

VIRUS SYMMETRY

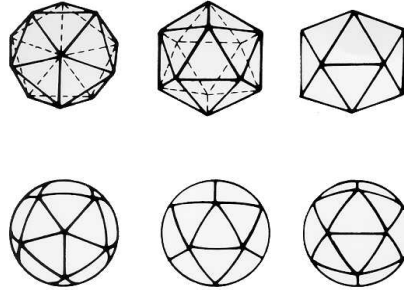
The orderly structural arrangement of similar protein to protein interface in viruses gives rise to a symmetrical structure. With the help of electron microscopy, it has been found that the morphology of nearly all viruses conforms to one of two basic symmetrical patterns which could be:

1. Cubic/icosahedral
2. Helical

These are the two capsid symmetries described for all viruses

Cubic/Icosahedral symmetry

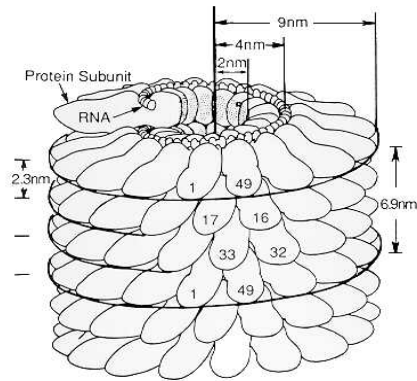
- Highly structured capsid in which capsomeres are arranged in form of an icosahedrons
- In the icosahedrons, there are 20 triangular faces and 12 apices/corners
- The capsomeres of each face form an equilateral triangle
- The capsomeres contribute to the rigidity of the capsid and help protect the nucleic acid genome
- Each individual capsomere may consist of several polypeptides (in poliovirus, the capsomere is made up of three proteins)
- All DNA viruses of animals except poxviruses as well as some RNA viruses possess icosahedral symmetry
- Viruses with icosahedral symmetry could be naked (without envelope) or enveloped
- Icosahedral capsids are generally assembled in the host cell prior to incorporation of the viral nucleic acid. Some viral preparations may contain capsids devoid of nucleic acids.



Icosahedral models (left to right) on fivefold, threefold, and twofold axes of rotational symmetry (Copyright © 1996 The University of Texas Medical Branch at Galveston)

Helical Symmetry

- Single stranded RNA viruses such as paramyxoviruses, orthomyxoviruses and rhabdoviruses have helical symmetry
- The capsid is in form of a helix
- Helical viruses resemble long rods that may be rigid or flexible
- The flexuous helical nucleocapsid is always contained within a lipoprotein envelope
- The envelope is lined internally by a matrix protein (M-protein)
- The M-protein may be rigid as in the case of bullet shaped rhabdoviruses or readily distorted as in orthomyxoviruses and paramyxoviruses
- The capsid of helical viruses is formed by the insertion of protein units between each turn of the nucleic acid helix.
- The capsid protein helix thus coincides with that of the nucleic acid and the length of the helix is determined by the length of the RNA molecule
- Helical capsid devoid of nucleic acid cannot be formed.
- In RNA viruses, each capsomere consists of a single polypeptide molecule



The helical structure of the rigid tobacco mosaic virus rod (Copyright © 1996 The University of Texas Medical Branch at Galveston)

Complex Symmetry

- Large viruses with large genome have complicated symmetry
- For example, poxviruses have complex symmetry which is neither icosahedral nor helical

CLASSIFICATION OF VIRUSES

Following the discovery of viruses, earliest studies on them were based on their filterability, and observations on the diseases which they caused. Early classification systems were premised on pathogenic effects of the viruses and their transmission patterns. However, with the invention of electron microscope and sophisticated molecular techniques that permitted ultra-structural studies, details of the structures and compositions of viruses began to emerge. Thereafter, it became possible to group viruses on the basis of shared features of the virions.

Consequently, the following general parameters are have been used for classification of viruses:

1. Pathogenicity
2. Ecological characteristics

3. Physico-chemical characteristics

Pathogenicity:

In this classification, viruses affecting same tissues producing similar syndrome and pathological manifestations are grouped together.

- Viruses affecting the respiratory tract: Influenza, rhinoviruses, parainfluenza, adenovirus
- Vesicular viruses: Foot-and-Mouth-Disease, vesicular stomatitis
- Central nervous system viruses: rabies, equine encephalitis, enteroviruses (polio), mumps
- Mucous membrane viruses: Myxomaviruses
- Enteric viruses: rotaviruses,
- Limitations of this classification system: some viruses affect more than one system of the body and they will belong to several groups. Pantropic viruses affecting multiple systems such as canine distemper, Newcastle disease, rinderpest, pestes des petits ruminants will belong to respiratory, enteric and CNS groups.

Ecological characteristics:

Ecological features of viruses such as the involvement of vectors or vertebrate reservoirs in their transmission cycles and maintenance in nature can be used for classification. Viruses are classified into arboviruses and non-arboviruses or roboviruses and non-roboviruses.

Arboviruses: these are viruses that are transmitted biologically between blood sucking arthropods (such as ticks, culicoides, mosquitoes) and vertebrate hosts. They cause disease in the vertebrate host but not in the arthropods. Examples include African swine fever virus (soft ticks), Yellow fever virus (mosquitoes), Equine encephalitis virus (mosquitoes), African horse sickness virus (culicoides).

Reboviruses: These are viruses with rodent reservoirs. Infected rodents are asymptomatic. They shed the virus in their urine and contaminate the human surroundings, food, drinks and fomites.

Example include Lassa fever virus with rat as reservoir.

Physico-chemical characteristics:

These are the most reliable, verifiable and satisfactory parameters for classifying viruses. Viruses are classified based on the following criteria:

- Type of nucleic acid (RNA or DNA)
- Number of strands of the nucleic acid (single or double stranded)
- Physical construction of the nucleic acid (linear, circular, circular with break, segmented, non-segmented)
- Polarity of the viral genome: positive polarity (viral genome can be used directly as mRNA) and negative polarity(viral genome must be transcribed into mRNA)
- Symmetry of the nucleocapsid
- Presence or absence of envelope
- Size of the virus
- Antigenic and chemical compositions
- Susceptibility to physical and chemical changes

Based on these criteria, viruses are grouped into families, subfamilies and genera. Further subdivision is based on the degree of antigenic similarity and serological tests. Antigenically identical viruses can be further grouped by differences in biological characteristics including virulence, cellular receptors and nucleotide sequences.

VIRUS NOMENCLATURE

The nomenclature of viruses has been in a constant state of flux for many years. This is may not be unconnected with emerging facts about the composition and morphology of viruses with advanced studies made possible by new technologies.

- Some viruses are named according to the type of disease they cause. Examples include poxviruses, herpesviruses (creeping lesions)
- Other are named based on acronyms of disease (papovavirus -papilloma, -polyoma -vacuolating) or acronym of observable characteristics (picornavirus -pico/small -rna -virus)
- Viruse are also named based on morphology as revealed by electron microscopy. Coronaviruses (halo or corona/crown of spikes), Togavirus (Toga/cloak), Rhabdovirus (Rhabdo/Rod-shaped), Calicivirus (Calix/cup-shaped depression)
- Some viruses are named after geographical regions where they were first isolated (E. g. Coxsackie-, Marburg-, Gumboro-, Mokola- virus)
- Occasionally, viruses are named after individual discoverer (Epstein-Barr virus)

The International Committee on Taxonomy of Viruses (ICTV) was established in 1973 to develop and expand the universal scheme in which characteristics of virions are used to assign them to five hierarchical levels (order, family, subfamily, genus and species). The hierarchical levels are denoted with the following suffixes:

Order: -virale

Family: -viridae

Subfamily: -virinae

Genus: -virus

Species: -virus

The primary considerations for virus taxonomy are the type and nature of the genome, the mode and site of replication and the structure and morphology of the virion.

Virus orders are designated by the suffix –virale. Phylogenetically-related families are grouped together. Many virus families are yet to be assigned into orders. Only two orders containing viruses of animals are so far recognized. The virus order Mononegavirale is made up the families Paramyxoviridae, Rhabdoviridae, Bornaviridae and Filoviridae. Members of the order Mononegavirale have common attributes including a single stranded, non-segmented, negative sense RNA genome. Their replication strategies are also similar. The second viral order is the Nidovirale comprising of the families Coronaviridae and Arteriviridae.