

Viruses occur universally. It is likely that every living organism on this planet is infected by a species-specific range of viruses.

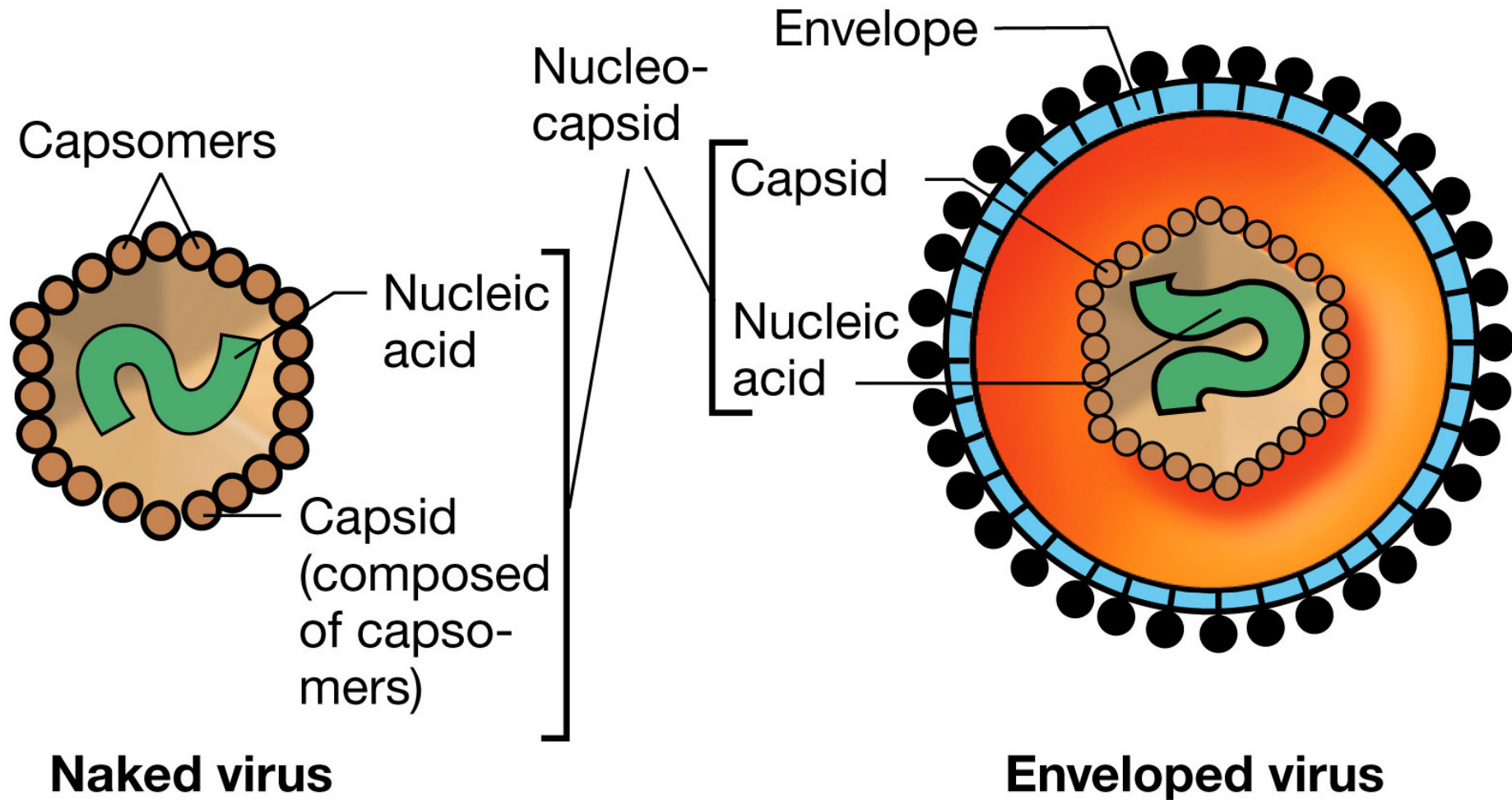
Viruses are obligate intracellular parasites that require a host within which they replicate.

Although they are well known for causing disease, most viruses coexist peacefully with their hosts.

# Properties common to all viruses

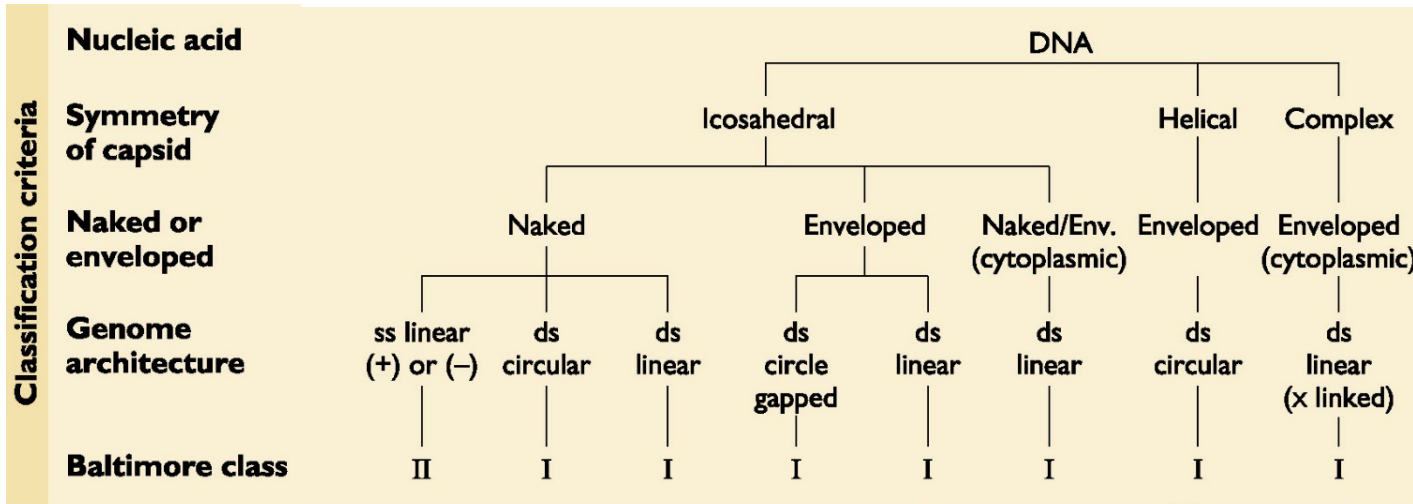
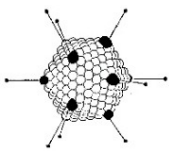
- Viruses have a nucleic acid genome of either DNA or RNA.
- Compared with a cell genome, viral genomes are small, but genomes of different viruses range in size by over 100-fold (ca 3000 nt to 1,200,000 bp)
- Small genomes make small particles – again with a 100-fold size range.
- Viral genomes are associated with protein that at its simplest forms the virus particle, but in some viruses this nucleoprotein is surrounded by further protein or a lipid bilayer.
- The outermost proteins of the virus particle allow the virus to recognise the correct host cell and gain entry.
- Viruses can only reproduce in living cells: they are obligate parasites.

# Diagrammatic structure of virus particles



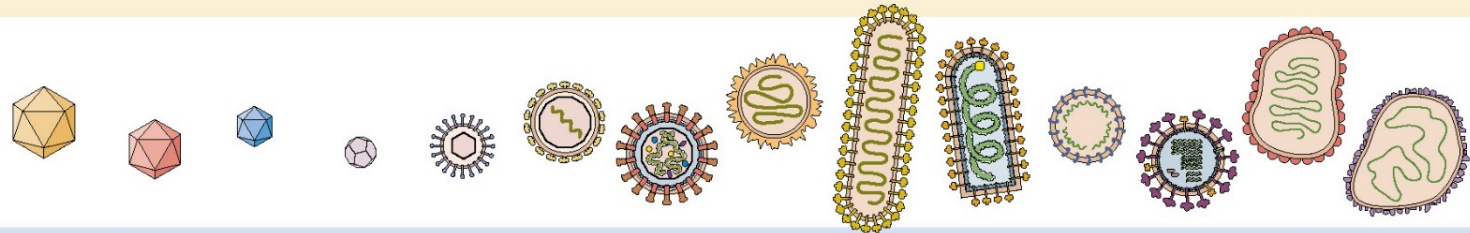
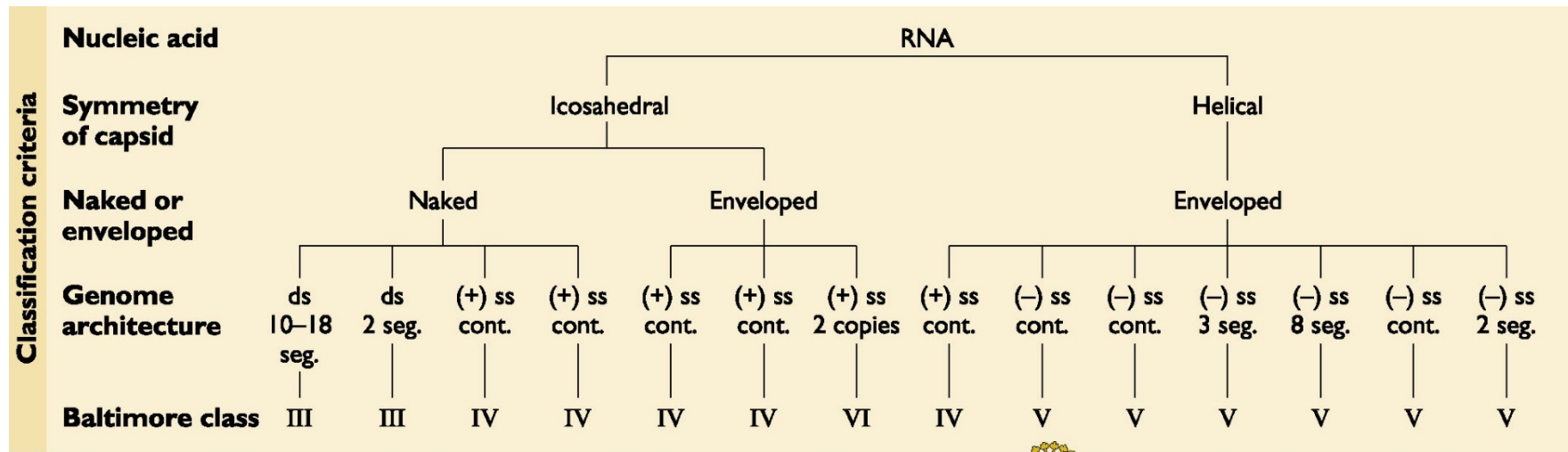
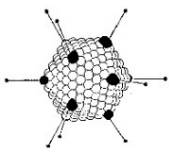
# Classification criteria

- Nature of the nucleic acid
- Protein coat symmetry (capsid)
- Presence or absence of lipid envelope
- Genome architecture



<b>Properties</b>	<b>Family name</b>	Parvo	Papova	Adeno	Hepadna	Herpes	Irido	Baculo	Pox
	<b>Virion polymerase</b>	(-)	(-)	(-)	(+)	(-)	(-)	(-)	(+)
	<b>Virion diameter (nm)</b>	18-26	45-55	70-90	42	150-200	125-300	60 X 300	170-200 x 300-450
	<b>Genome size (total in kb)</b>	5	5-8	36-38	3.2	120-200	150-350	100	130-280

From Flint et al. *Principles of Virology* (2000), ASM Press

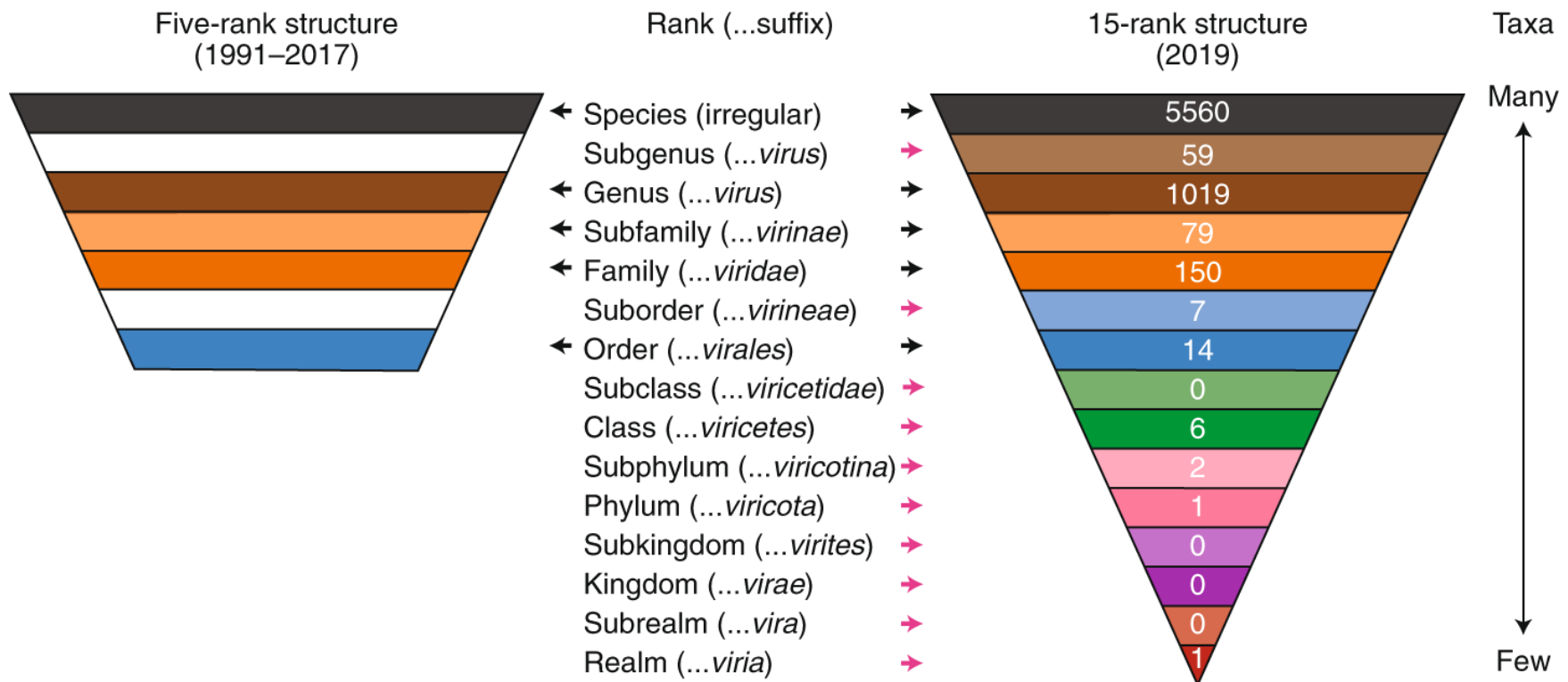


Properties	Family name	Reo	Birna	Calici	Picorna	Flavi	Toga	Retro	Corona	Filo	Rhabdo	Bunya	Orthomyxo	Paramyxo	Arena
	Virion polymerase	(+)	(+)	(-)	(-)	(-)	(-)	(+)	(-)	(+)	(+)	(+)	(+)	(+)	(+)
	Virion diameter (nm)	60-80	60	35-40	28-30	40-50	60-70	80-130	80-160	80 x 790-14,000	70-85 x 130-380	90-120	90-120	150-300	50-300
	Genome size (total in kb)	22-27	7	8	7.2-8.4	10	12	3.5-9	16-21	12.7	13-16	13.5-21	13.6	16-20	10-14

From Flint et al. *Principles of Virology* (2000), ASM Press

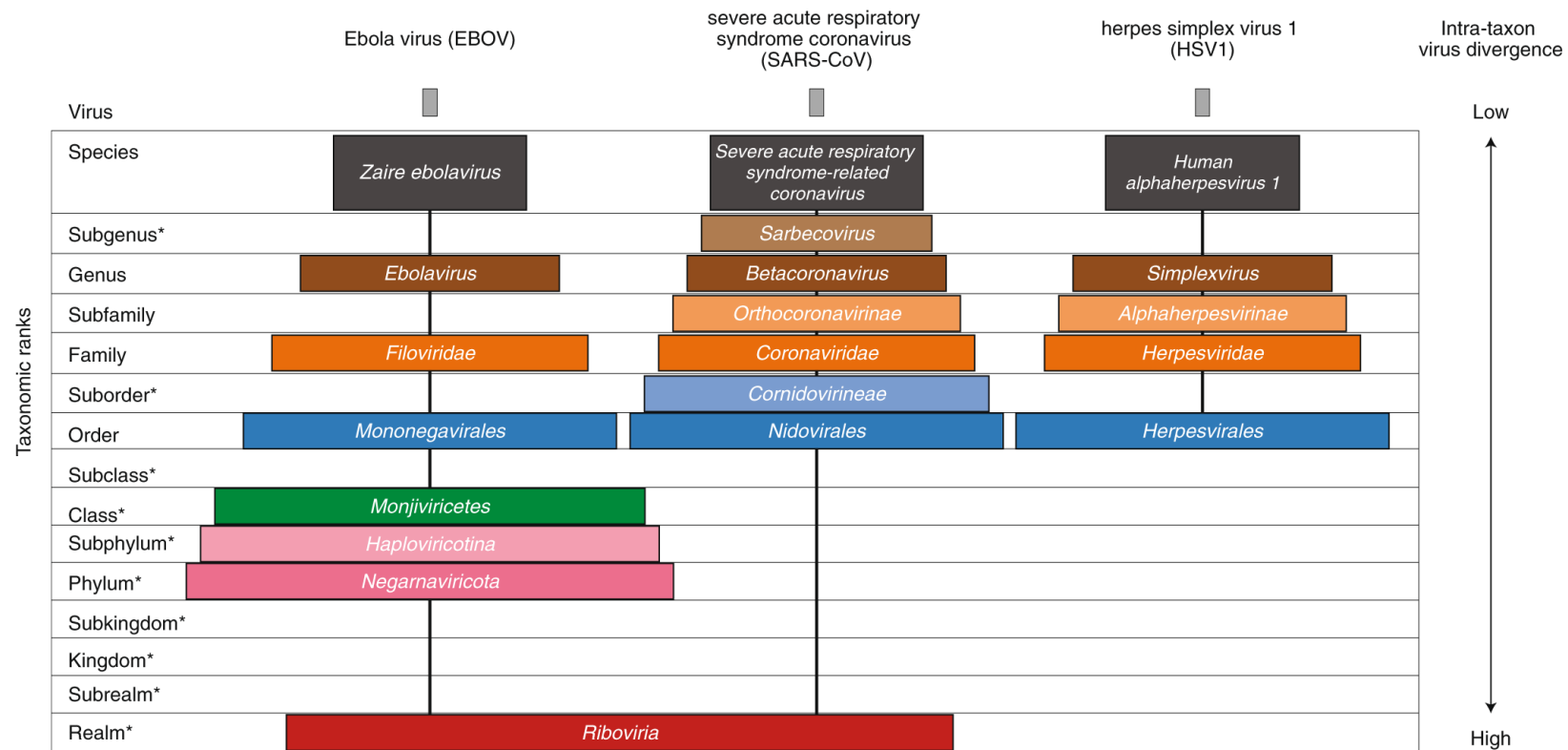
- A comparison of the ICTV (International Committee on Taxonomy of Viruses) taxonomic rank hierarchy in 1991–2017 and 2019

Taxonomic ranks are shown in relation to the distribution pattern of taxa. The number of taxa assigned to each rank (as recorded in the current ICTV Master Species List, release 2018b, MSL34) are shown in white font on the 15-rank structure. When the ranks are described as a hierarchy, the species rank is often referred to as the lowest rank and the realm rank as the highest rank. However, when the ranks are used as phylogenetic terms, the realm rank can be described as basal and the species rank as apical or terminal. Both conventions are used in this Consensus Statement. Black arrows, ranks common to the five- and 15-rank structure; pink arrows, ranks introduced in the 15-rank structure





# Classification of EBOV, SARS-CoV and herpes simplex virus 1 in the 15-rank taxonomic hierarchy



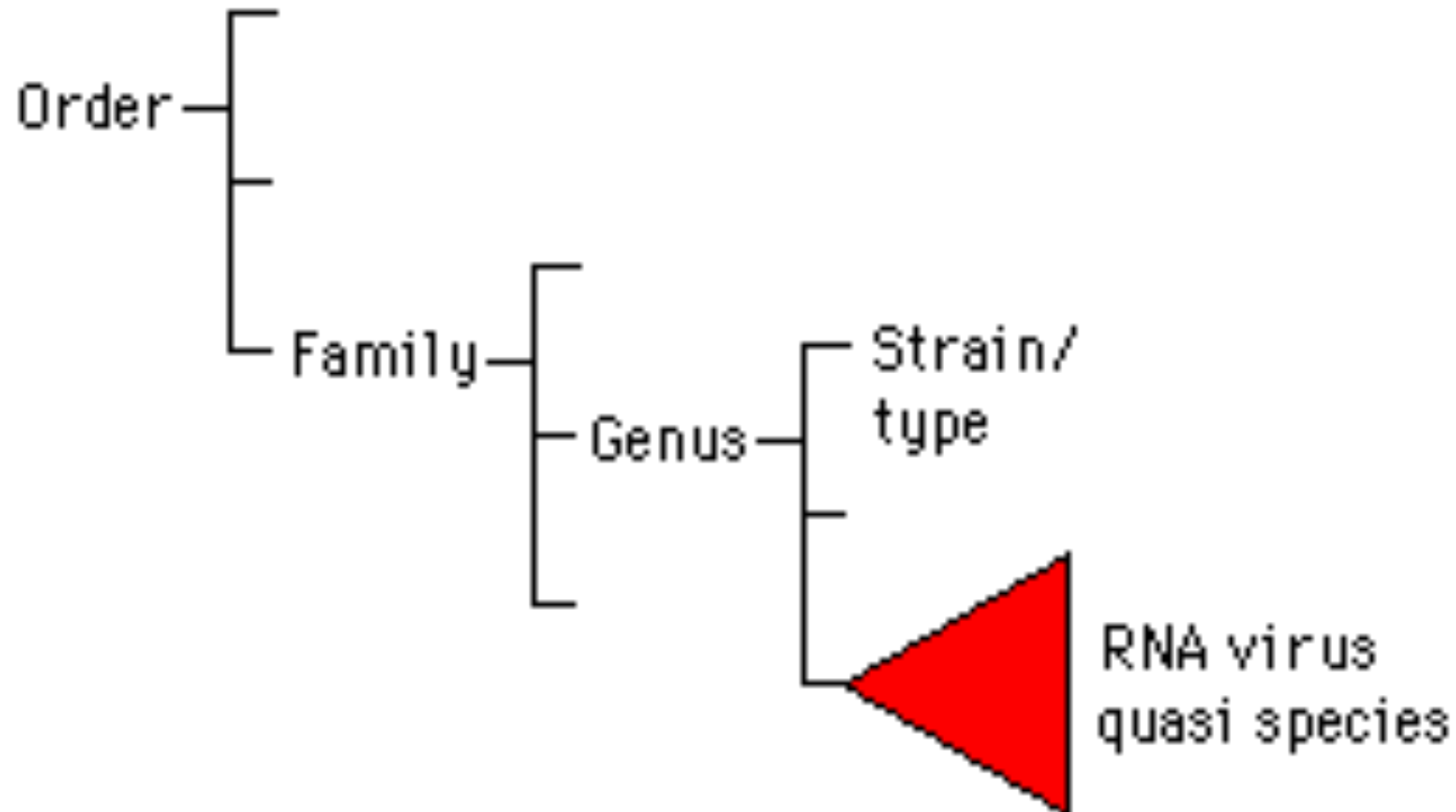
Intra-cluster virus divergence, which increases from the virus species rank to the realm rank, is represented by the increasing width of the respective rectangles, which are not drawn to scale. EBOV is most closely related to, but distinct from, Bombali, Bundibugyo, Reston, Sudan and Tai Forest viruses, which belong to separate species included in the *Ebolavirus* genus. SARS-CoV is one of several closely related coronaviruses isolated from humans and animals, such as palm civets and bats, and are included in the species *Severe acute respiratory syndrome-related coronavirus*. Herpes simplex virus 1 is one of two human herpesviruses belonging to different species in the *Simplexvirus* genus. Ranks that were introduced with the extended rank structure are indicated by an asterisk.



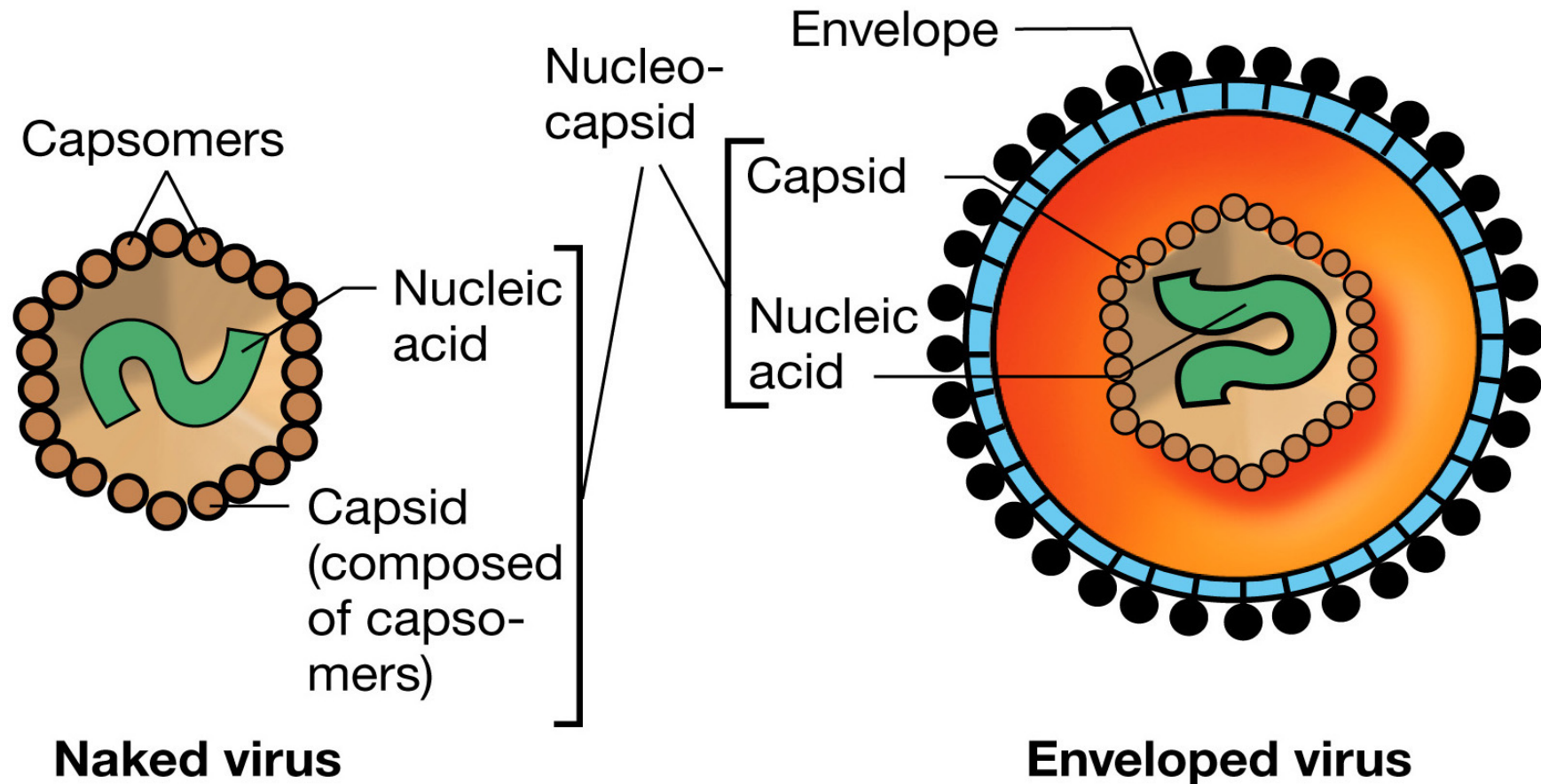
# Virus taxonomy

(ICTV fondato fine anni '60)

L'ordine ha suffisso –virales. La famiglia ha suffisso -viridae. La sottofamiglia ha suffisso –virinae. Il genere ha suffisso -virus. La specie?



# Diagrammatic structure of virus particles



# The diversity of viral genomes

## DNA Genomes

*Double-Stranded DNA (dsDNA)*

*Gapped DNA*

*Single-Stranded DNA (ssDNA)*

## RNA Genomes

*dsRNA*

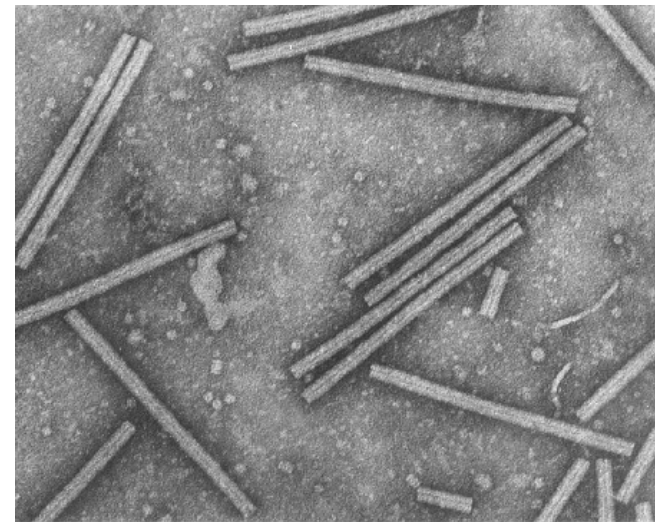
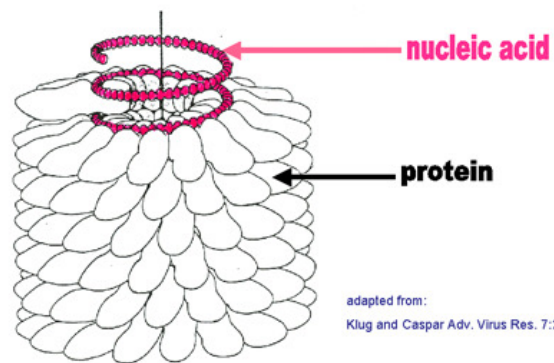
*(+) Strand RNA*

*(-) Strand RNA*

# Capsid symmetry

The **helical symmetry** is very common among plant viruses

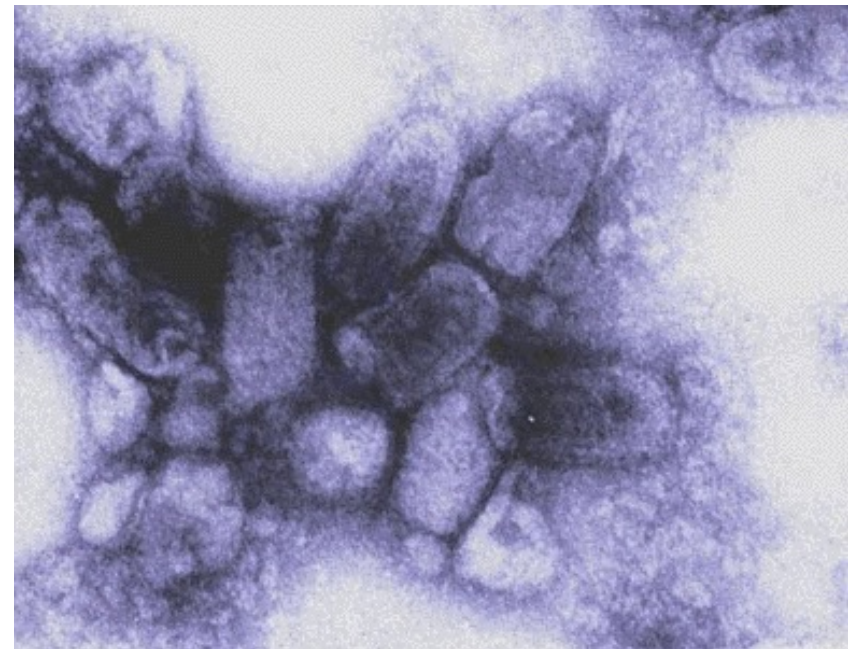
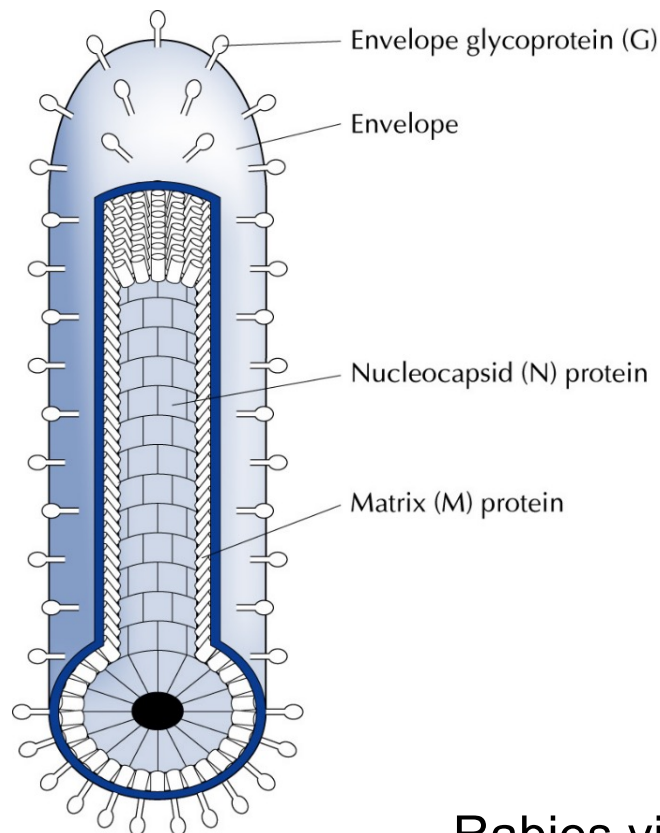
TOBACCO MOSAIC VIRUS



# Capsid symmetry

Helical animal viruses are all enveloped viruses.

Many of them are pathogenic to humans: influenza virus (*Orthomyxoviridae*), viruses that cause measles and mumps (*Paramyxoviridae*), the rabies virus (*Rhabdoviridae*) Ebola and Marburg viruses (*Filoviridae*)



Rabies virus

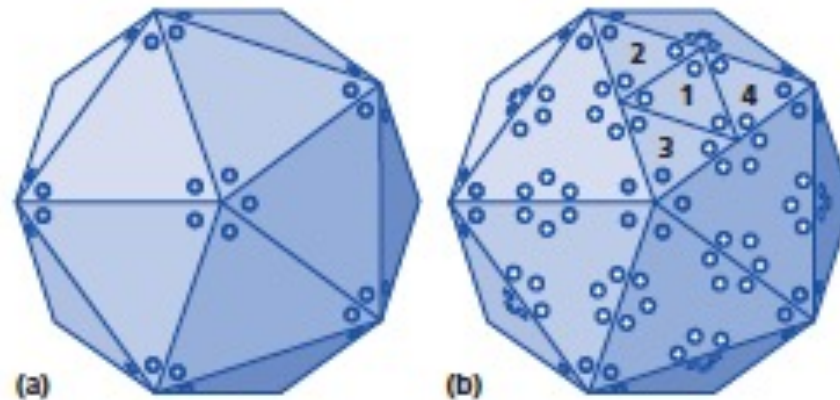
From Cann *Principles of molecular virology* (2001). Academic Press

# Capsid symmetry

**Icosahedral symmetry.** The simplest capsids are formed by 60 protomers. They are distributed such that there is one subunit at the vertices of each of the triangular faces. Five protomers around each vertex of the icosahedron form the capsomer, the morphological units (in this case named **penton**). Icosahedral viruses with capsid consisting of 60 protomers are known, but they are not independently replicating viruses

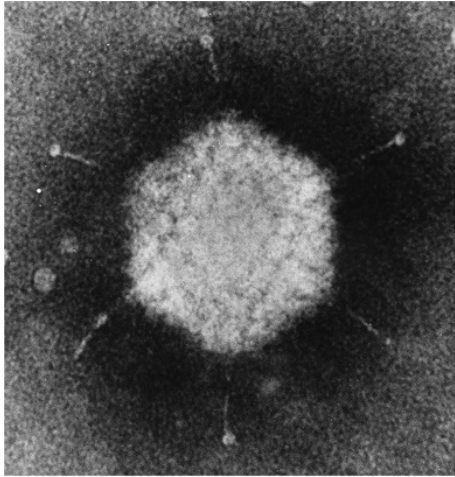


# Capsid symmetry

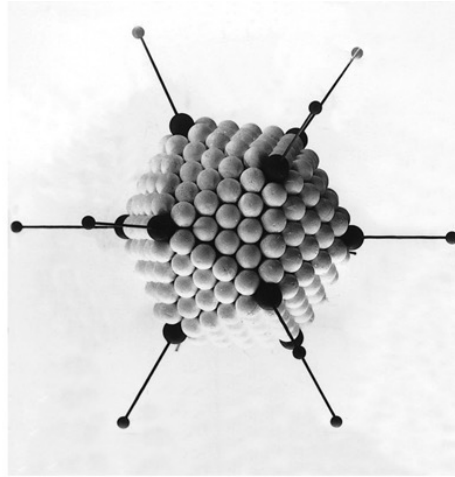


Arrangement of  $60n$  identical subunits on the surface of an icosahedron. (a)  $n = 1$  and the 60 subunits are distributed such that there is one subunit at the vertices of each of the 20 triangular faces. Note that each subunit has the same arrangement of neighbours and so all the subunits are equivalently related. (b)  $n = 4$ . Each triangular face is divided into 4 smaller, but identical, equilateral triangular facets and a subunit is again located at each vertex. In total, there are 240 subunits. Note that each subunit, whether represented by an open or closed circle, has the identical arrangement of neighbours: see the face in which triangles 1–4 have been drawn. However, since some subunits are arranged in pentamers and others in hexamers, the members of each set are quasi-equivalently' related.

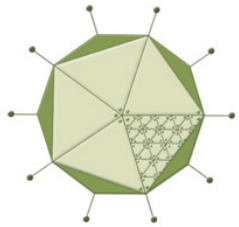




(a)

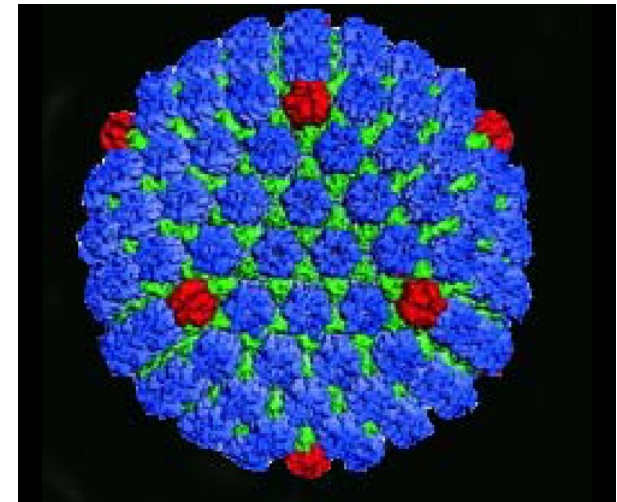
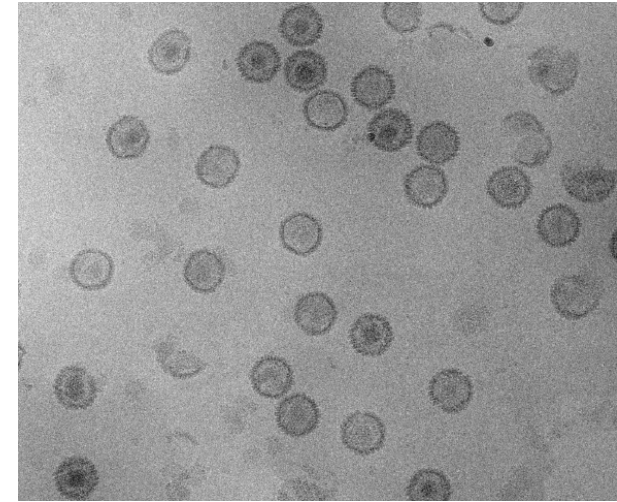


(b)

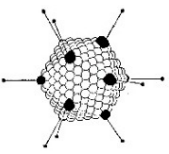


(c)

Adenovirus  $T=25$



HSV-1  $T=16$



# VIRAL ENVELOPE

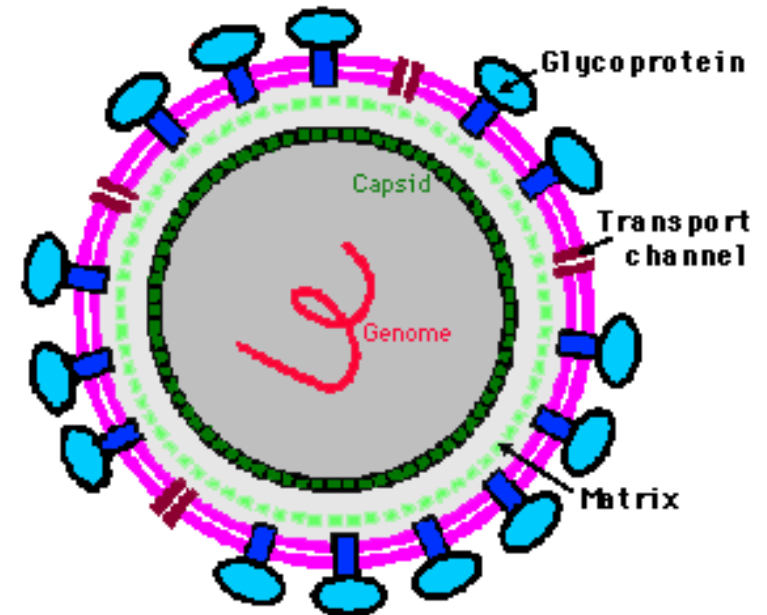
The envelope is made up of a **lipid bilayer** that is acquired by budding from the cell membranes and contains virus-specific proteins:

**Surface glycoproteins (all enveloped viruses)**

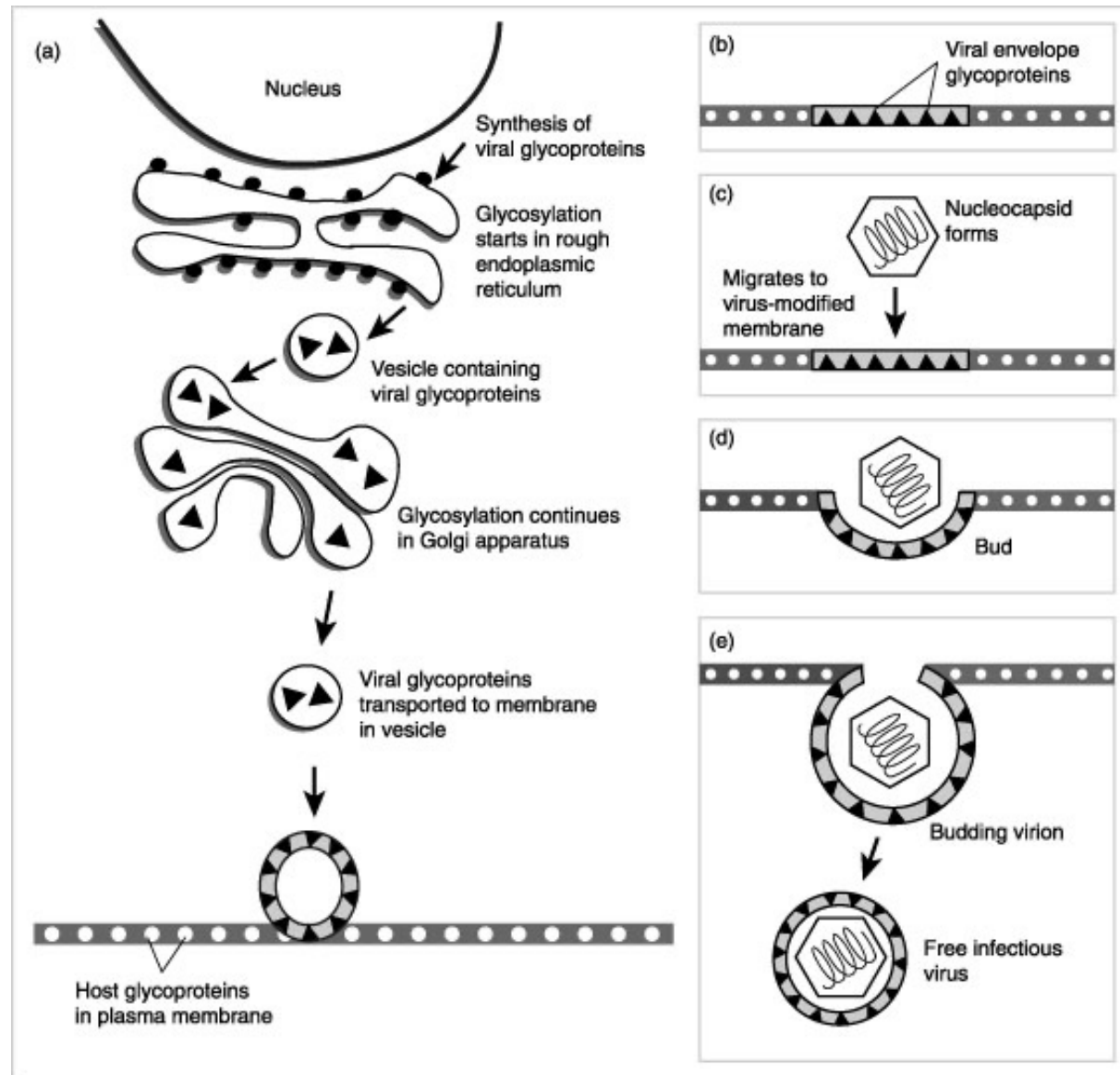
**Transmembrane glycoproteins**

**Transport channel**

Most enveloped viruses are characterized by the presence of a **matrix** that connects the capsid to the lipid envelope.



# Budding



# Envelope acquisition - Budding

