5 tail tube before (6.2 Å resolution, B) and after (5.8 Å resolution, C) interaction with the host receptor, leading to the expulsion of the TMP. C. Cryo EM reconstruction of pb6 tubes at 8.8 Å resolution. Middle: side view, right: top view. Bar 20 Å.