DNA structure and phase transitions in the bacteriophage capsid

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Tailed bacteriophages are complex macromolecular machineries that deliver their genome into the host cytoplasm while their capsid and tail remain bound to the cell surface. Although several models have been proposed, DNA organization is still unknown in the phage head but dimensions of the capsids are adjusted to keep DNA at a concentration close to 500mg/ml independently of the species. DNA ejection from the capsid is triggered by specific interaction of a phage tail protein with a receptor inserted in the wall of the bacteria. DNA is injected into the cytoplasm through the tail. The bacterial receptor of the T5 bacteriophage has been isolated (1), allowing to reconstitute the ejection process *in vitro* (2) and to investigate the underlying mechanisms (3) that show differences compared to Lambda and SPP1 bacteriophages (4). The T5 genome is almost 40µm long (113.9kbp) and confined in a capsid 80nm in diameter.

Using cryoElectron microscopy (cryoEM), we follow the organization of DNA inside the capsid at different steps of the ejection process and correlate these observations with the lengths and concentrations of encapsidated DNA. The DNA chain occupies the total volume of the capsid and reorganizes under confinement. The structure turns from crystalline hexagonal to 2D hexagonal, cholesteric and isotropic, following the sequence reported for solutions of short DNA fragments (5).

The interactions between DNA strands can also be monitored and turned from repulsive to attractive by addition of multivalent cations that diffuse through the protein capsid. After partial ejection of DNA, each individual DNA chain (3000 to 55000bp *i.e.* 1.4-18µm long) is collapsed inside each capsid. The structure of toroidal DNA is analyzed. We show how the frustration arising between chirality and hexagonal packing combined with the strong curvature imposed by the small volume of the container impose phasing of the helices and variations the DNA helical pitch (6).

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