

Commentary

Precise note on sizes and shapes of viral capsids

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DESCRIPTION

Capsid is a viral protein shell, which closes its genes. It contains several oligomeric (repetitive) structural units made up of proteins called protomers. The apparent subunits of 3-dimensional morphological, which may or may not interact with individual proteins, are called capsomeres. Capsid-forming proteins are called capsid proteins or viral coat proteins (VCP). The capsid and the inner genome are called nucleocapsid.

Capsids are broadly classified according to their structure. Most capsid-containing bacteria have a helical or icosahedral structure. Some bacteria, such as bacteriophages, develop complex structures due to elasticity limitations and electrostatics. The icosahedral shape, with 20 equal triangular faces, is almost circular, while the helical shape resembles a spring shape, replacing the cylinder but not the cylinder itself. The capsid surface may contain one or more proteins. For example, the capsid of the foot-and-mouth virus has a surface that contains three proteins called VP1–3.

Some bacteria are covered, meaning that the capsid is covered with a lipid membrane known as a viral envelope. The envelope is found by the capsid in the intracellular membrane at the host. Examples include the inner cell membrane, the Golgi membrane, and the outer cell membrane.

Once the virus has invaded the cell and begins to replicate, new capsid subunits are synthesized using the cell protein biosynthesis method. In some viruses, including those with helical capsids and especially those with RNA genomes, capsid proteins interact with their genomes. In some bacteria, especially complex viruses with double DNA genomes, capsid proteins combine to form procapsids that form a special portal structure at one vertex. Through this portal, viral DNA is transferred to capsid.

Specific shapes of capsid

1. Icosahedral: Icosahedral structure is most common among bacteria. The icosahedron has 20 triangular faces divided by 12 five-vertexes and contains 60 asymmetric units. Thus, the icosahedral virus is made up of 60N protein subunits. The number and arrangement of capsomeres in the icosahedral capsid can be divided using the “quasi-equity principle” proposed by Donald Caspar and Aaron Klug. Like Goldberg polyhedra, the icosahedral structure can be considered to be composed of pentamers and hexamers.

2. Prolate: Long icosahedron is a common form of bacteriophages. Such a structure is built with a cylinder with a cap on either end. The cylinder is made up of a long triangular surface. The Q-number, which can be any positive number, specifies the number of triangles, comprised of small unequal units, making up 10 triangular cylinders. Caps are divided by the number T.

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3. Helical: Many rod-shaped and filamentous plant viruses have capsids with helical symmetry. The helical structure can be described as a n 1-D set of molecular helices related to n -fold axial symmetry. The helical modification is divided into two categories. Single-dimensional and two-dimensional helical systems. Creating a helical structure based on a set of translation and rotation matrixes encoded in a protein data bank. Helical symmetry is given the formula $P = \mu \times \rho$, where μ is the number of units of structure per turn of the helix, ρ is the axial elevation per unit and P is the height of

the helix. The structure is said to be open due to the fact that any volume can be closed by changing the length of the helix. The most common helical virus is the tobacco mosaic virus. The virus is a single molecule of (+) strand RNA. Each coating protein inside the helix binds three nucleotides of the RNA genome. Influenza A viruses are synthesized by combining multiple ribonucleoproteins, the viral NP protein organizes RNA into a helical structure. Sizes are also different the tobacco mosaic virus has 16.33 protein subunits in each helical rotation, while the flu virus A has a tail loop of 28 amino acids.