

Structure of the bacteriophage T4 long tail fiber needle-shaped receptor-binding tip

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Bacteriophages are the most numerous organisms in the biosphere. They are exploited in an emergent array of applications including bactericidal and experimental phage therapy applications. In spite of their biological significance and the spectrum of potential applications, little high-resolution structural detail is available on their receptor-binding fibres. Here we present the crystal structure of the receptor-binding tip (D10 plus D11, Fig. 1) of the bacteriophage T4 long tail fibre, which is highly homologous to the tip of the bacteriophage lambda side tail fibres. It reveals an unusual elongated six-stranded anti-parallel beta-strand needle domain containing seven iron ions coordinated by histidine residues arranged co-linearly along the core of the biological unit (Fig. 2). At the end of the tip the three chains intertwine forming a broader head domain, which contains the putative receptor interaction site. The structure reveals a previously unknown beta-structured fibrous fold, explains the remarkable stability of the fibre and provides a framework for mutations to expand or modulate receptor-binding specificity.

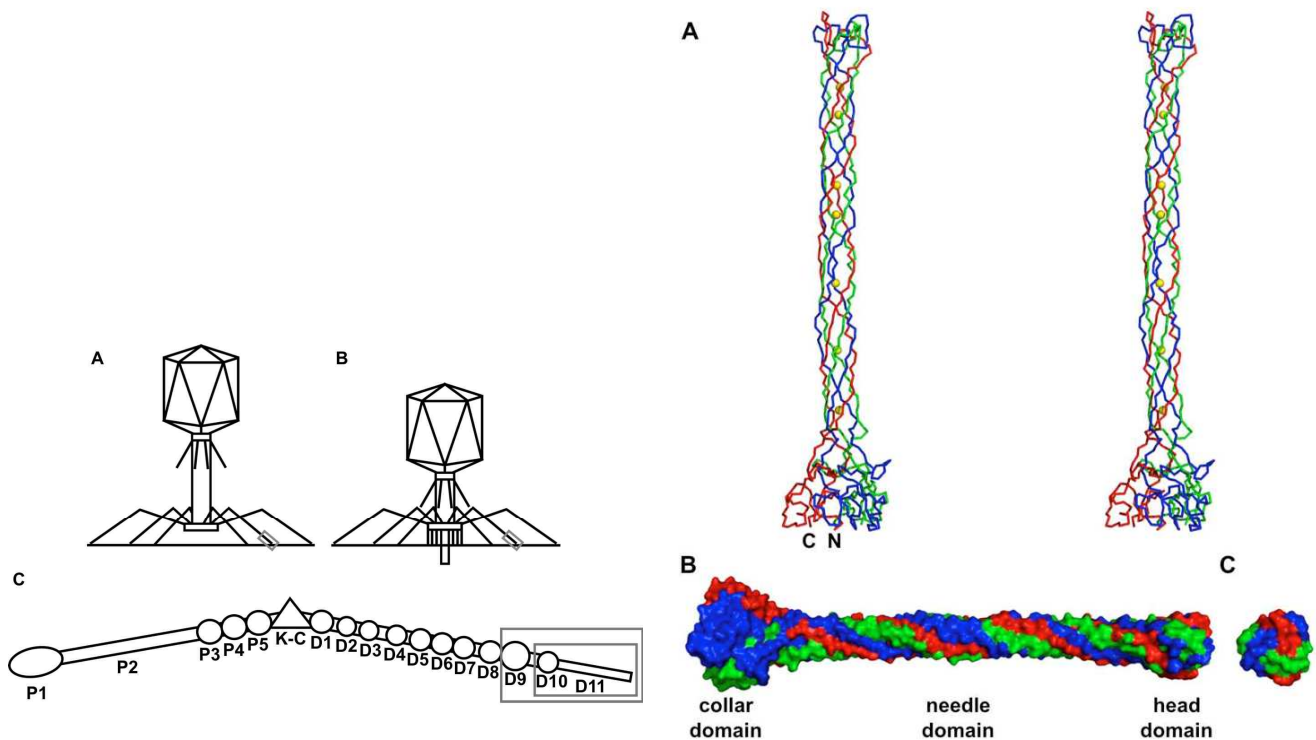


Fig. 1. Bacteriophage T4 and its long tail fibres. A-B. Schematic representations of bacteriophage T4 attached to a bacterial membrane before (left) and after (right) contraction of the outer tail tube. The tip domain of gp37 is boxed. C. Schematic representation of the bacteriophage T4 long tail fibre. Domains P1-5 correspond to gp34; the knee-cap domain (K-C) is formed by gp35, while the distal part of the fibre, consisting of gp36 and gp37, is divided into regions D1-11. The expressed protein, gp37(651-1026), corresponds to D9-11 (larger grey box), while the crystallised fragment, gp37(785-1026), corresponds to D10-11 (smaller grey box).

Fig. 2. Overview of the structure. A. Stereographic ribbon representation of gp37(785-1026). Chains A, B and C are coloured red, green and blue, respectively. The N- and C-termini of chain A are labelled. B-C. Surface representations of the structure of gp37(785-1026) seen from the side (B) and top (C) to illustrate the extensive intertwining of the three protein chains in the trimer.

Keywords fibrous fold; gene product 37 (gp37); iron binding; receptor binding; viral fibers; X-ray crystallography