



VIRUS TAXONOMY AND REPLICATION

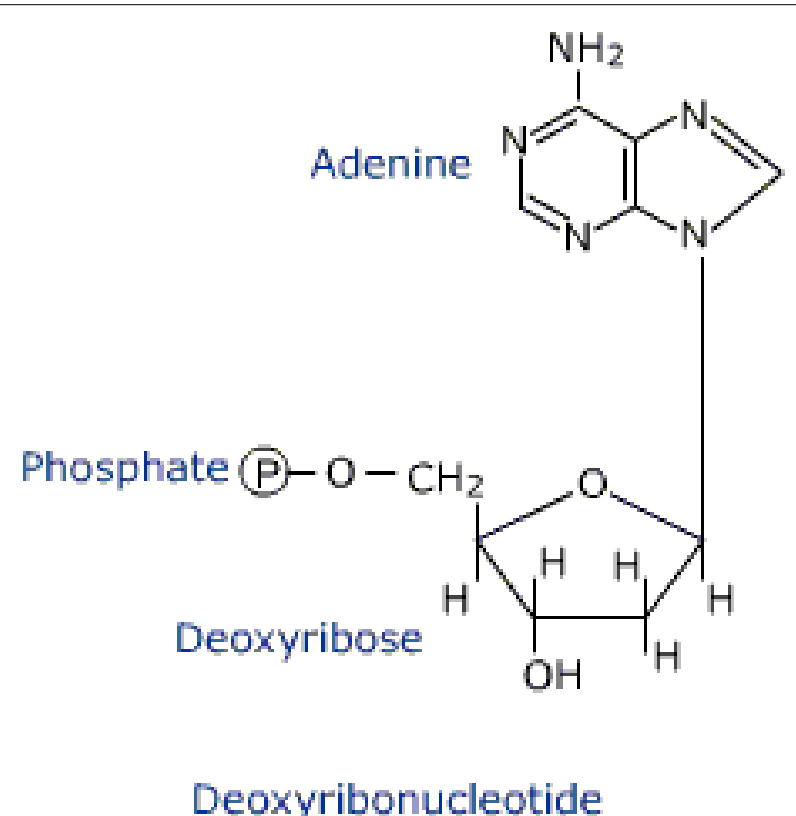
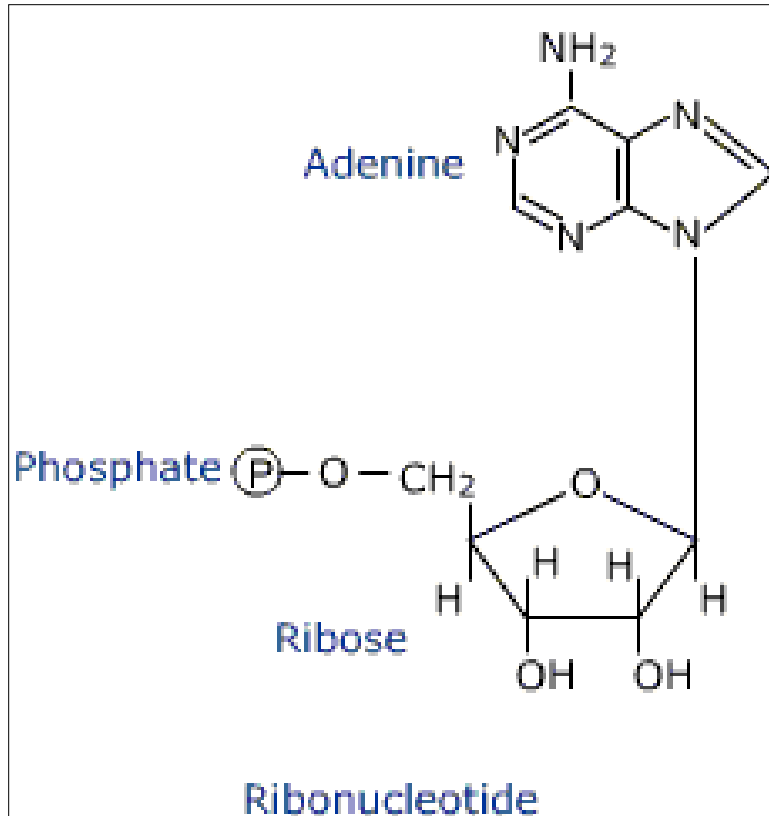
Paulo Eduardo Brandão, PhD
Department of Preventive Veterinary Medicine and Animal Health
School of Veterinary Medicine
University of São Paulo, Brazil

I. VIRUS STRUCTURE AND COMPOSITION

GENOME

EITHER RNA

OR DNA



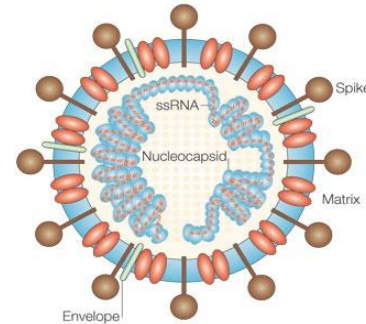
I. VIRUS STRUCTURE AND COMPOSITION

GENOME

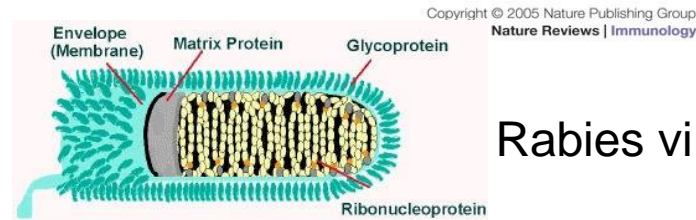
RNA VIRUSES: NUMBER OF
RNA STRANDS = 1 or 2

3.5 to 32 kb

SINGLE-STRANDED RNA

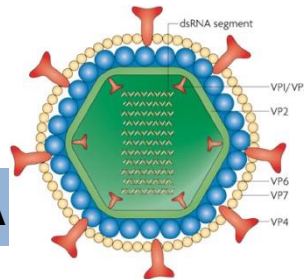


Coronaviruses

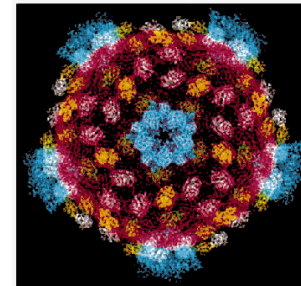


Rabies virus

DOUBLE-STRANDED RNA



Rotavirus



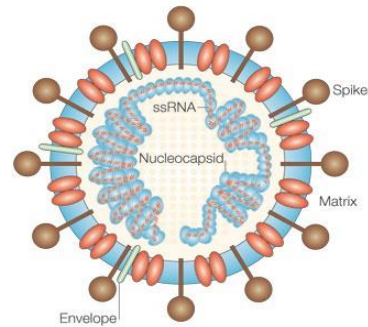
Reovirus

I. VIRUS STRUCTURE AND COMPOSITION

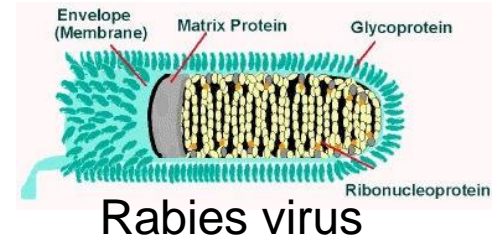
GENOME

RNA VIRUSES: NUMBER OF
RNA SEGMENTS = 1 TO 11

NON-SEGMENTED
RNA



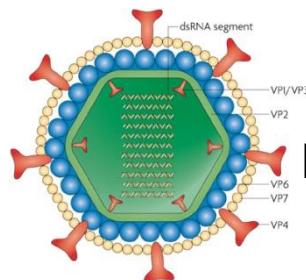
Coronaviruses



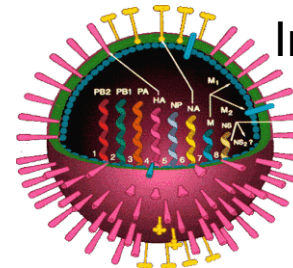
Rabies virus

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Nature Reviews | Immunology

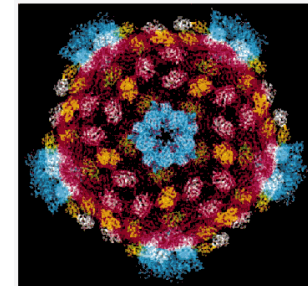
SEGMENTED RNA



Rotavirus



Influenzavirus



Reovirus

I. VIRUS STRUCTURE AND COMPOSITION

GENOME

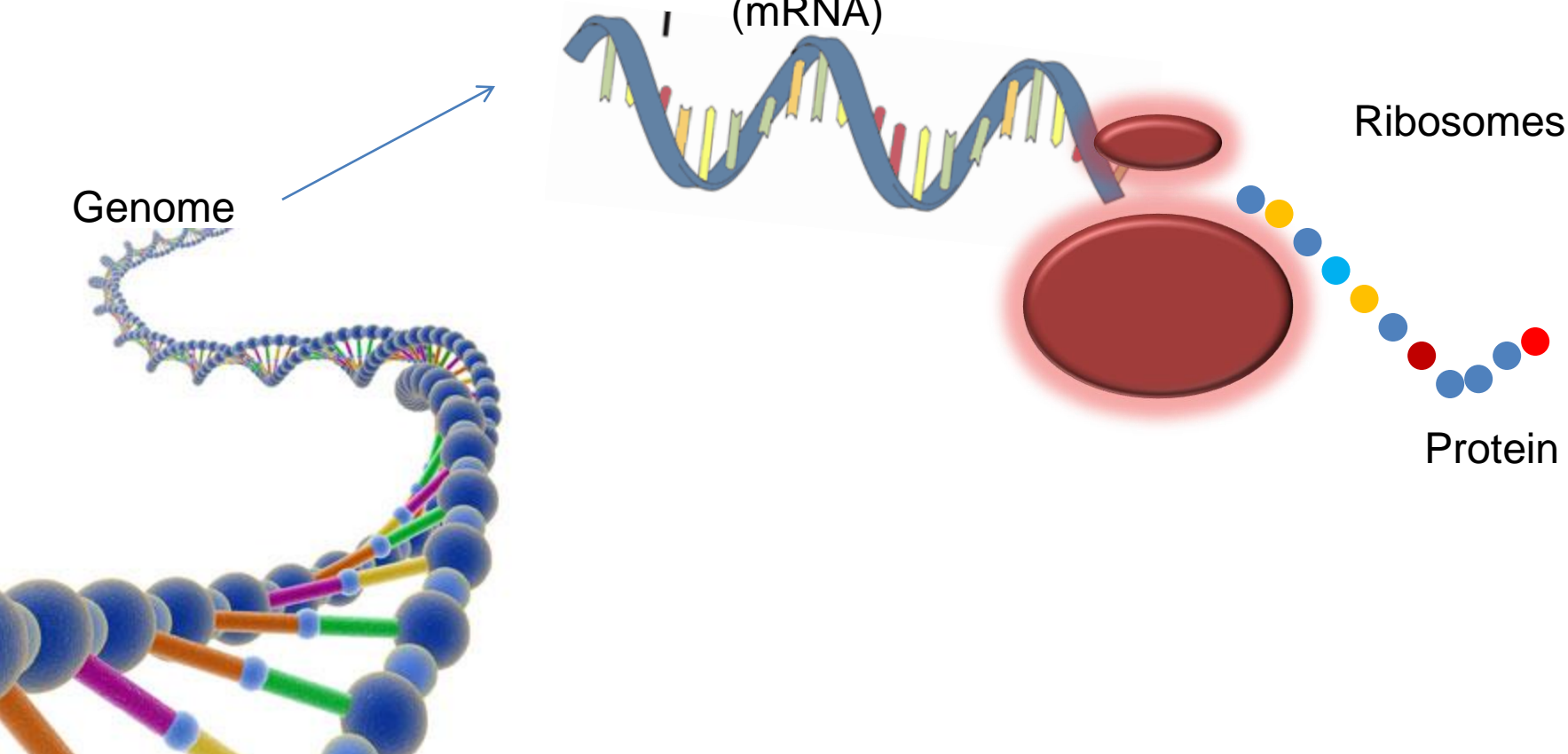
RNA VIRUSES: RNA POLARITY

Messenger
RNA
(mRNA)

Ribosomes

Genome

Protein



I. VIRUS STRUCTURE AND COMPOSITION

GENOME

RNA VIRUSES: RNA POLARITY

POSITIVE-SENSE RNA

VIRUS GENOME SERVES AS mRNA AND IS DIRECTLY TRANSLATED BY RIBOSOMES INTO VIRUS PROTEINS

- ☞ **Coronaviruses**
- ☞ **Classical swine fever**
- ☞ **Foot-and-mouth disease virus**

NEGATIVE-SENSE RNA

A mRNA MUST BE SYNTHESIZED AND ONLY THEN TRANSLATED BY RIBOSOMES

- ☞ **Rabies virus**
- ☞ **Influenzaviruses**
- ☞ **Canine distemper virus**

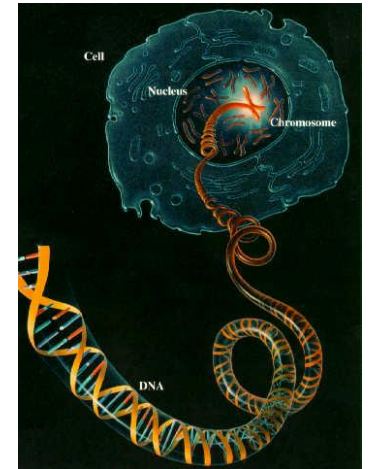
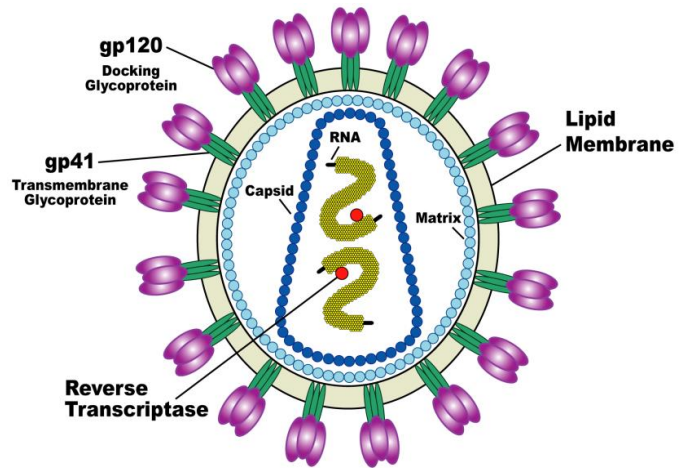
I. VIRUS STRUCTURE AND COMPOSITION

GENOME

RETROVIRUSES: QUITE DIFFERENT!

Reverse transcriptase

RNA GENOME → COMPLEMENTARY DNA → **INTEGRATION**
TO HOST CELL
DNA



I. VIRUS STRUCTURE AND COMPOSITION

GENOME

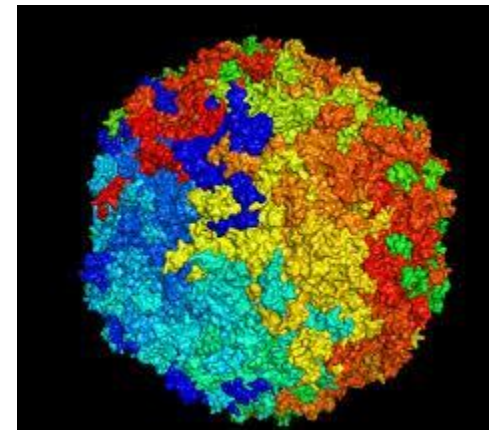
DNA STRANDS AND POLARITY

(1.8 thousand to 2.8 million base pairs)

DOUBLE-STRANDED: MOST DNA VIRUSES

**SINGLE-STRANDED
(NEGATIVE SENSE OR POSITIVE SENSE): *e.g.* PARVOVIRUS**

In this case, a dsDNA will be produced during infection



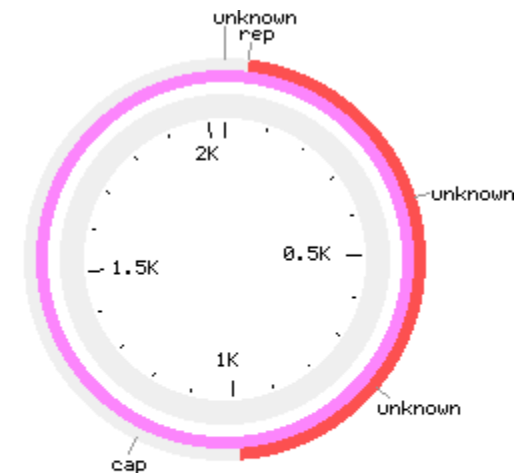
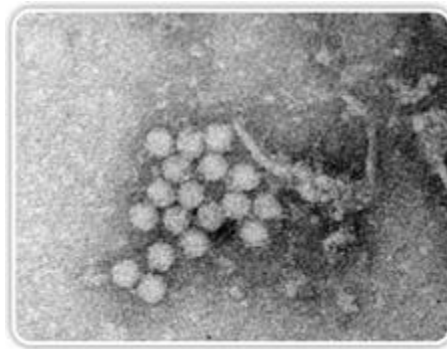
I. VIRUS STRUCTURE AND COMPOSITION

GENOME

DNA MORPHOLOGY

LINEAR: MOST DNA VIRUSES

CIRCULAR: CIRCOVIRUS

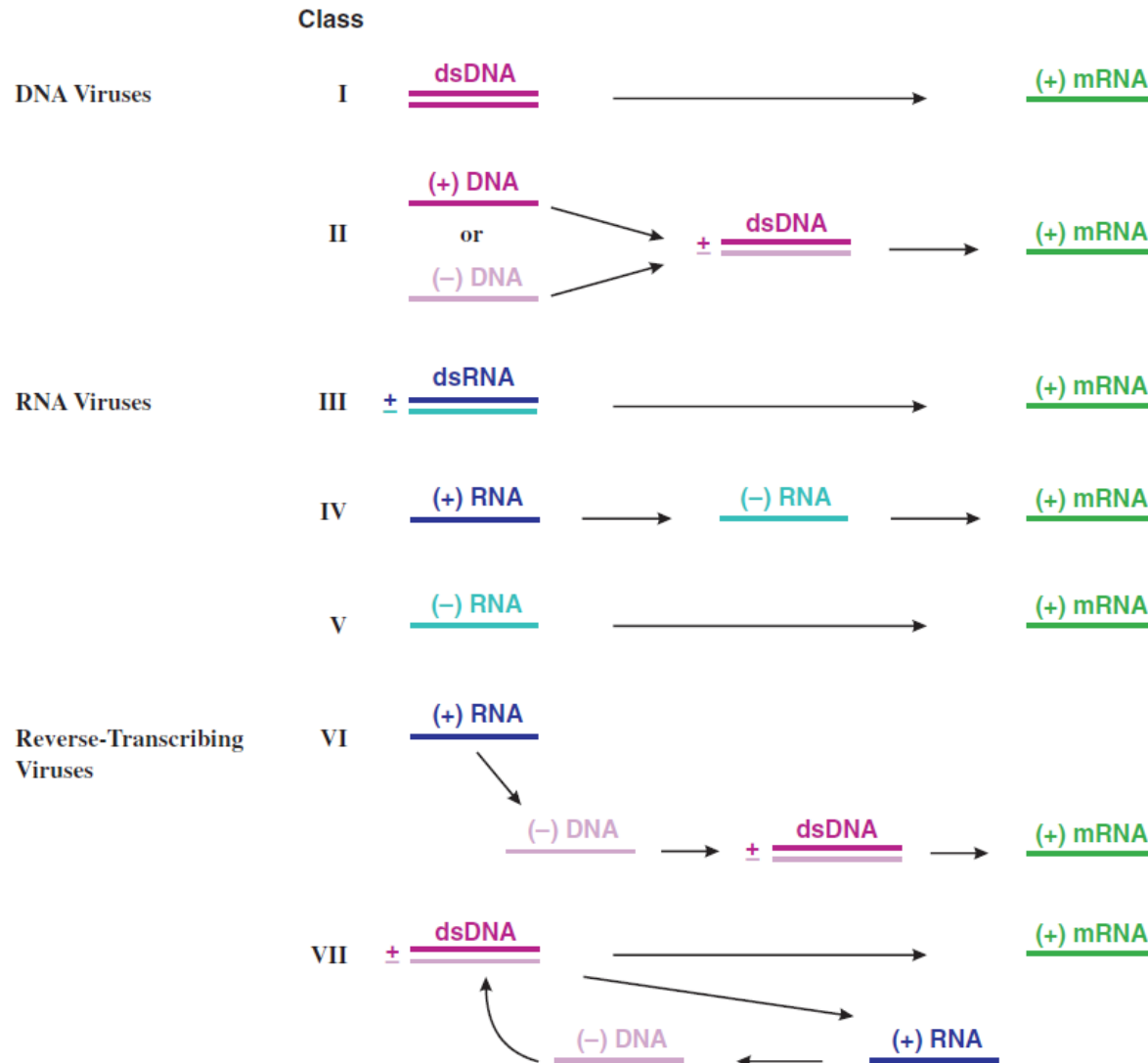


Legend:

- CDS +strand
- CDS -strand

I. VIRUS STRUCTURE AND COMPOSITION

GENOME



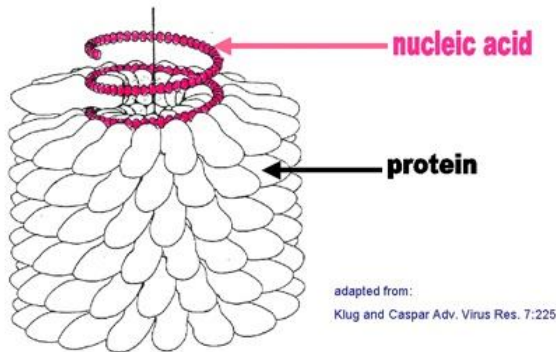
The Baltimore classification of viruses based on genome type

I. VIRUS STRUCTURE AND COMPOSITION

CAPSID

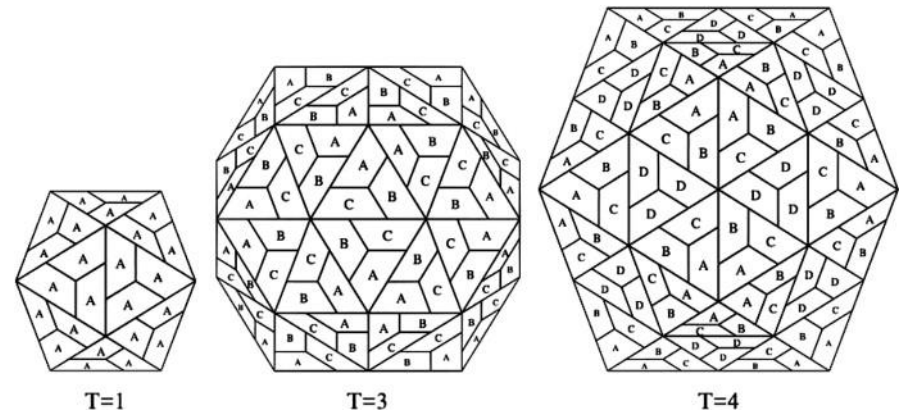
THE CAPSID IS THE GENOME PROTEIN COAT

Helical simetry



Icosahedral simetry

Mateu MG 2013



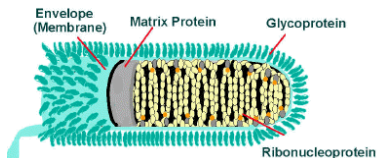
T=triangulation number: number of pentagons and hexagons in the icosahedron

I. VIRUS STRUCTURE AND COMPOSITION

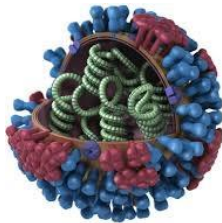
CAPSID

Helical simetry

Rabies virus



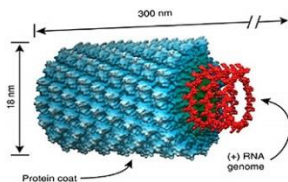
Influenzavirus



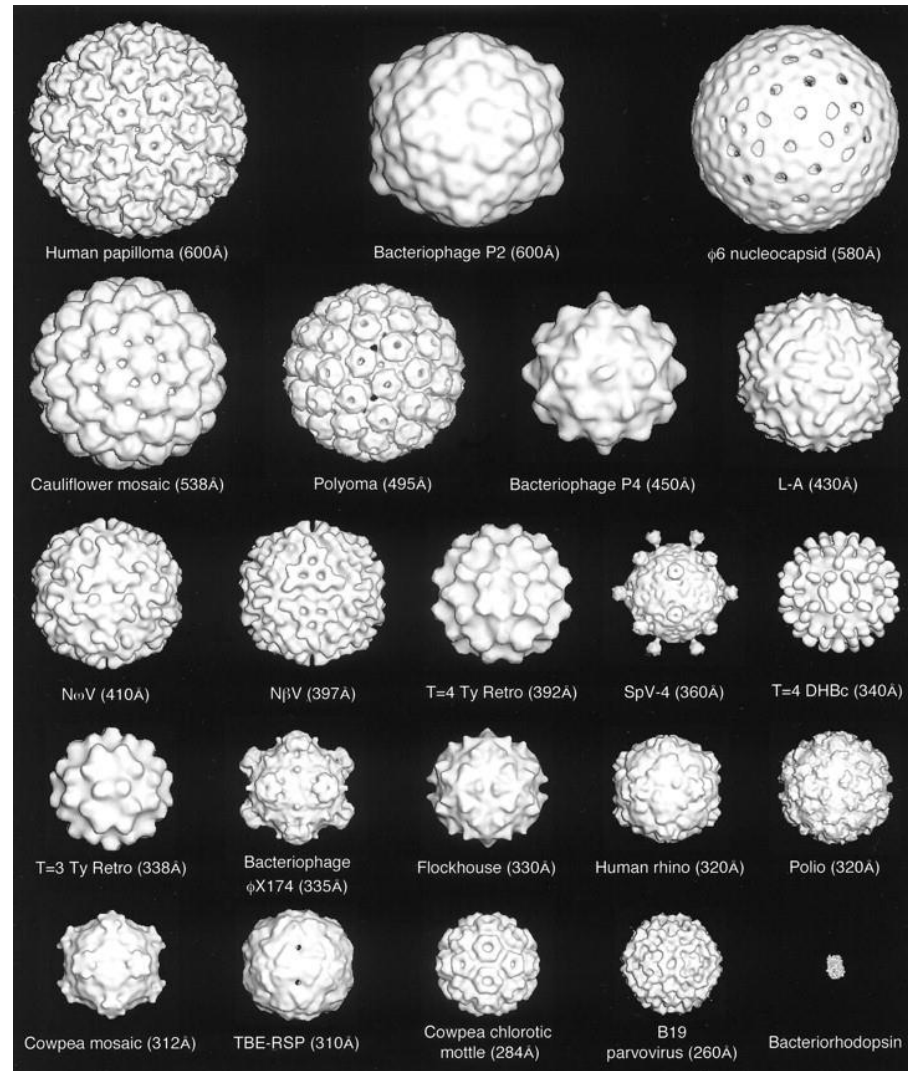
Marburg virus



Tobacco mosaic virus



Icosahedral simetry

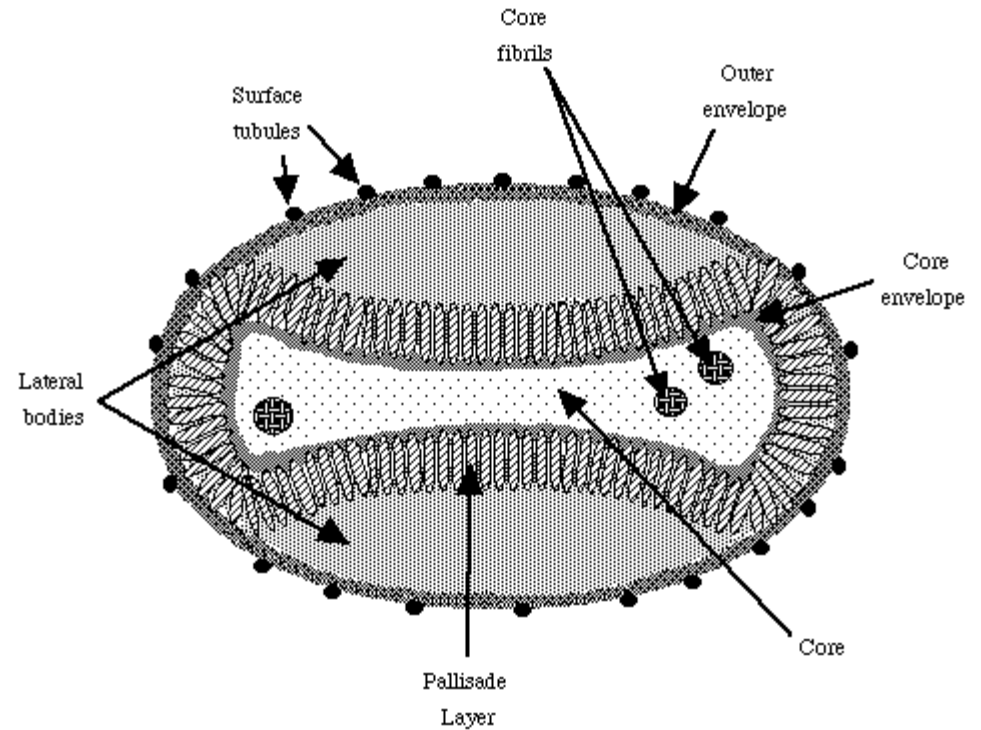
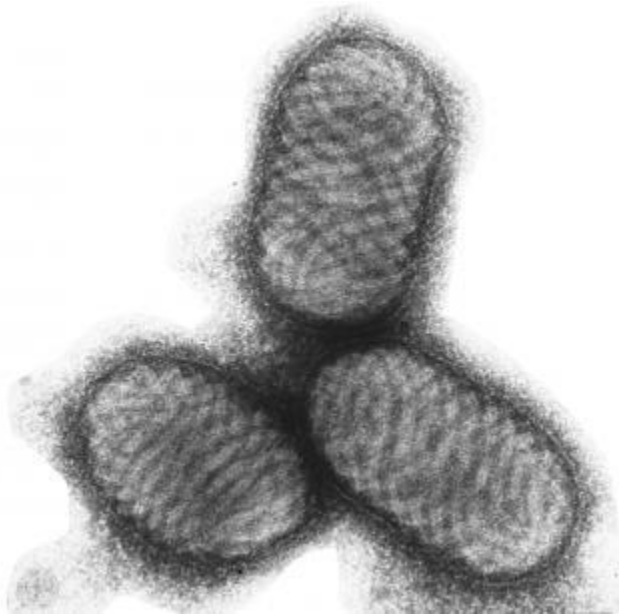


II. VIRUS STRUCTURE AND COMPOSITION

CAPSID

COMPLEX SIMETRY (NOT HELICAL, NOT ICOSAHERDRAL EITHER)

Poxviruses



I. VIRUS STRUCTURE AND COMPOSITION

ENVELOPE

✓DOUBLE-LAYERED LIPID MEMBRANE

✓FROM CELL MEMBRANE OR FROM ORGANELLES MEMBRANES

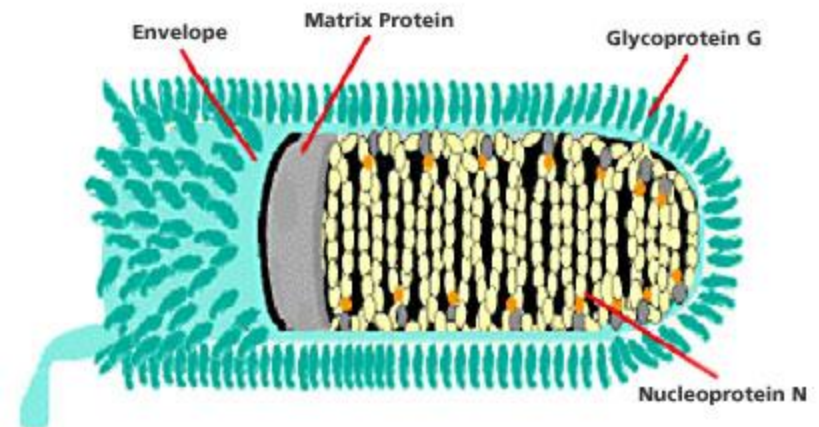
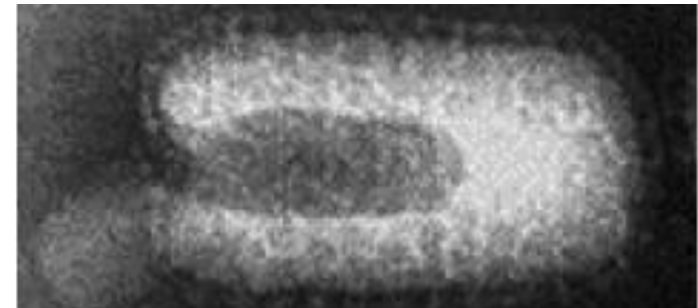
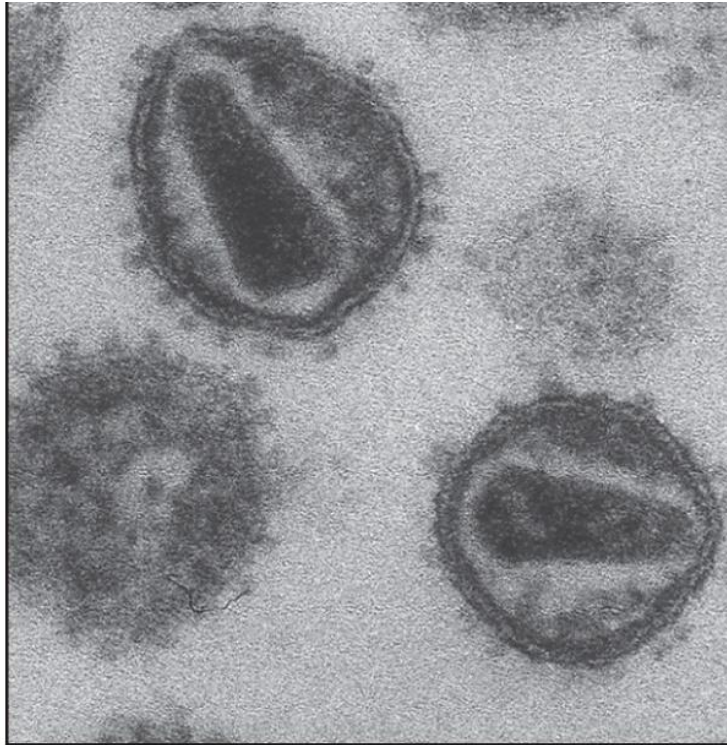


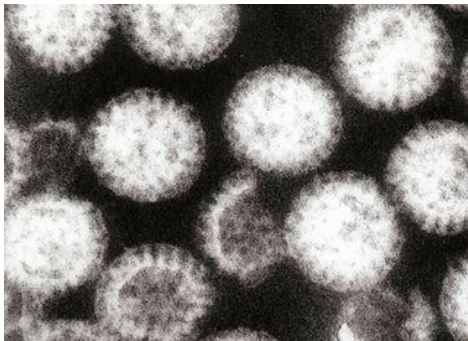
Figure 11.20 The Immune System, 3ed. (© Garland Science 2009)

I. VIRUS STRUCTURE AND COMPOSITION

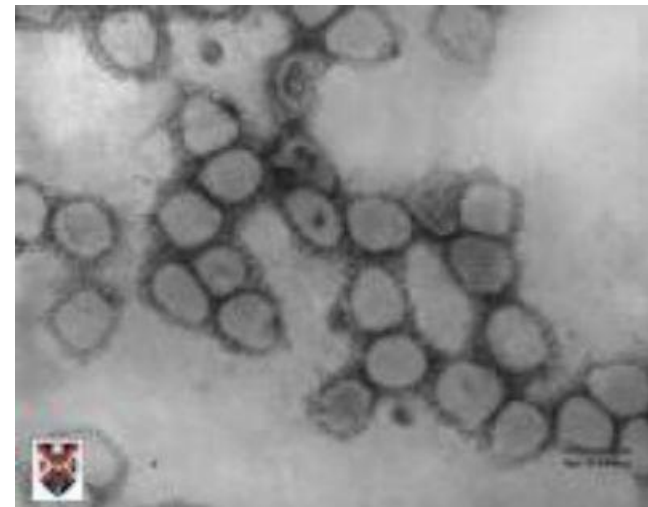
MORPHOLOGY

✓HOW THE VIRION LOOKS LIKE UNDER ELECTRON MICROSCOPE

✓MORPHOLOGY IS NOT THE SAME AS SIMETRY



- ✓ Round-shaped
- ✓ Bullet-shaped
- ✓ Filamentous
- ✓ pleomorphic
- etc*



II. TAXONOMY

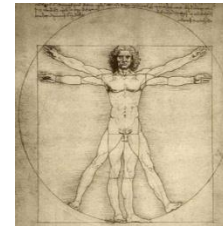
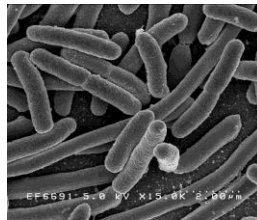
2,000 VIRUS SPECIES



30,000 STRAINS,
ISOLATES, VARIANTS



A virus in a virus:
Sputnik virus lives
inside Mimivirus



II. TAXONOMY

1966, Moscow: International
Committee on the Taxonomy of
Viruses :

[Home](#) | [Contact](#)

International Committee on Taxonomy of Viruses

VIROLOGY DIVISION - IUMS

[The ICTV](#) | [Taxonomy](#) | [ICTV Files](#) | [ICTV Discussions](#) | [News and Information](#) | [ICTV Directory](#)

Virus Taxonomy



Virus Taxonomy
Ninth Report of the International Committee on Taxonomy of Viruses
International Union of Microbiological Societies
Virology Division
Editors:
Andrew M.Q. King · Michael J. Adams
Eric B. Carstens · Eike J. Lefkowitz

NOW AVAILABLE!

Virus Taxonomy
Ninth Report of the International Committee on Taxonomy of Viruses

Congratulations to everyone involved in this monumental effort. Preparation of the Ninth Report has encompassed 6 years of work and has involved hundreds of virologists putting together the most up-to-date, internationally accepted taxonomy and nomenclature of all viruses. At 1327 pages, it is the largest report the ICTV has ever published including 6 orders, 87 families, 19 subfamilies, 349 genera, and 2284 virus and viroid species. It can be ordered from Amazon or directly from Elsevier.



Taxonomy lies at the uneasy interface between biology and logic. The processing of information follows somewhat different rules in these two systems and the role of taxonomy is to reconcile them as tidily as possible. To this end, the [Virology Division](#) of the [International Union of Microbiological Societies](#) (IUMS) charged the International Committee on Taxonomy of Viruses (ICTV) with the task of developing, refining, and maintaining a universal virus taxonomy. The goal of this undertaking is to categorize the multitude of known viruses into a single classification scheme that reflects their evolutionary relationships, i.e. their individual phylogenies. The most recent report of the ICTV: "Virus taxonomy: classification and nomenclature of viruses: Ninth Report of the International Committee on Taxonomy of Viruses. (2012) Ed: King, A.M.Q., Adams, M.J., Carstens, E.B. and Lefkowitz, E.J. San Diego: [Elsevier Academic Press](#)", is the standard and definitive reference for virus taxonomy.

The official ICTV 2012 taxonomy is now available.
Select the taxonomy menu above or click [here](#).

www.ictvdb.org

II. TAXONOMY

LEVELS OF TAXONOMY FOR VIRUSES

***-virales* = order**

***-viridae* = family**

***-virinae* = sub family**

***-virus* = genus**

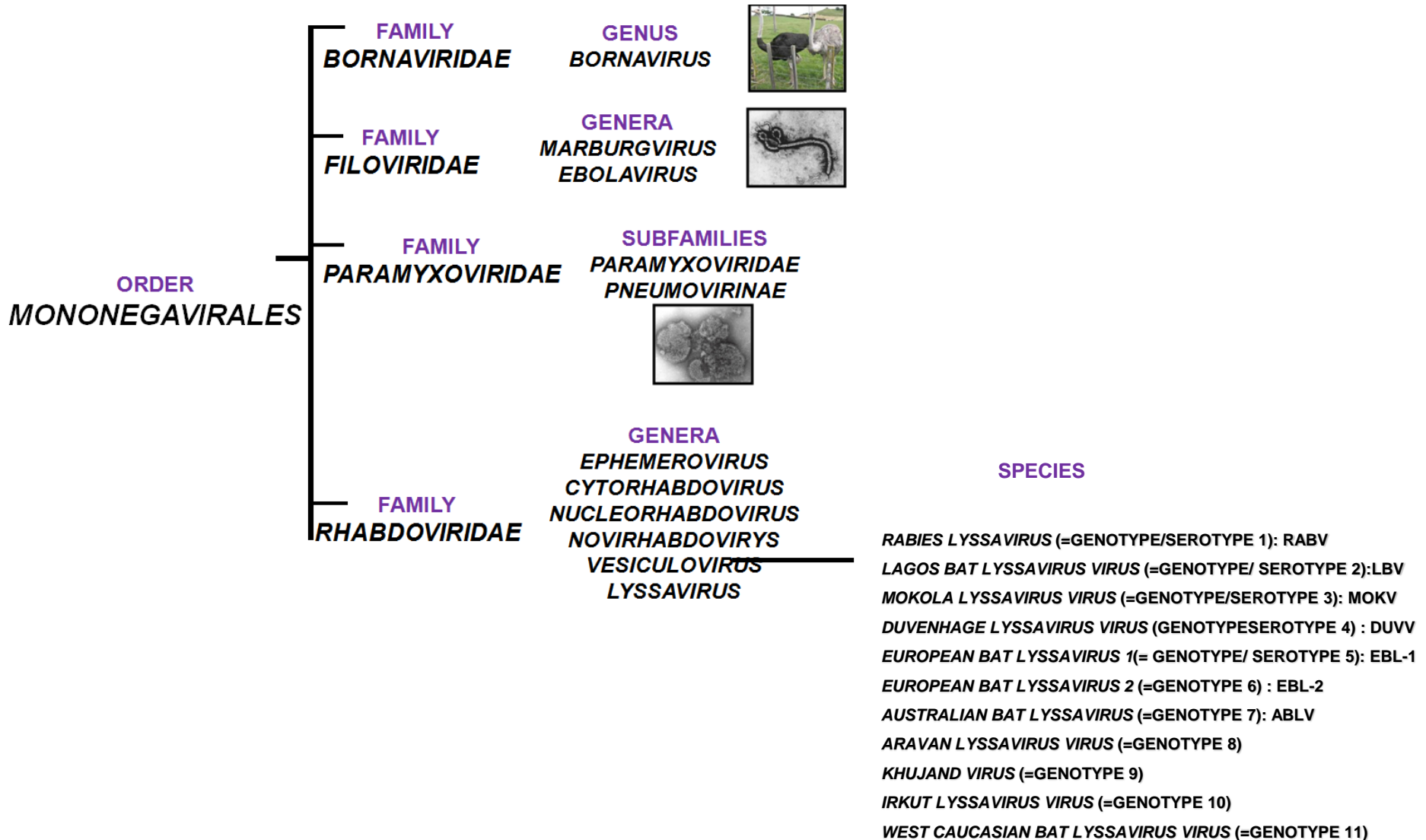
***virus* = species**

II. TAXONOMY

+ Order: <i>Bunyavirales</i>	(9 Families)
+ Order: <i>Caudovirales</i>	(4 Families)
+ Order: <i>Herpesvirales</i>	(3 Families)
+ Order: <i>Ligamenvirales</i>	(2 Families)
+ Order: <i>Mononegavirales</i>	(9 Families)
+ Order: <i>Nidovirales</i>	(4 Families)
+ Order: <i>Ortervirales</i>	(5 Families)
+ Order: <i>Picornavirales</i>	(7 Families)
+ Order: <i>Tymovirales</i>	(5 Families)
+ Order: Unassigned	(86 Families)

II. TAXONOMY

For instance,



A clash of ideas – the varying uses of the ‘species’ term in virology and their utility for classifying viruses in metagenomic datasets

Peter Simmonds*

Abstract

Species definitions of viruses are frequently descriptive, with assignments often being based on their disease manifestations, host range, geographical distribution and transmission routes. This method of categorizing viruses has recently been challenged by technology advances, such as high-throughput sequencing. These have dramatically increased knowledge of viral diversity in the wider environment that dwarfs the current catalogue of viruses classified by the International Committee for the Taxonomy of Viruses (ICTV). However, because such viruses are known only from their sequences without phenotypic information, it is unclear how they might be classified consistently with much of the existing taxonomy framework. This difficulty exposes deeper incompatibilities in how species are conceptualized. The original species assignments based on disease or other biological attributes were primarily descriptive, similar to principles used elsewhere in biology for species taxonomies. In contrast, purely sequence-based classifications rely on genetic metrics such as divergence thresholds that include or exclude viruses in individual species categories. These different approaches bring different preconceptions about the nature of a virus species, the former being more easily conceptualized as a category with a part/whole relationship of individuals and species, while species defined by divergence thresholds or other genetic metrics are essentially logically defined groups with specific inclusion and exclusion criteria. While descriptive species definitions match our intuitive division of viruses into natural kinds, rules-based genetic classifications are required for viruses known from sequence alone, whose incorporation into the ICTV taxonomy is essential if it is to represent the true diversity of viruses in nature.

The current ICTV definition of a species has been recently amended to:

‘A species is the lowest taxonomic level in the hierarchy approved by the ICTV. A species is a monophyletic group of viruses whose properties can be distinguished from those of other species by multiple criteria’

Table 1. Descriptive and sequence-based classification of viruses

Examples of species with descriptive definitions – typically one virus member per species	Sequence-based species assignment examples typically multiple members per species
<i>Flavivirus</i> genus, family <i>Flaviviridae</i>	<i>Enterovirus</i> genus, family <i>Picornaviridae</i> : 35 % amino acid sequence divergence in P1 and 25 % in non-structural genes
<i>Alphavirus</i> genus, family <i>Togaviridae</i>	<i>Hepacivirus</i> genus, family <i>Flaviviridae</i> : 25 % amino acid sequences divergence in NS3 and 30 % divergence in NS5B
Species in the plant virus families: <i>Benyviridae</i> , <i>Bromoviridae</i> , <i>Caulimoviridae</i> , <i>Closteroviridae</i> , <i>Geminiviridae</i> , <i>Iridoviridae</i> , <i>Luteoviridae</i> , <i>Nanoviridae</i> , <i>Partitiviridae</i> , <i>Potyviridae</i> , <i>Secoviridae</i> , <i>Tombusviridae</i> , <i>Tymoviridae</i> , <i>Virgaviridae</i>	<i>Alpha-</i> , <i>Beta-</i> , <i>Gammatorquetenovirus</i> genera, family <i>Anelloviridae</i> : 35 % nucleotide sequence divergence in ORF1
And many others...	<i>Lyssavirus</i> genus, family <i>Rhabdoviridae</i> : 18–20 % sequence divergence in N gene

II. TAXONOMY

WHAT IS TAKEN INTO ACCOUNT?

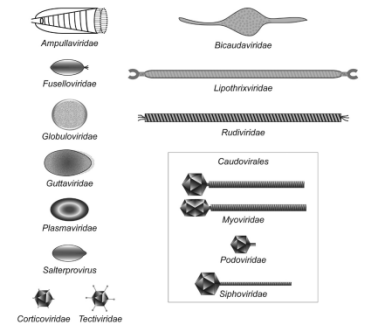
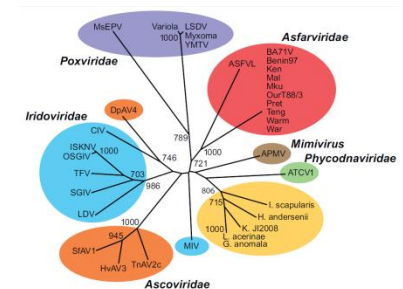
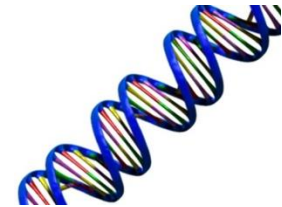
✓ GENOME TYPE

✓ GENOME IDENTITY

✓ CAPSID, ENVELOPE

✓ REPLICATION AND TRANSCRIPTION ROUTES

✓ HOST RANGE



II. TAXONOMY

WHAT ABOUT STRAINS, LINEAGES, ISOLATES?

STRAIN: A GIVEN SUBPOPULATION INSIDE A VIRUS SPECIES

LINEAGE: A TAXON SEPARATE FROM OTHER IN A PHYLOGENETIC TREE

ISOLATE: A VIRUS POPULATION ISOLATED AND MAINTAINED IN A LAB

BUT...THESE DEFINITIONS ARE NOT USED BY THE ICTV

III. REPLICATION

✓ ATTACHMENT/ BINDING

✓ ENTRY

✓ UNCOATING

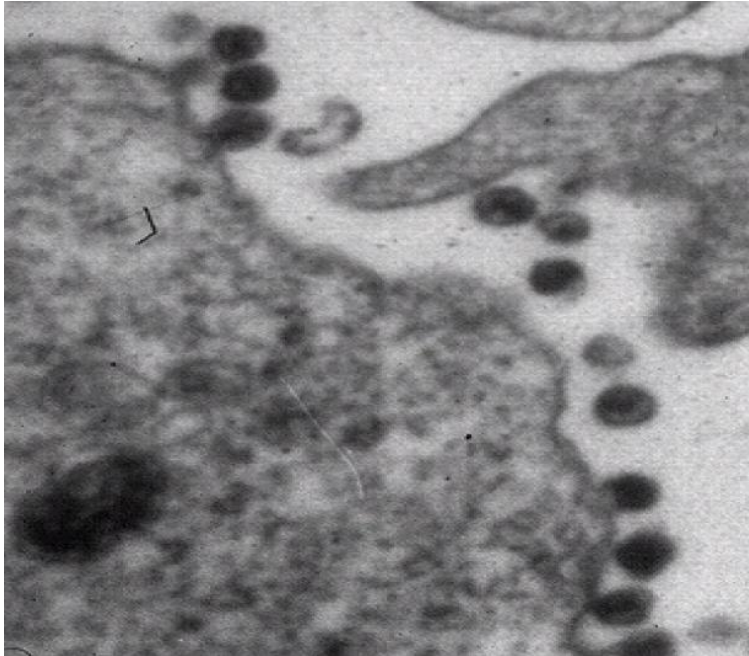
✓ TRANSCRIPTION/TRANSLATION

✓ ASSEMBLY

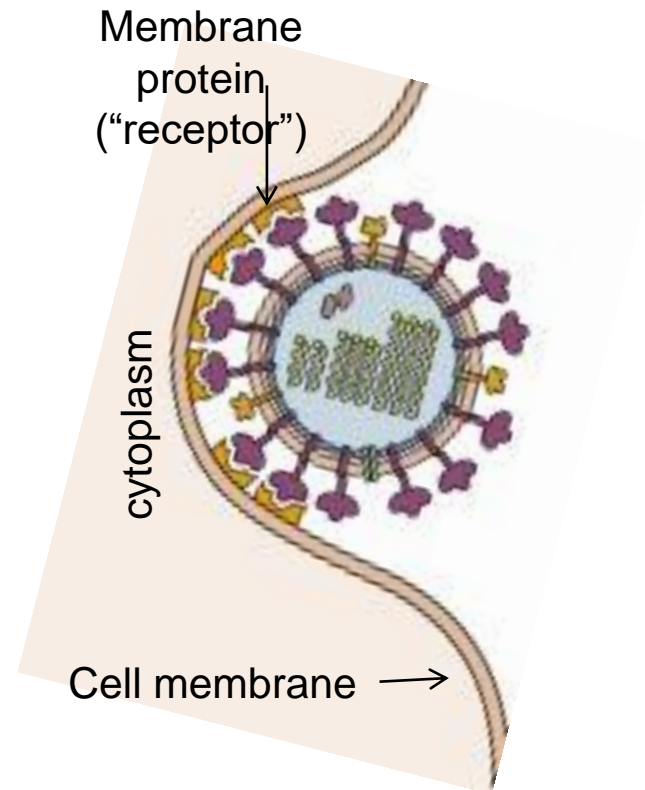
✓ EXIT

III. REPLICATION

ATTACHMENT/ BINDING



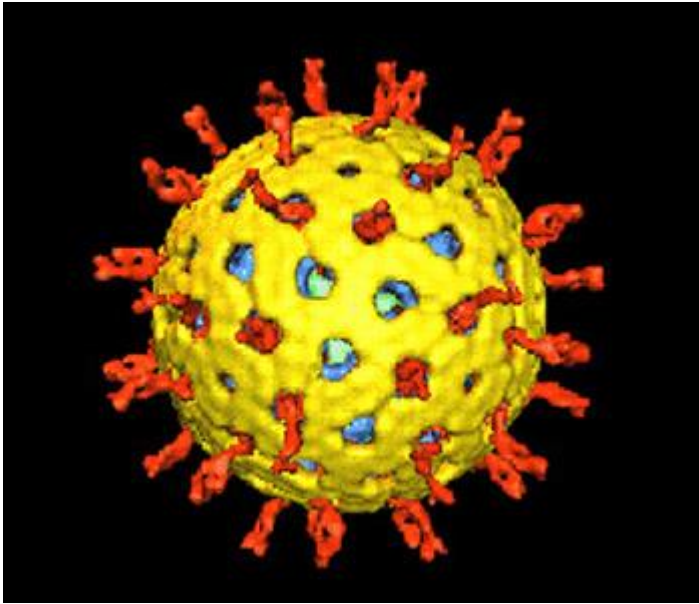
A VIRUS SURFACE PROTEIN BINDS NON-COVALENTLY TO A CELL MEMBRANE SURFACE PROTEIN



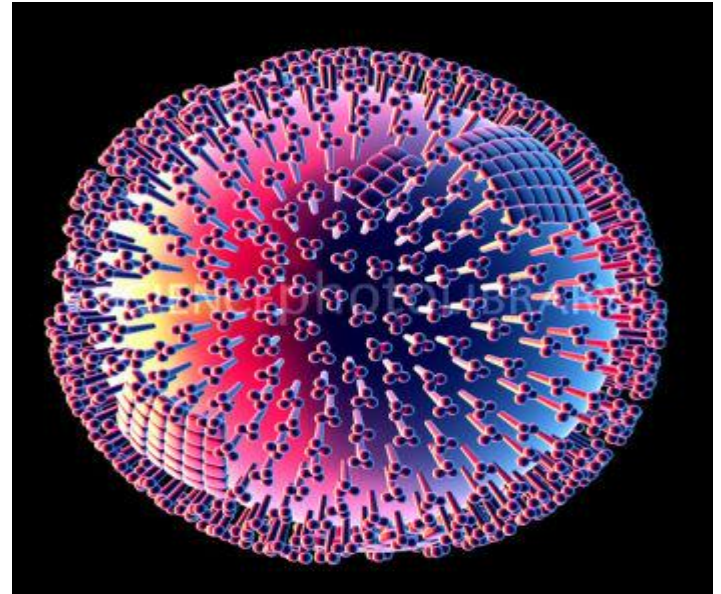
III. REPLICATION

ATTACHMENT/ BINDING

VIRAL PROTEINS ABLE TO ATTACH TO CELL RECEPTORS:



Capsid proteins in non-enveloped viruses



Envelope proteins in enveloped viruses

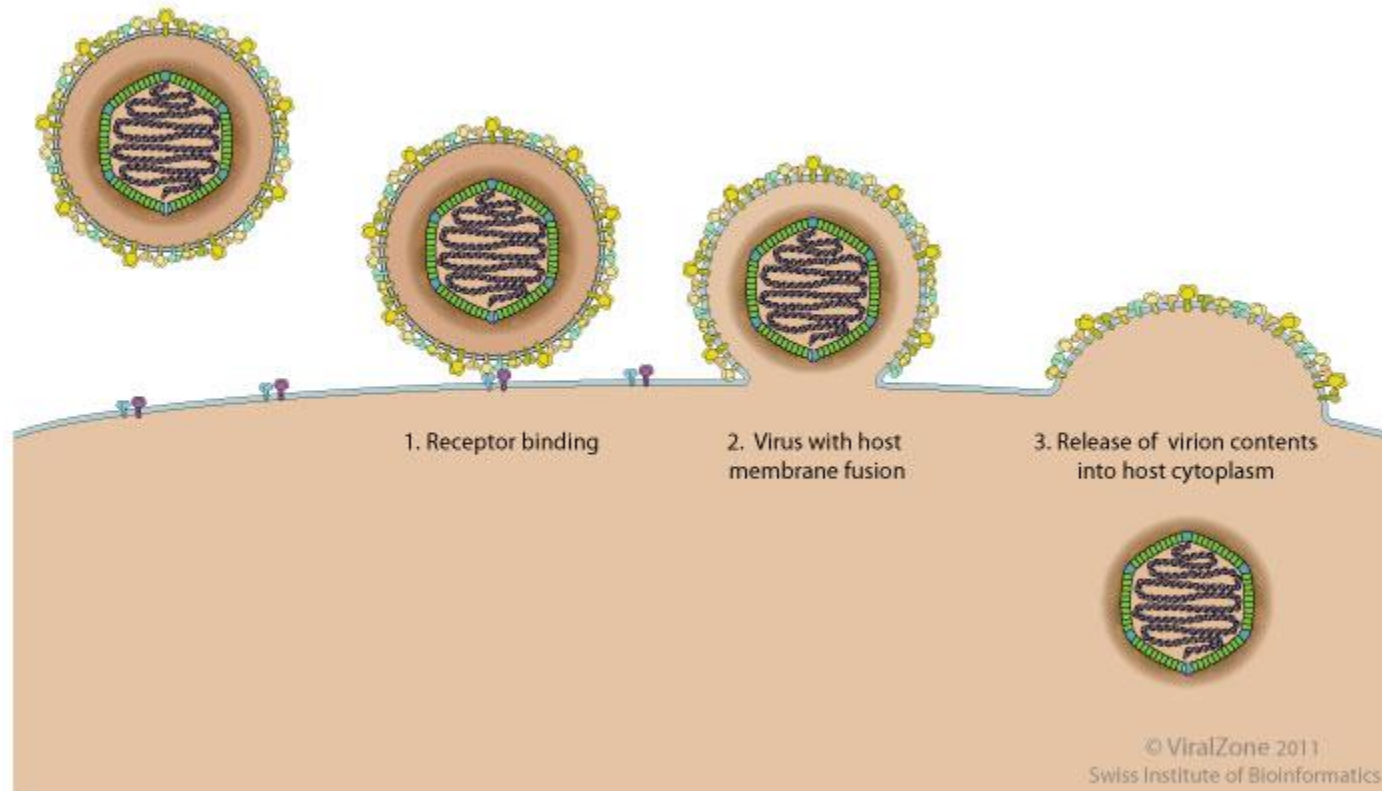
III. REPLICATION

VIRUS ENTRY

FOUR POSSIBLE MECHANISMS; DIFFERENT VIRUSES, DIFFERENT MECHANISMS

1. CELL FUSION

e.g. retroviruses,
canine
distemper virus

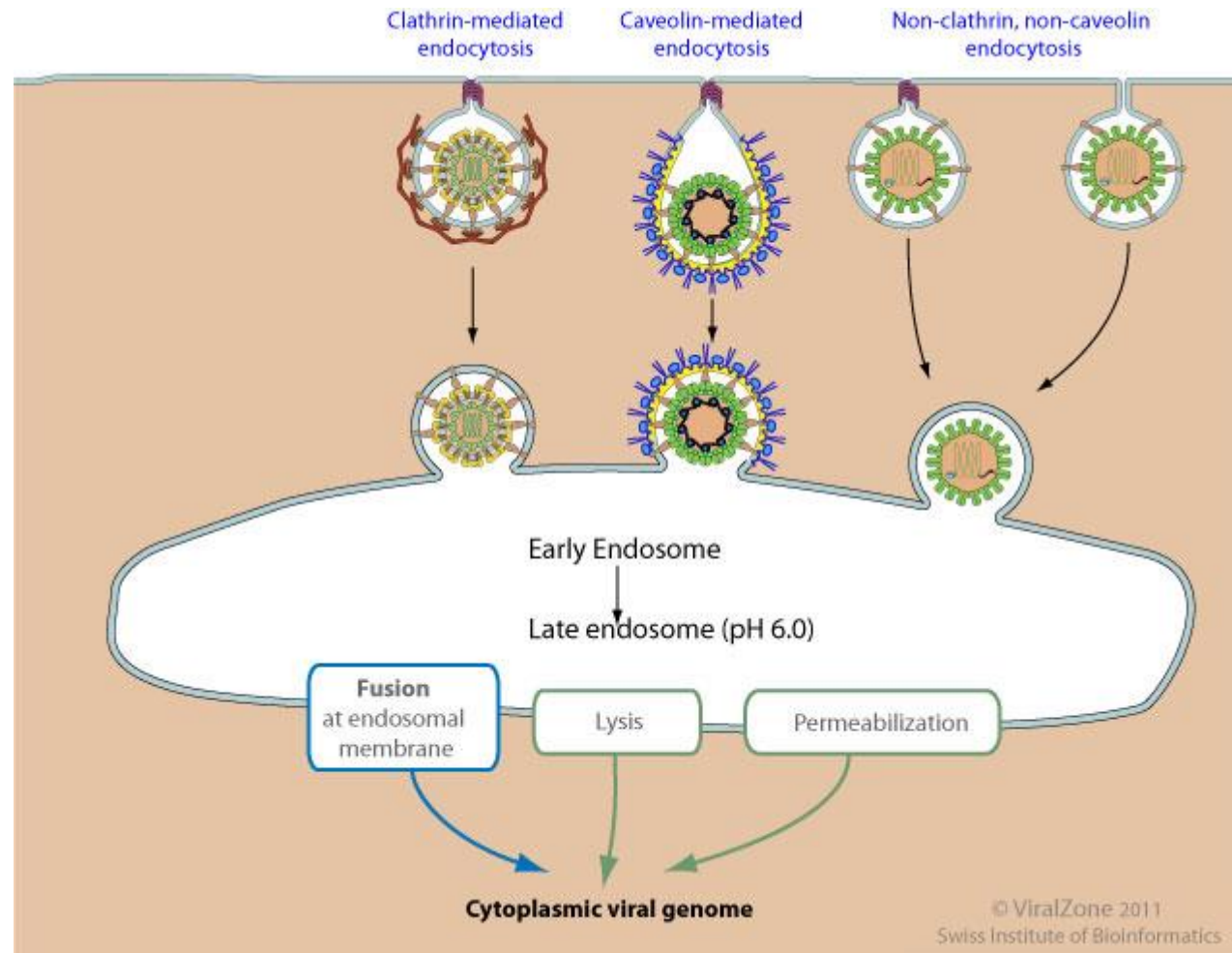


III. REPLICATION

VIRUS ENTRY

2. ENDOCYTOSIS

e.g. influenza virus,
yellow fever virus



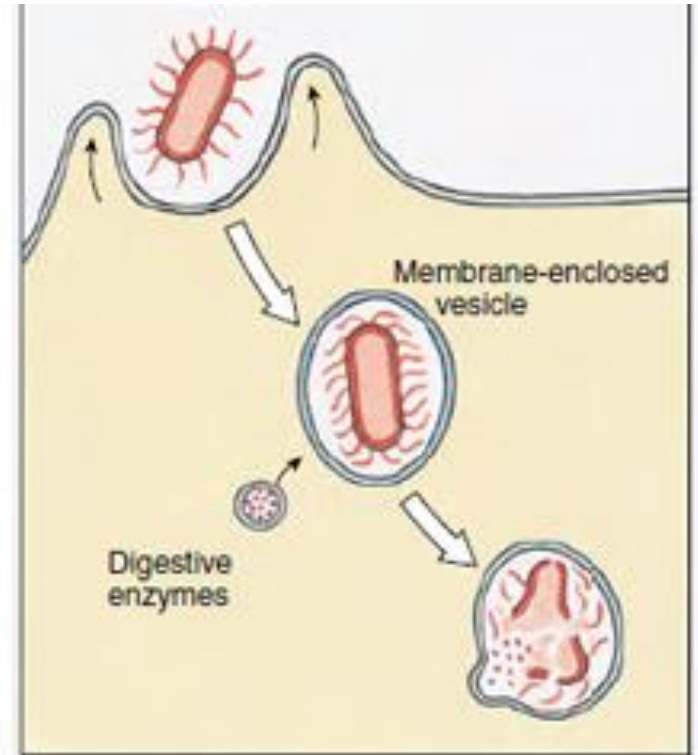
III. REPLICATION

VIRUS ENTRY

3. PHAGOCYTOSIS

e.g. poxviruses

Macrophages, dendritic cells



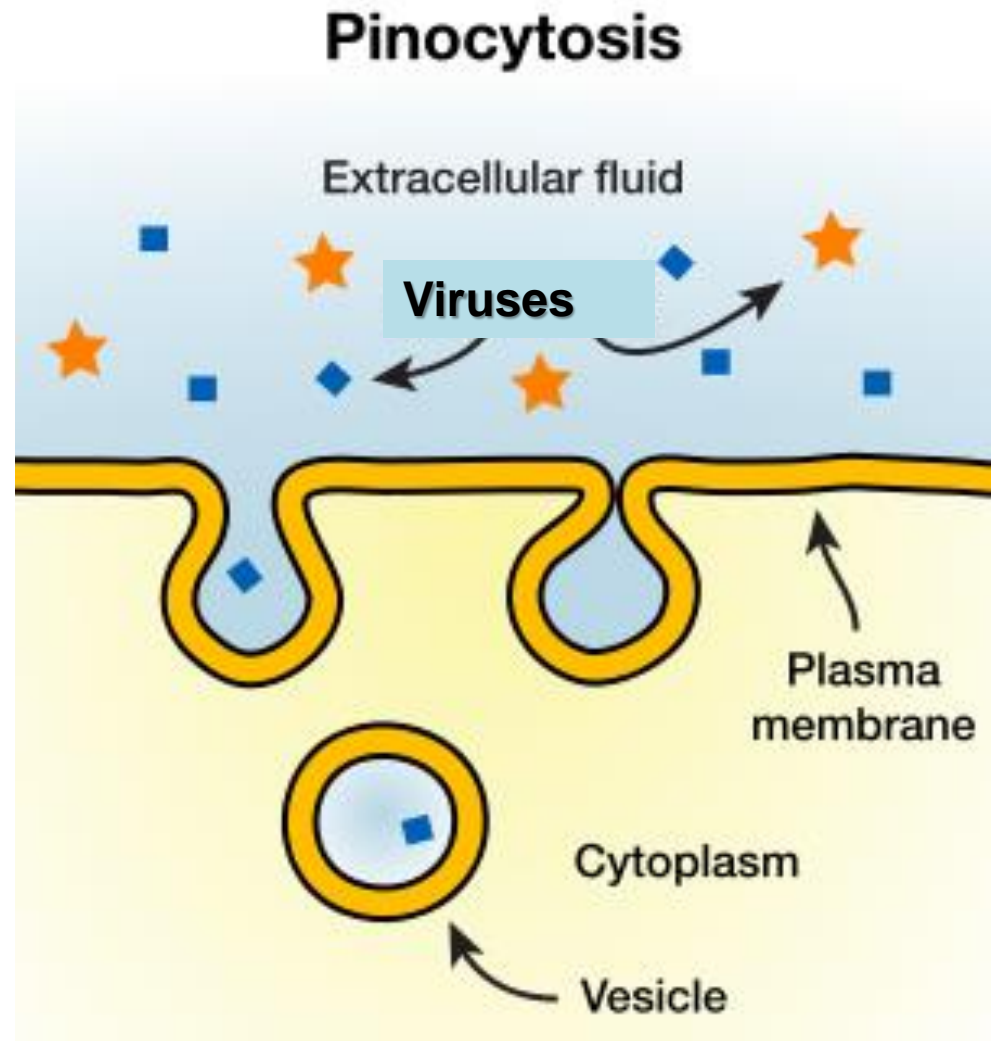
III. REPLICATION

VIRUS ENTRY

4. PINOCYTOSIS

✓ Internalization of liquids

✓ Large viruses
(e.g. HIV, some
adenoviruses, some
herpesviruses)



III. REPLICATION

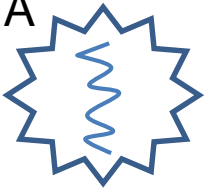
UNCOATING

LIBERATION OF THE GENOME

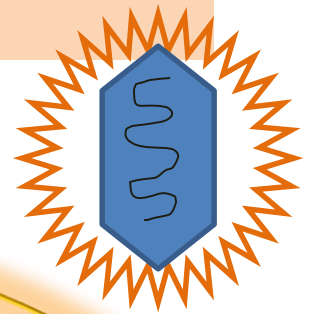
✓ ON THE CYTOPLASM (FOR RNA VIRUSES)

✓ IN THE CELL NUCLEUS (FOR DNA VIRUSES)

RNA



DNA



pH goes down → proteins denature

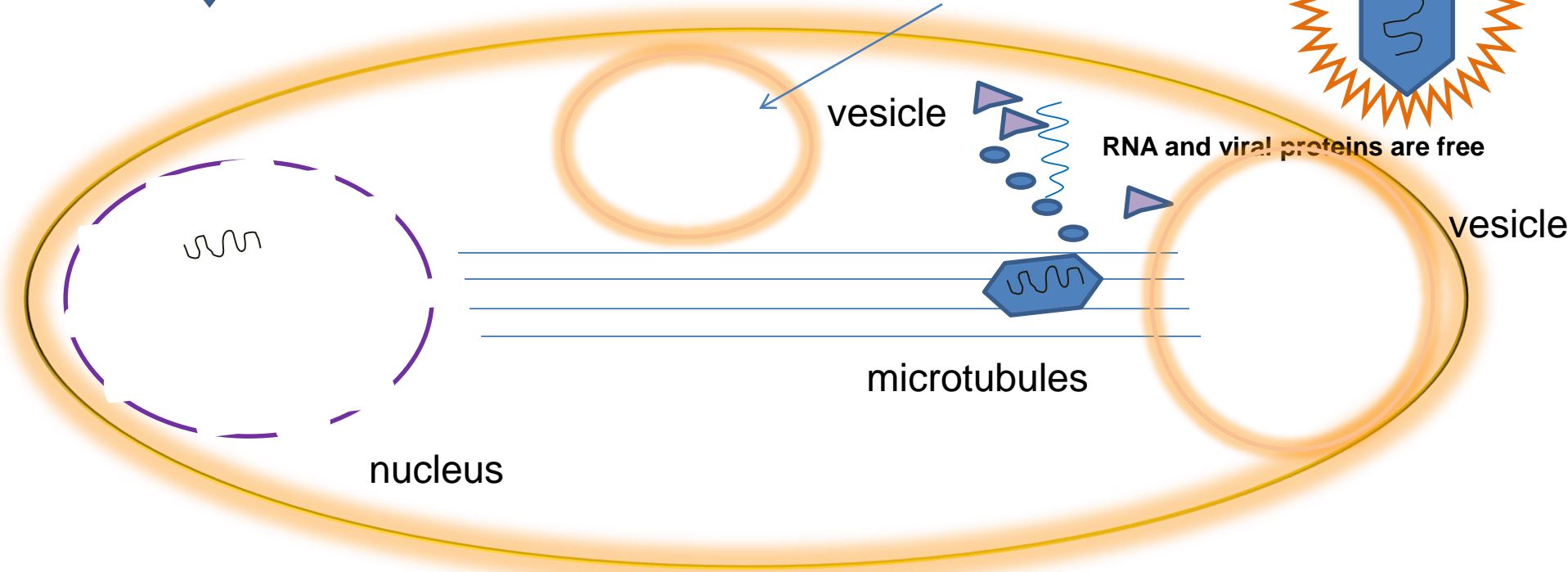
vesicle

RNA and viral proteins are free

vesicle

microtubules

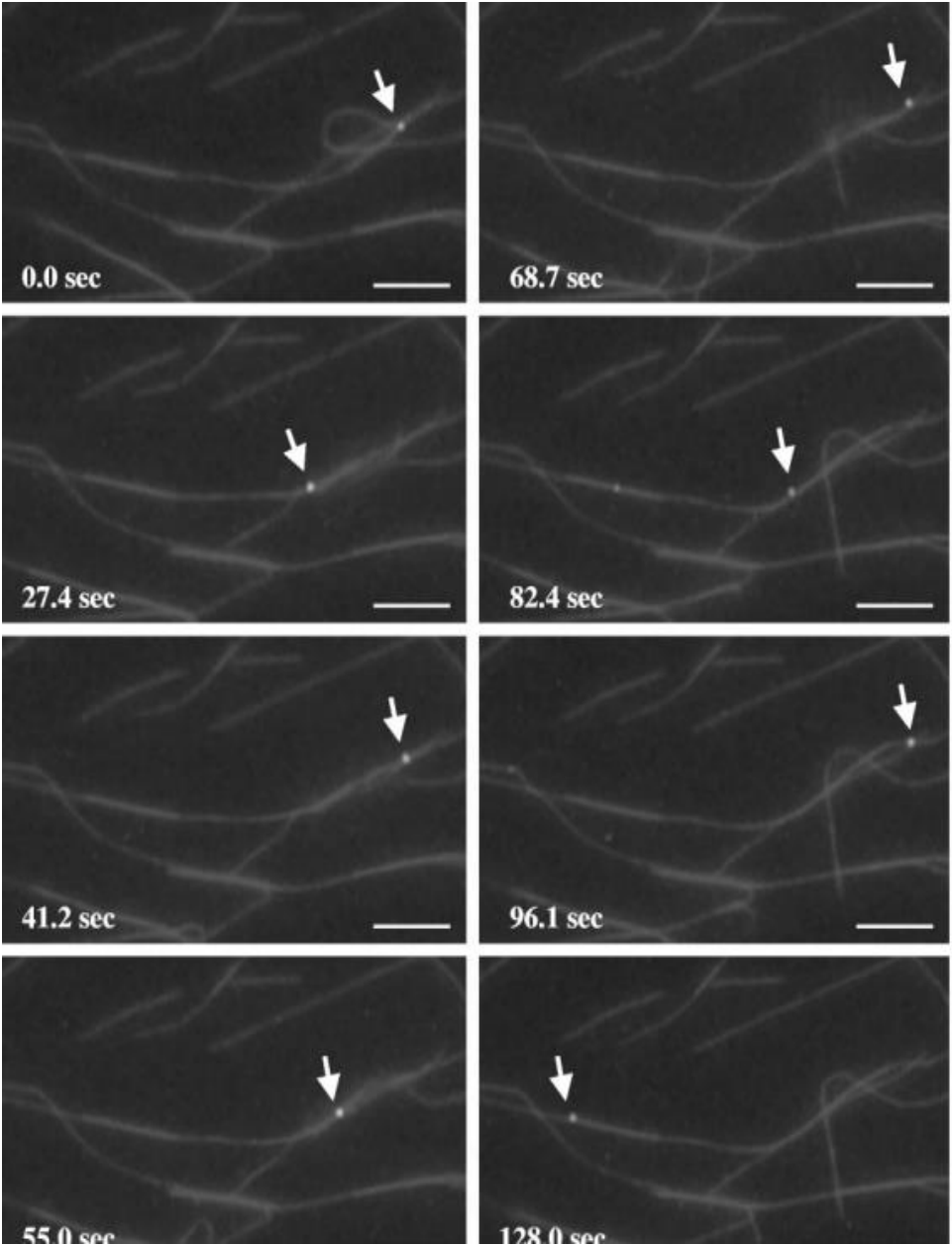
nucleus

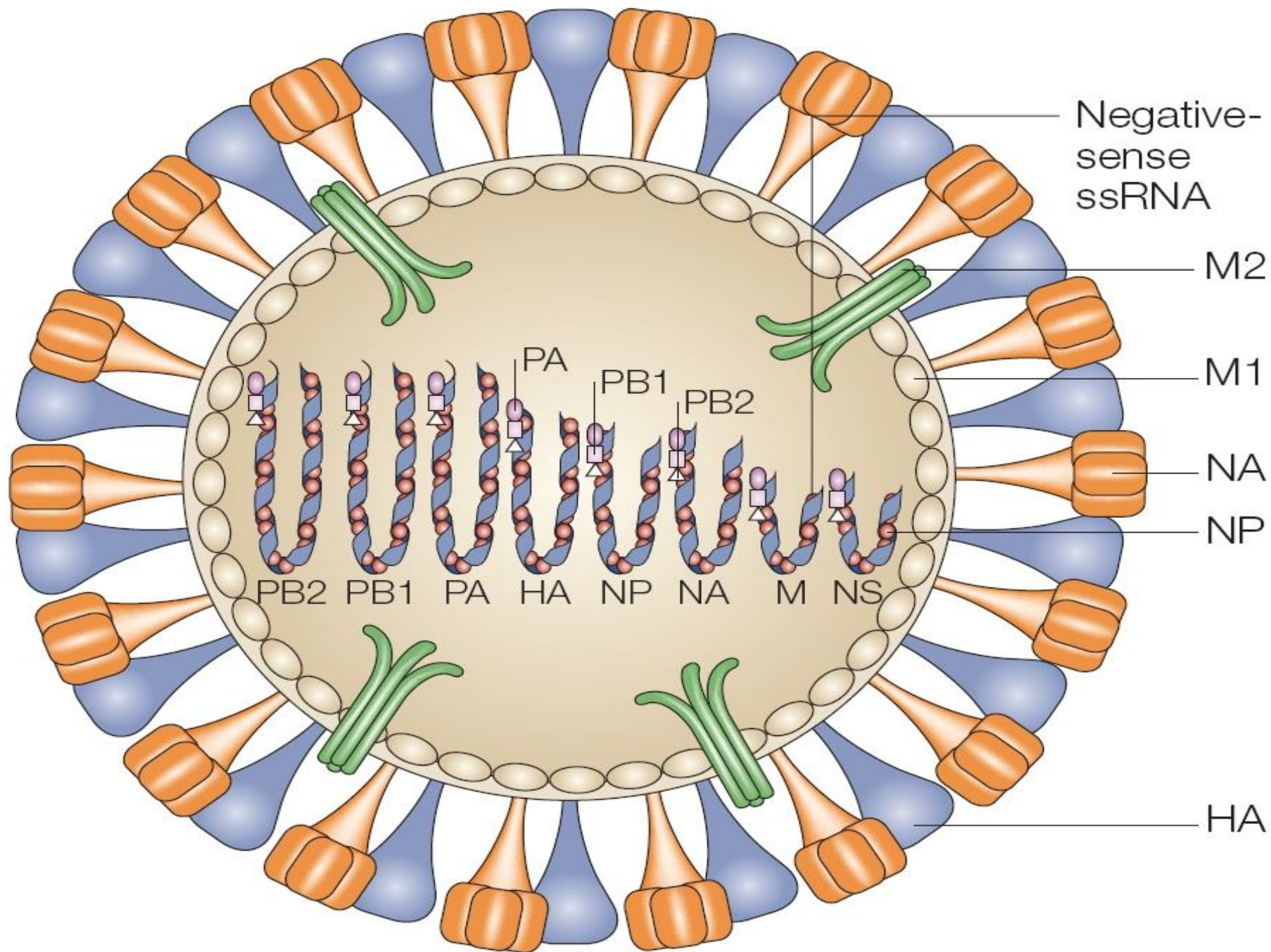


Reconstitution of Herpes Simplex Virus Microtubule-Dependent Trafficking In Vitro†

Grace E. Lee,¹ John W. Murray,² Allan W. Wolkoff,² and Duncan W. Wilson^{1*}
Department of Developmental and Molecular Biology,¹ and Marion Bessin Liver Research Center and Department of Anatomy and Structural Biology,² Albert Einstein College of Medicine, Bronx, New York 10461

Received 27 September 2005/Accepted 31 January 2006

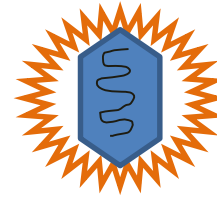




III. REPLICATION

TRANSCRIPTION/TRANSLATION AND ASSEMBLY

DNA VIRUS



Structural and non-structural viral proteins

exocytosis

Envelope is acquired

Viral DNA polymerase

Virus genome

Viral mRNAs

Cellular RNA polymerase

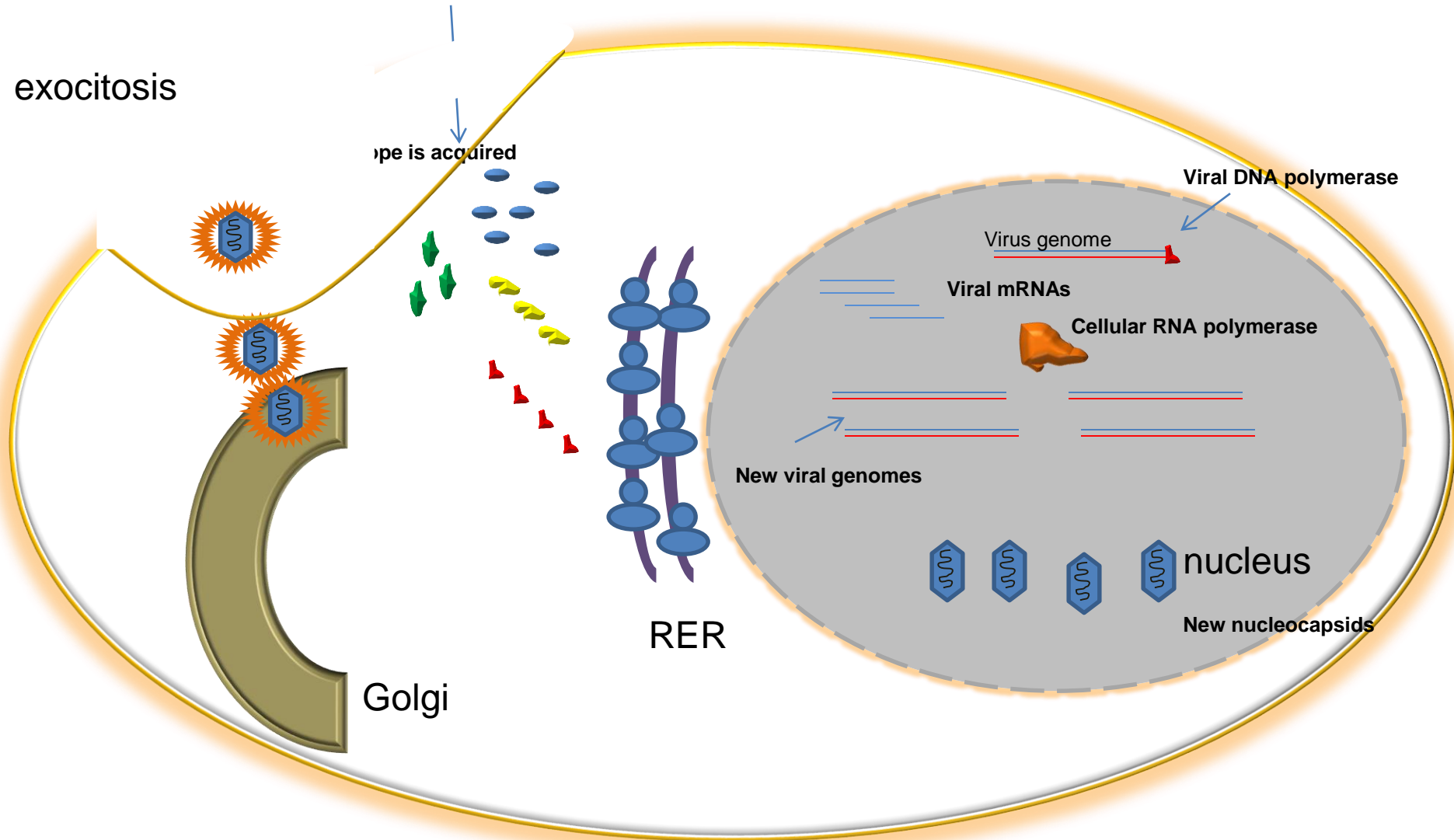
New viral genomes

nucleus

New nucleocapsids

RER

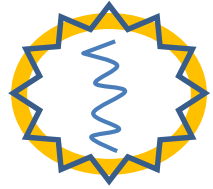
Golgi



III. REPLICATION

1st: in cases the polyprotein is only non-structural, all subunits have a role on transcription and replication

POSITIVE-SENSE RNA VIRUS



A polyprotein is translated (containing only non-structural or both non-structural and structural proteins, depending on the virus species)

The polyprotein cleavages itself

Viral genome (=mRNA)

Negative version of the genome

Subgenomic mRNAs are synthesized

Positive-sense genomes are also synthesized

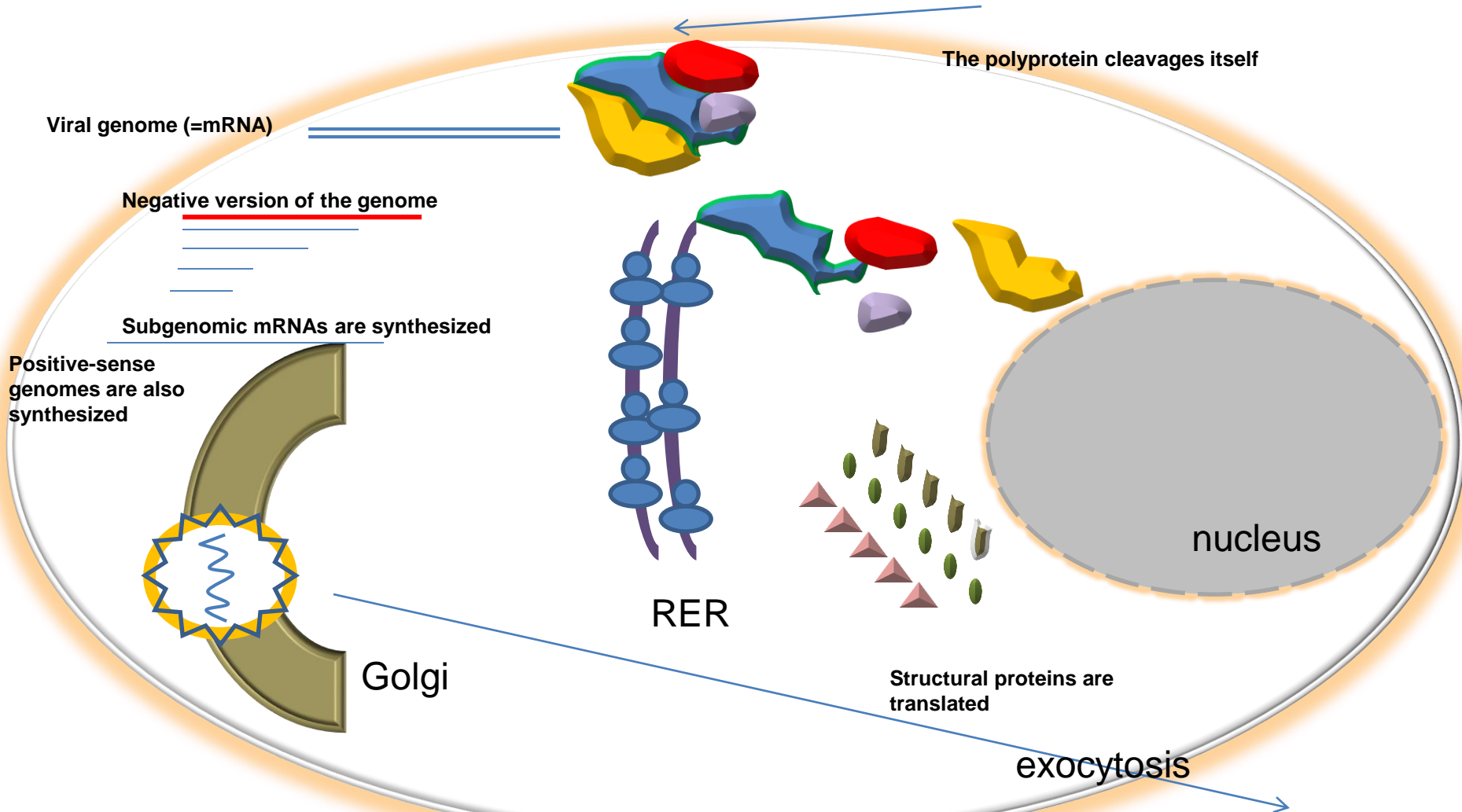
RER

nucleus

Golgi

Structural proteins are translated

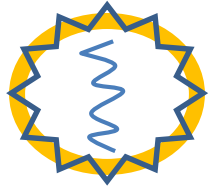
exocytosis



III. REPLICATION

TRANSCRIPTION/TRANSLATION
AND ASSEMBLY

POSITIVE-SENSE RNA VIRUS



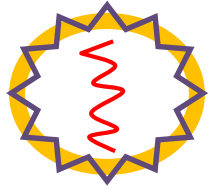
**2nd: IN CASES THE POLYPROTEIN IS
NOT ONLY NON-STRUCTURAL, ALL
SUBUNITS HAVE A ROLE ON
TRANSCRIPTION AND REPLICATION**

**SIMILAR ROUTES TAKE PLACE,
BUT STRUCTURAL PROTEINS
ARE ALREADY PART OF THE
LARGE POLYPROTEIN**

III. REPLICATION

TRANSCRIPTION/TRANSLATION
AND ASSEMBLY

NEGATIVE-SENSE RNA VIRUS



**THE RNA POLYMERASE IS ALREADY PRESENT
IN THE VIRION WHEN IT ENTERS THE
CYTOPLASM AND IS READY TO TRANSCRIBE
mRNAs**

**SO...NEGATIVE-SENSE RNA VIRUSES NEED A FURTHER
STEP BEFORE TRANSLATING PROTEINS**

III. REPLICATION

EXIT

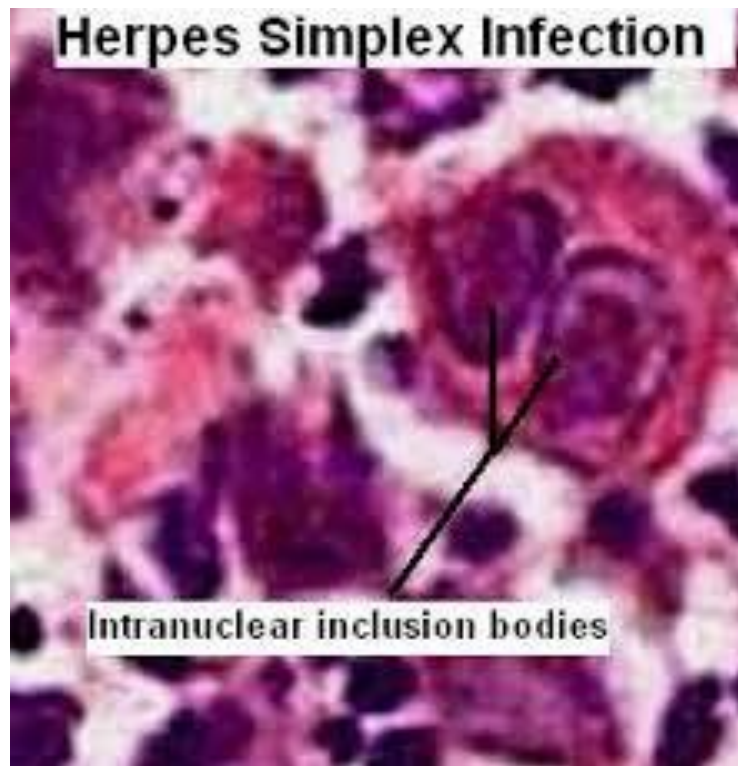
NON-ENVELOPED VIRUSES:

- ✓ MORPHOGENESIS IS COMPLETED IN THE CYTOPLASM(RNA) OU NUCLEUS (DNA)
- ✓ FULLY MATURE AT THESE SITES
- ✓ LYSIS OF THE INFECTED CELL

ENVELOPED VIRUSES:

- ✓ MORPHOGENESIS IS ONLY COMPLETED AT THE GOLGI-ROUGH ENDOPLASMIC RETICULUM, CYTOPLASMIC MEMBRANE OR NUCLEAR MEMBRANE (DNA)
- ✓ BUDDING TROUGH THE MEMBRANES AND EXIT BY EXOCITOSIS: NO CELL LYSIS

Herpes Simplex Infection



Purkinje cell - Negri body

