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# Bacteriophage T5 tail tube structure suggests a trigger mechanism for Siphoviridae DNA ejection

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## Résumé

The vast majority (96%) of bacteriophages - bacterial viruses - possess a tail that allows host recognition, cell wall perforation and safe viral DNA channelling from the capsid to the cytoplasm of the bacterium. The majority of tailed phages, the *Siphoviridae*, bear a long flexible tail formed of stacked tail tube proteins (TTP) that polymerise around and along the tape measure protein (TMP). At the distal end of the tail, the tail tip complex harbours the receptor binding proteins (RBP). Little is known on the mechanisms that trigger DNA ejection after binding of *Siphoviridae* to their host. Here, we report the overall structure of siphophage T5 tail tube by determining the crystal structure of T5 TTP pb6 at 2.2 Å resolution and the structure of T5 tail tube by cryo electron microscopy (EM) at 6 Å resolution. Fitting the crystal structure of the TTP into the EM map made it possible to propose a pseudo-atomic model of the tail tube. We also observe that the structure of the tail tube remains unchanged after interaction of T5 tails with the host receptor, showing that host binding information is not propagated to the capsid by the tail tube. We rather suggest that the TMP, folded in a metastable state, would transmit the signal. RBP-host receptor interactions and subsequent tail tip rearrangements would destabilise the TMP, leading to its ejection from the tube and ultimately to capsid opening and DNA release. Although pb6 is unusually formed of three domains, structure analysis reveals homology of pb6 with all classical TTPs and related tube proteins of bacterial puncturing devices (type VI secretion system and R-pyocin) extending thus our findings to most of biological tailed-like structures.

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