

Physico-Chemical Structure of T4 Bacteriophage:

T4 is a dsDNA bacteriophage virus which belongs to the family Myoviridae. Frederick Twort and Félix d'Hérelle independently discovered Bacteriophages. The detail Physico-chemical structure of the virion is as follows-

Symmetry:

It is a tadpole shaped virion with binal symmetry. It is said binal symmetry because the virion contains head with icosahedron symmetry and tail with helical symmetry.

Size: 90 × 200 nm

Components: The virion has a prolate head inside which the genome is packaged.

An elongated Contractile Tail is attached to the head and a short neck with collar is also present in between. A Base plate is present to the other end of the tail to which Several Tail Fibres are attached.

Head:

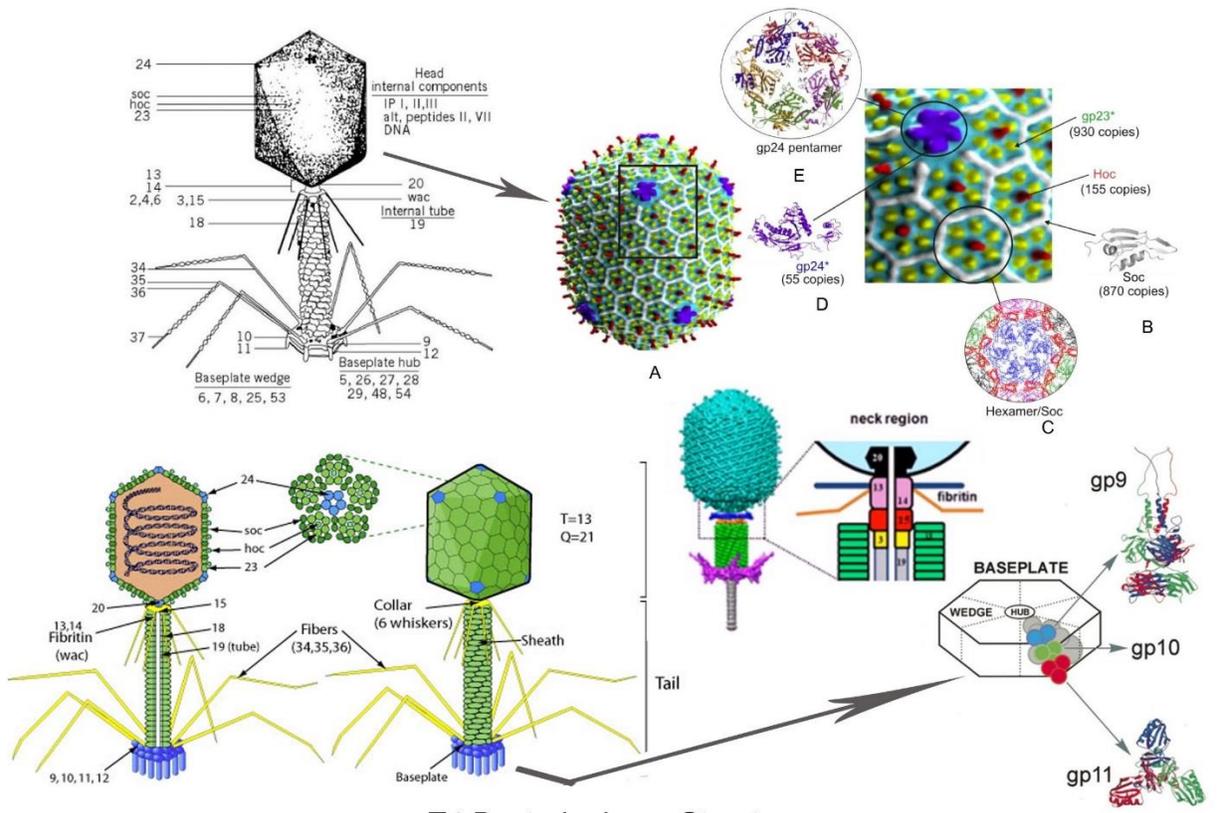
- T4 head is prolate shaped which is actually an elongated icosahedron (*i.e. a structure with 20 equilateral triangle with 12 vertices*)
- A total of 24 different types of Proteins involved in the formation of head among which 16 involved in formation of Prohead and its maturation, 5 for DNA packaging and 3 are required to complete and stabilize the head.
- Inside the head a linear dsDNA molecule is tightly packed.
- The proteins involved in structural formation and stability of the Head are gp23, gp24, HOC (*Highly antigenic Outer Capsid Protein*), SOC (*Small Outer Capsid Protein*) etc.

Neck:

- The Neck is the region which unites the two part Head and the tail.
- It is ring like structure of proteins composed of proteins 13, 14, wac and fibritin.

Tail:

- The tail of T4 Phage is contractile (*i.e. it can contract and expand like a muscle*) and that is why T4 phage belong to the Myoviridae group (*Myo~Muscle*).



T4 Bacteriophage Structure

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- The tail is made up of two co-cylinder arranged like a manner that there is a second cylinder (Outer Cylinder) present around the inner Cylinder which is present at the core.
- Among this two cylinder the Inner Cylinder is made up of protein gp19 and there are 144 subunits of this gp19 protein is arranged in 24 stacked hexameric rings. It is to be note here that the inner Cylinder is **not Contractile**.
- The Outer Cylinder is sheath like structure and made up of 144 subunits of gp18 protein. This ring is **contractile**. The subunits are arranged in helical fashion in a manner that the entire ring can rotate and as a result the intra subunit distance is reduced. Thus the ring contracts.

Base Plate:

- The Base plate is a hexagonal structure and the central part of the base to which the tail is attached to is called Hub and the corners are called wedges.
- There are Six different types of Protein is involved in formation of Base Plate, these are gp5, gp27, 29, 26, 28 and 51).

- Among these proteins gp5-gp27 complex attached to the tube has a lysozyme activity (so that it can degrade the glycosidic bonds of Peptidoglycan present in the cell wall of Bacteria)

Tail Fibres:

- There are two different types of Fibres in T4- Short Tail Fibres(STF) and Long Tail Fibres (LTF).
- The Short Tail Fibres are made up of gp9 and gp12 as a trimer and act as a socket of Long Tail Fibre.
- The Long Tail Fibre which involved in attachment to the Bacterial Cell Wall consisting of protein products from four different genes – 34, 35, 36 and 37). It is to be note that the terminal polypeptide of gp37 is very much specific (785-1026) as it interacts with Lipopolysaccharide of Bateriaum.

Genome :

- The T4 phage's genome is double-stranded DNA which is tightly packaged inside the Head.
- The genome is about 169 kbp long and encodes (produces or codes for) 289 proteins.
- T4 dsDNA contains a modified base **5-Hydroxy-methyl-Cytosine(5-HMC)** instead of Cytosine(C).
- The T4 genome is terminally redundant that means a sequence of 1.6 kbp is repeated at both ends.
- The genome is first replicated as a unit, then several genomic units are recombined end-to-end to form a concatemer.
- When packaged, the concatemer is cut at unspecific positions of the same length, leading to several genomes that represent **circular permutations** of the original.
- The T4 genome bears eukaryote like intron sequences.

How T4 Bacteriophage infects *E.Coli*

The T4 phage initiates an *E.coli* infection by binding OmpC porin proteins and Lipopolysaccharide (LPS) on the surface of *E. coli* cells with its long tail fibers (LTF). A recognition signal is sent through the LTFs to the baseplate. This unravels the short tail fibers (STF) that bind irreversibly to the *E. coli* cell surface. The baseplate changes conformation and the tail sheath contracts, causing GP5 at the end of the tail tube to puncture the outer membrane of the cell. The lysozyme domain of GP5 is activated and degrades the periplasmic peptidoglycan layer. The remaining part of the membrane is degraded and then DNA from the head of the phage can travel through the tail tube and enter the *E. coli* cell.