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Function and origin of Capsid

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DESCRIPTION

A capsid is that the protein shell of an epidemic, enclosing its genetic material. It consists of several oligomeric structural subunits made from protein called protomers. The observable 3-dimensional morphological subunits, which can or might not correspond to individual proteins, are called capsomeres. The proteins making up the capsid are called capsid proteins or Viral Coat Proteins (VCP). The capsid and inner genome is named the nucleocapsid. Capsids are broadly classified consistent with their structure. The bulk of the viruses have capsids with either helical or icosahedral structure. Some viruses, like bacteriophages, have developed more complicated structures thanks to constraints of elasticity and electrostatics. The icosahedral shape, which has 20 equilateral triangular faces, approximates a sphere, while the helical shape resembles the form of a spring, taking the space of a cylinder but not being a cylinder itself. The capsid faces may contains one or more proteins. For instance, the hoof-and-mouth disease virus capsid has faces consisting of three proteins named VP1-3.

Some viruses are enveloped, meaning that the capsid is coated with a lipid membrane referred to as the viral envelope. The envelope is acquired by the capsid from an intracellular membrane within the virus' host; examples include the inner nuclear membrane, the Golgi membrane, and therefore the cell's outer membrane. Once the virus has infected a cell and begins replicating itself, new capsid subunits are synthesized using the protein biosynthesis mechanism of the cell. In some viruses, including those with helical capsids and particularly those with RNA genomes, the capsid proteins co-assemble with their genomes. In other viruses, especially more complex viruses with double-stranded DNA genomes, the capsid proteins assemble into empty precursor procapsids that has a specialized portal structure at one vertex. Through this portal, viral DNA is translocated into the capsid. Structural analyses of Major Capsid Protein (MCP) architectures are wont to categorise viruses into lineages. For instance, the bacteriophage PRD1, the algal virus Paramecium Bursaria Chlorella Virus (PBCV-1), Mimi virus and therefore the mammalian adenovirus are placed within the same lineage, whereas tailed, double-stranded DNA bacteriophages and herpesvirus belong to a second lineage.

FUNCTION

The functions of the capsid are to:
• Protect the genome,
• Deliver the genome, and
• Interact with the host.

The virus must assemble a stable, protective protein shell to guard the genome from lethal chemical and physical agents. These include sorts of natural radiation, extremes of pH or temperature and proteolytic and nucleolytic enzymes. For the non-enveloped viruses, the capsid itself could also be involved in interaction with receptors on the host cell, resulting in penetration of the host cell wall and internalization of the capsid. Delivery of the genome occurs by subsequent uncoating or disassembly of the capsid and release of the genome into the cytoplasm, or by ejection of the genome through a specialized portal structure directly into the host nucleus.

ORIGIN AND EVOLUTION

It has been suggested that a lot of viral capsid proteins have evolved on multiple occasions from functionally diverse cellular proteins. The recruitment of cellular proteins appears to possess occurred at different stages of evolution in order that some cellular proteins were captured and functionalized before the divergence of cellular organisms into the three contemporary domains of life, whereas others were hijacked relatively recently. As a result, some capsid proteins are widespread in viruses infecting distantly related organisms, whereas others are restricted to a specific group of viruses.

A computational model (2015) has shown that capsids may have originated before viruses which they served as a way of horizontal transfer between replicator communities since these communities couldn't survive if the amount of gene parasites increased, with certain genes being liable for the formation of those structures and people that favoured the survival of the self-replicating communities. The displacement of those ancestral genes between cellular organisms could favour the looks of latest viruses during evolution.