General Virology 304

Lecture Series XII

Virus Classification

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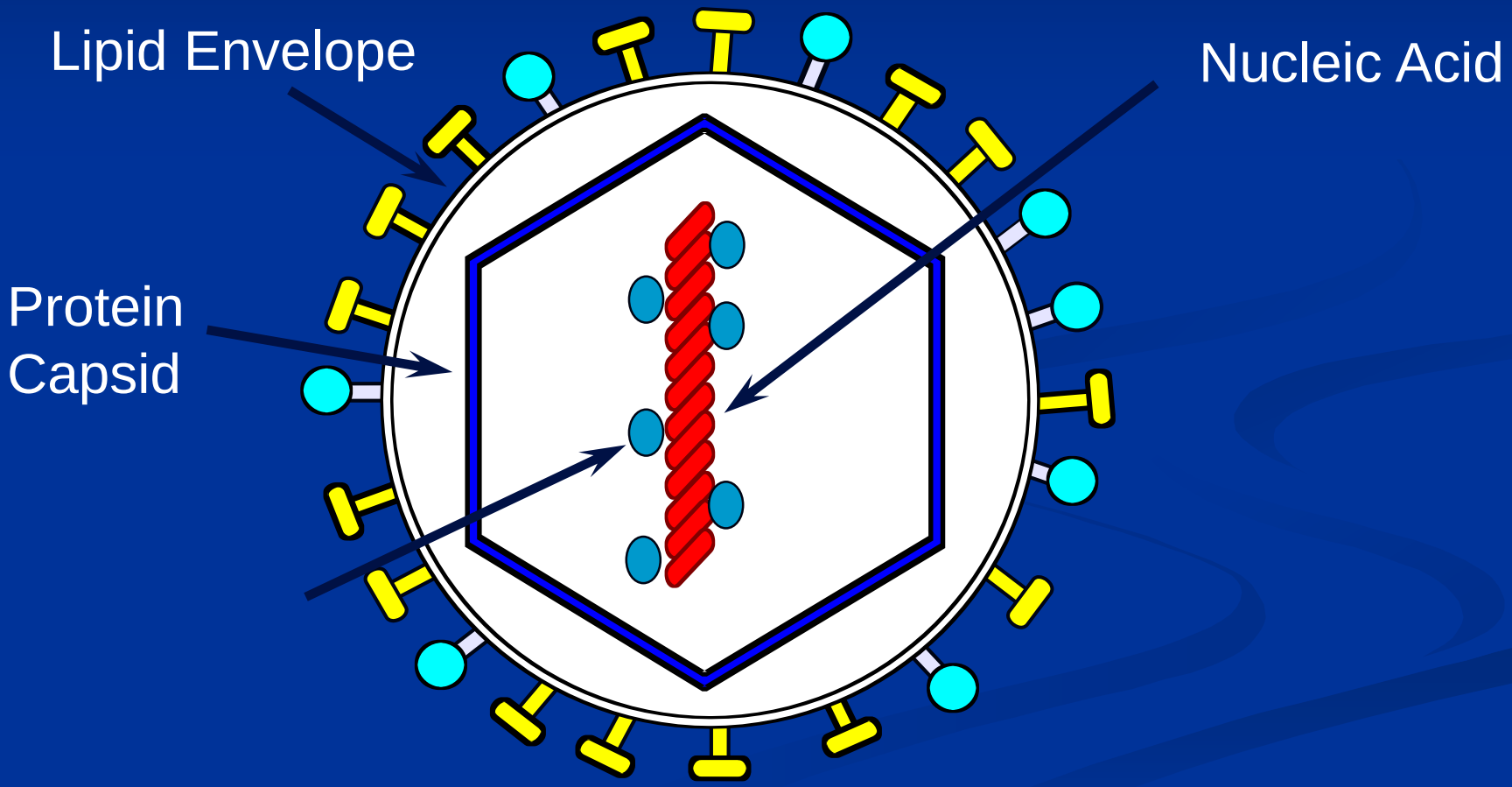
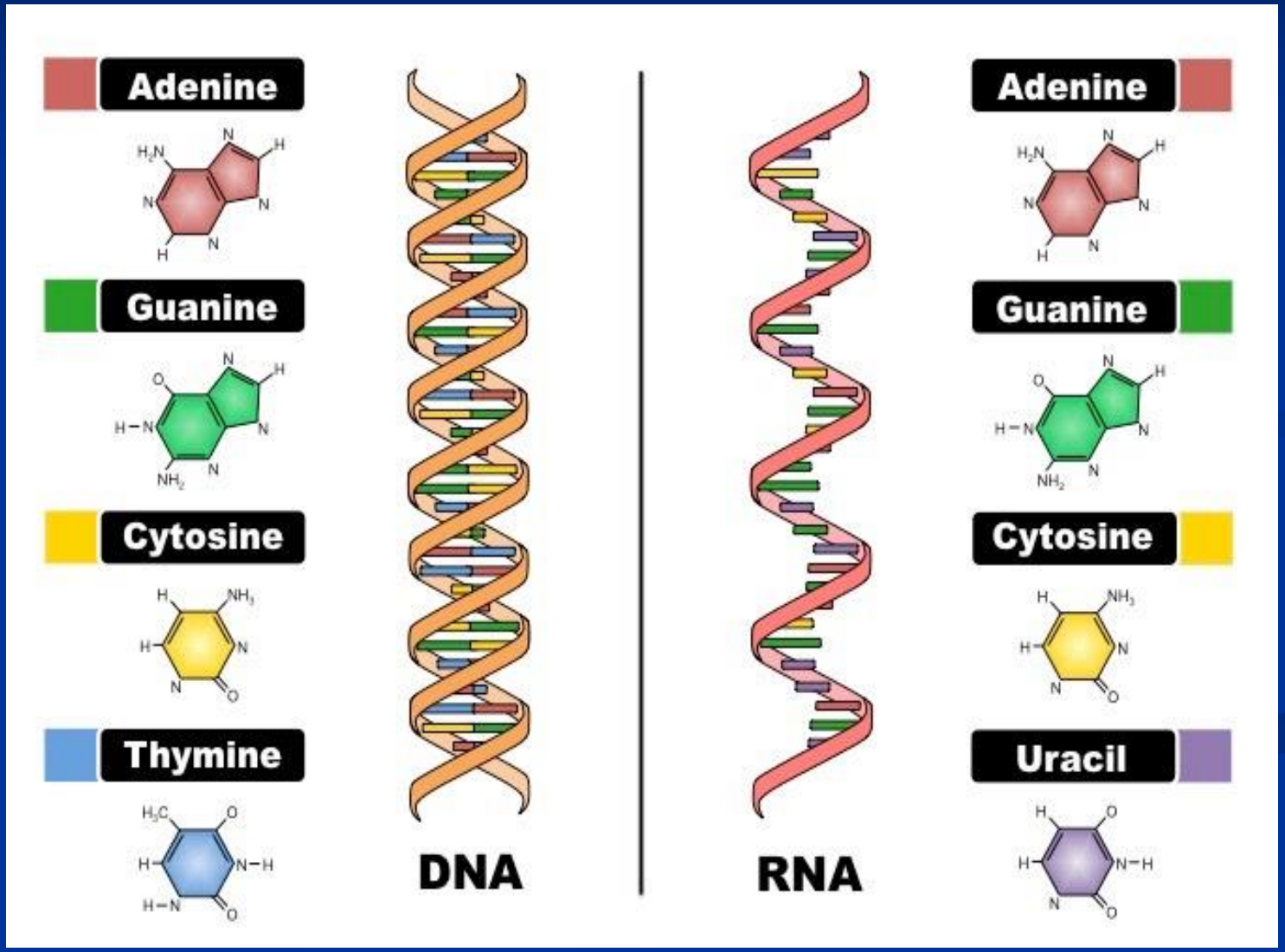
Virus



Virus Nucleic Acid (Genome)

1- Type:



Virus Nucleic Acid (Genome)

2- Strandness:

Most DNA Viruses

Pox - Herpes

Rare

Parvo - Circo

Rare

Reo - Birna

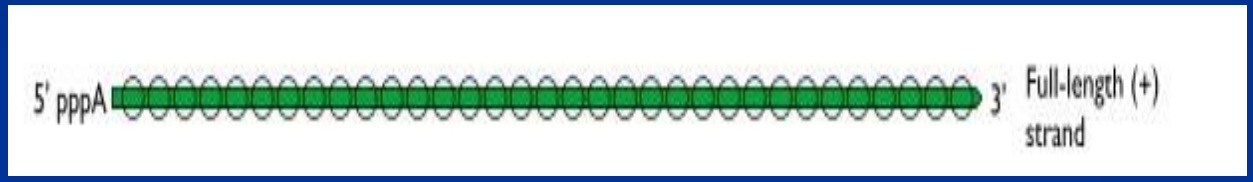
Most RNA Viruses

Influenza

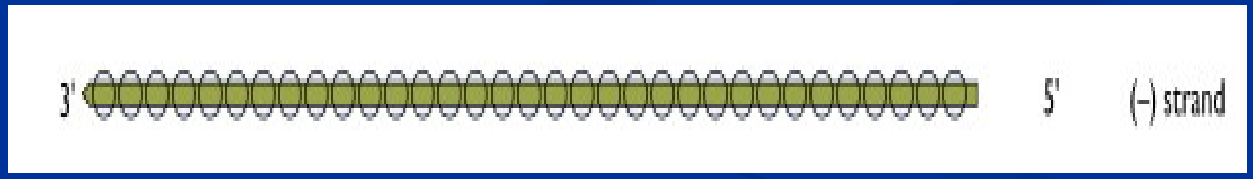
Virus Nucleic Acid (Genome)

3- Sense (polarity):

Positive Sense



Negative Sense



AmbiSense

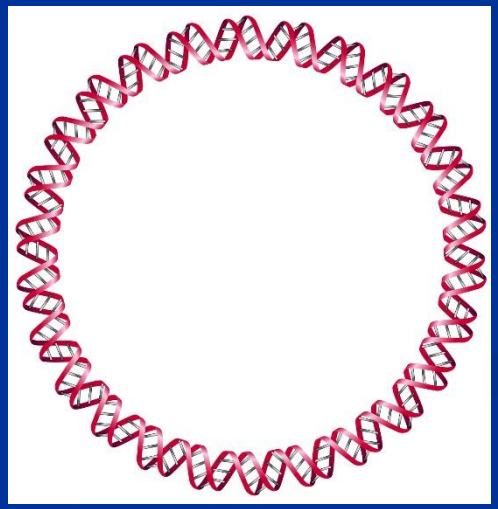
Virus Nucleic Acid (Genome)

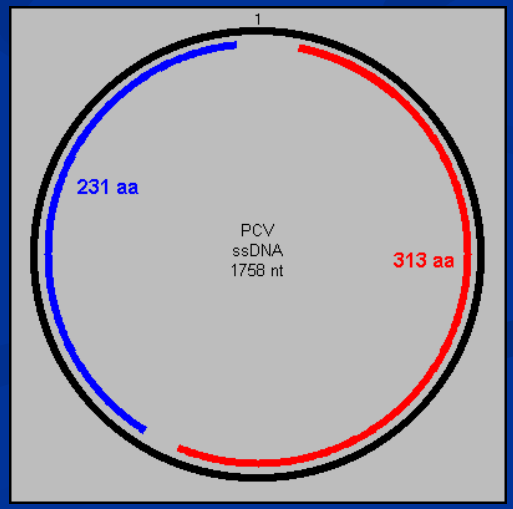
4- Linearity:

Linear:
HIV - HCV

Circular:

Circo - HBV

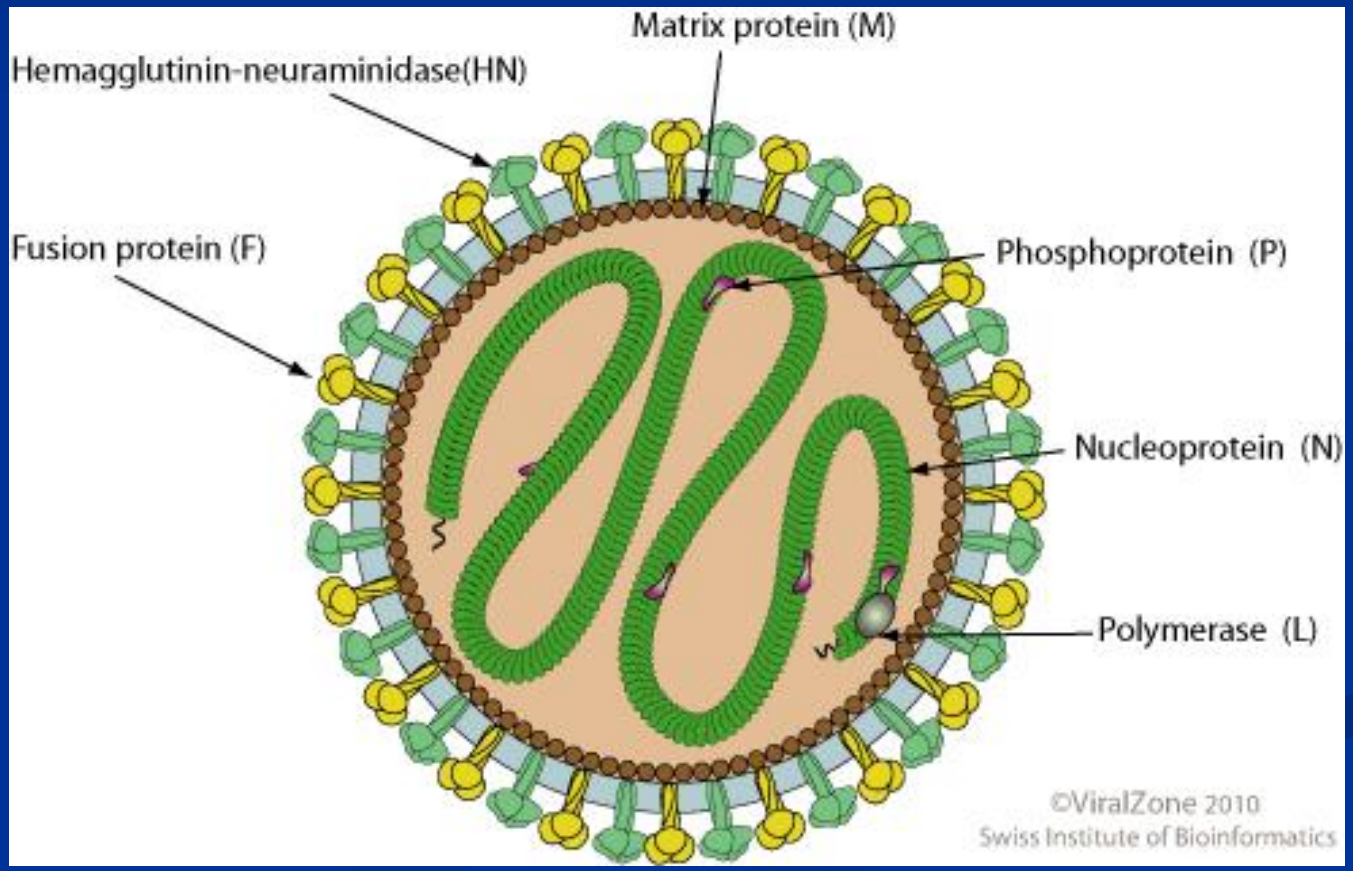




Virus Nucleic Acid (Genome)

5- Segmentation:

Single molecule:

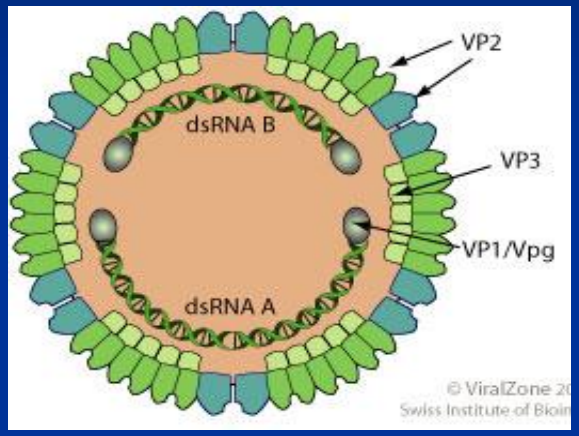


Newcastle Disease Virus

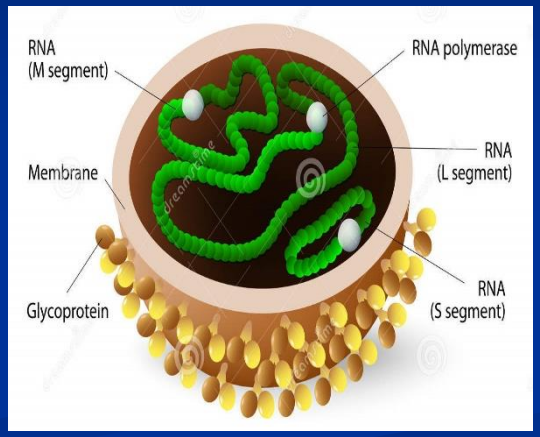
Virus Nucleic Acid (Genome)

5- Segmentation:

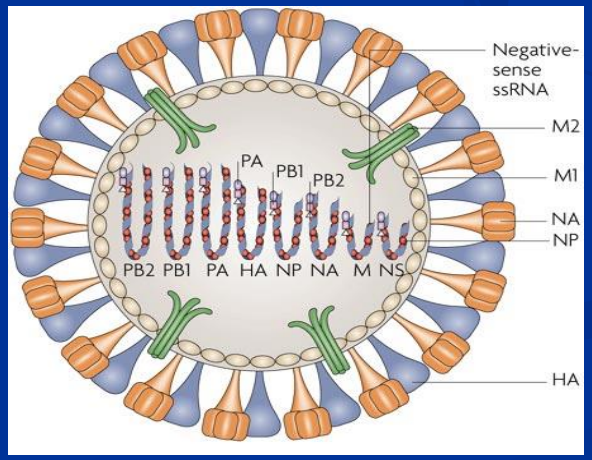
Segmented Genome:



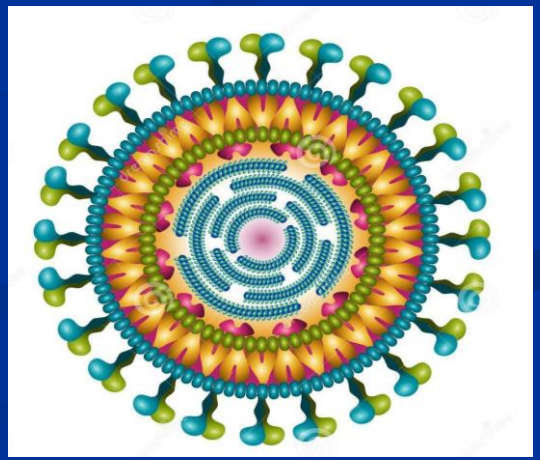
2 segments (IBDV)



3 segments (RVF)



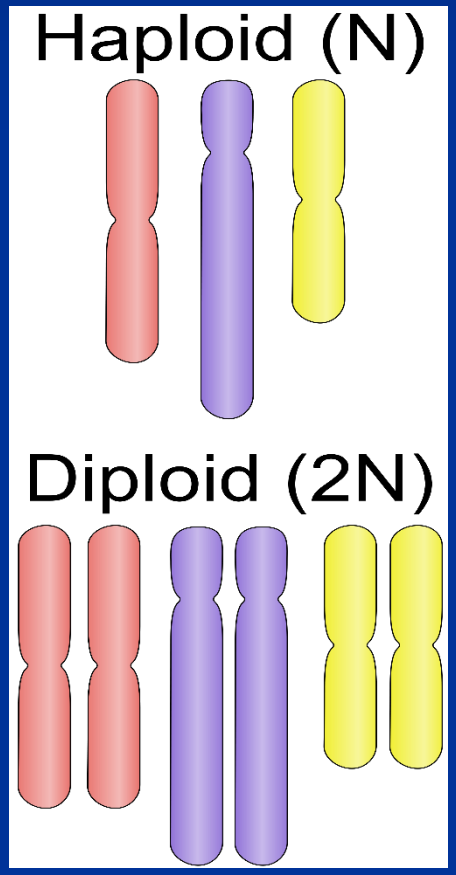
8 segments (Influenza)



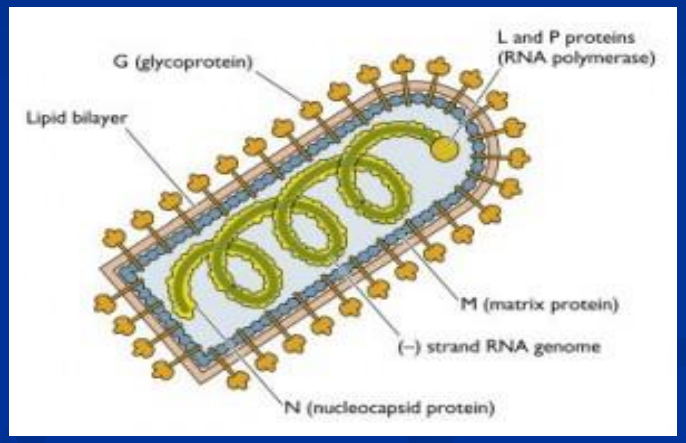
11 segments (Rota)

Virus Nucleic Acid (Genome)

6- Ploidy:

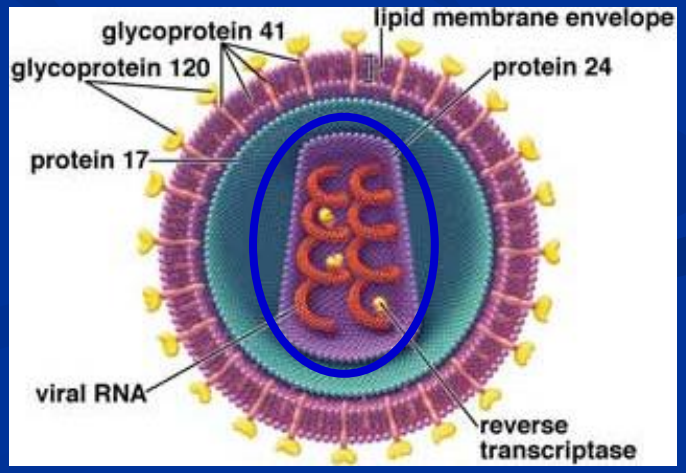


Haploid:



Diploid:

HIV



Example: Influenza Virus

RNA

Single stranded

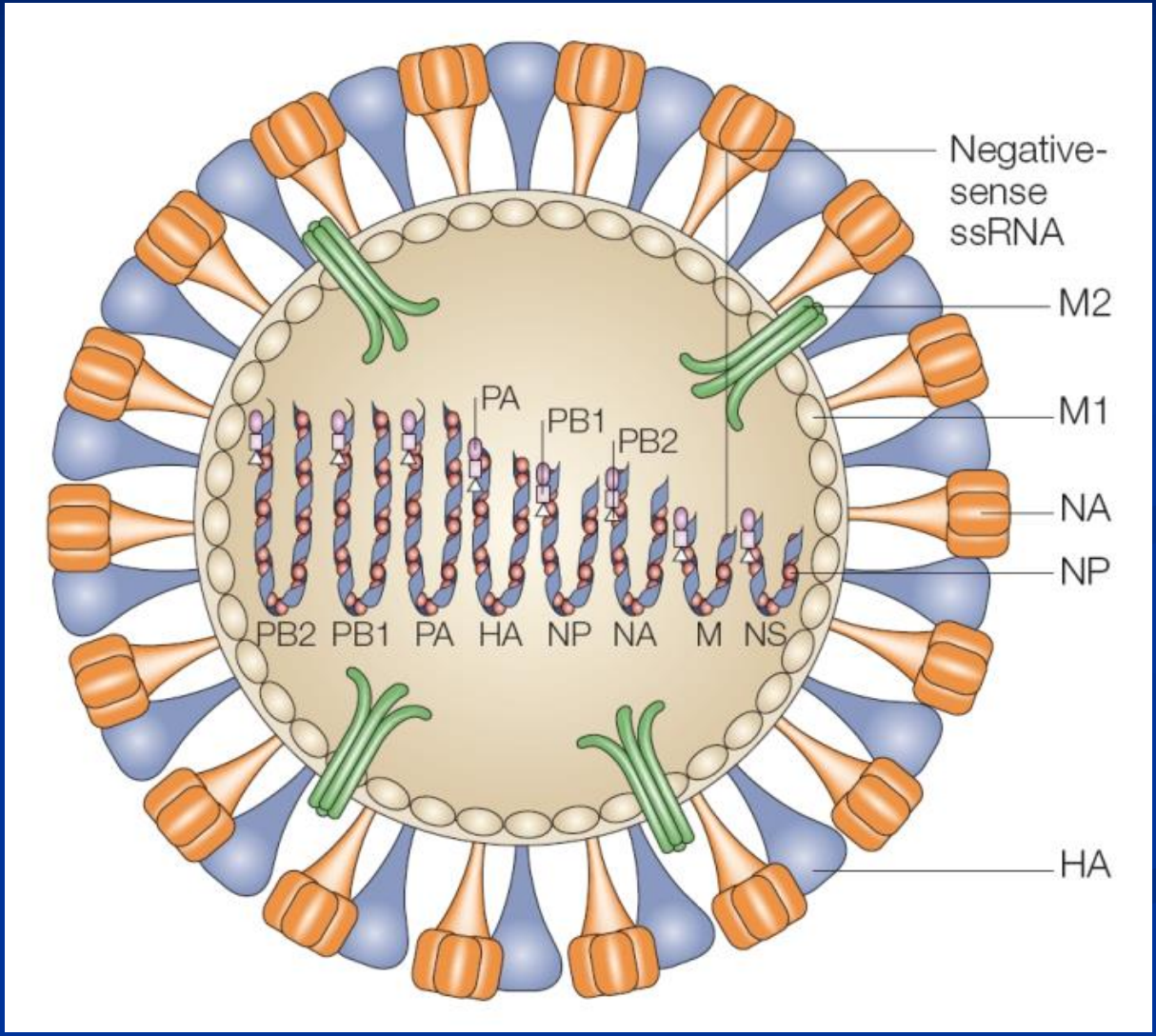
Negative sense

Linear

Segmented (6-8 segments)

Haploid

Example: Influenza Virus



Capsid

Two kinds of symmetry:

Correspond to two primary shapes

Rod:

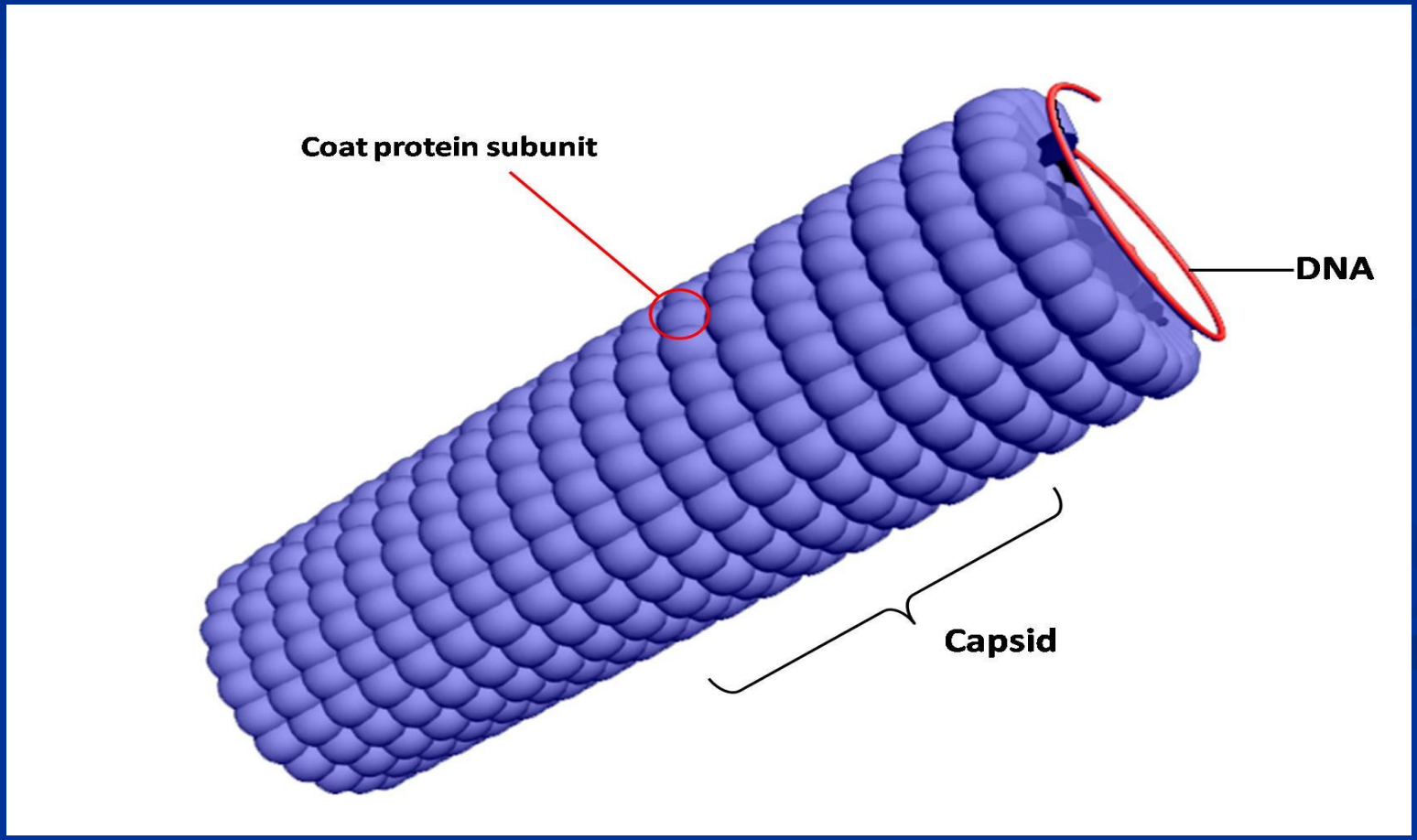
Helical symmetry

Spherical:

Icosahedral symmetry

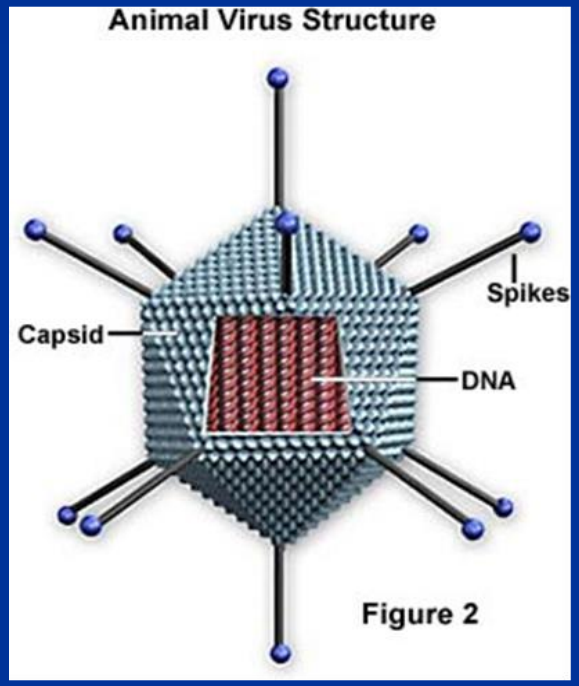
Capsid

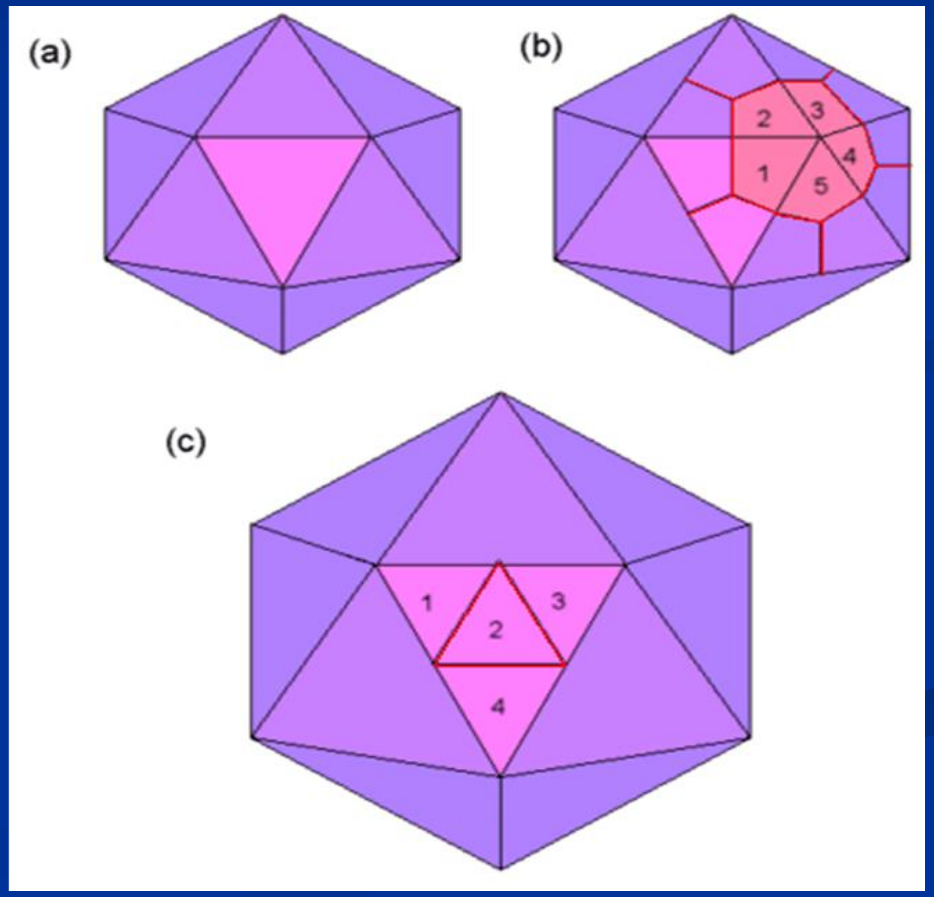
Helical Capsid:



2- Capsid

Icosahedral Capsid:

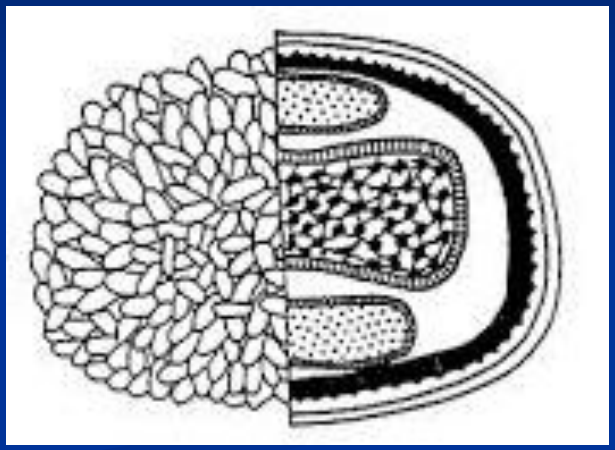




20 faces (equilateral triangle)
30 borders - 12 angles

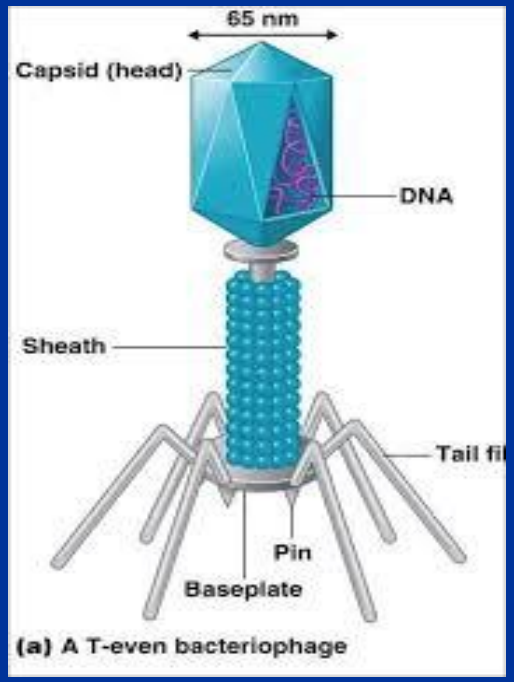
Capsid

Complex Capsid:



- **Neither icosahedral nor helical**

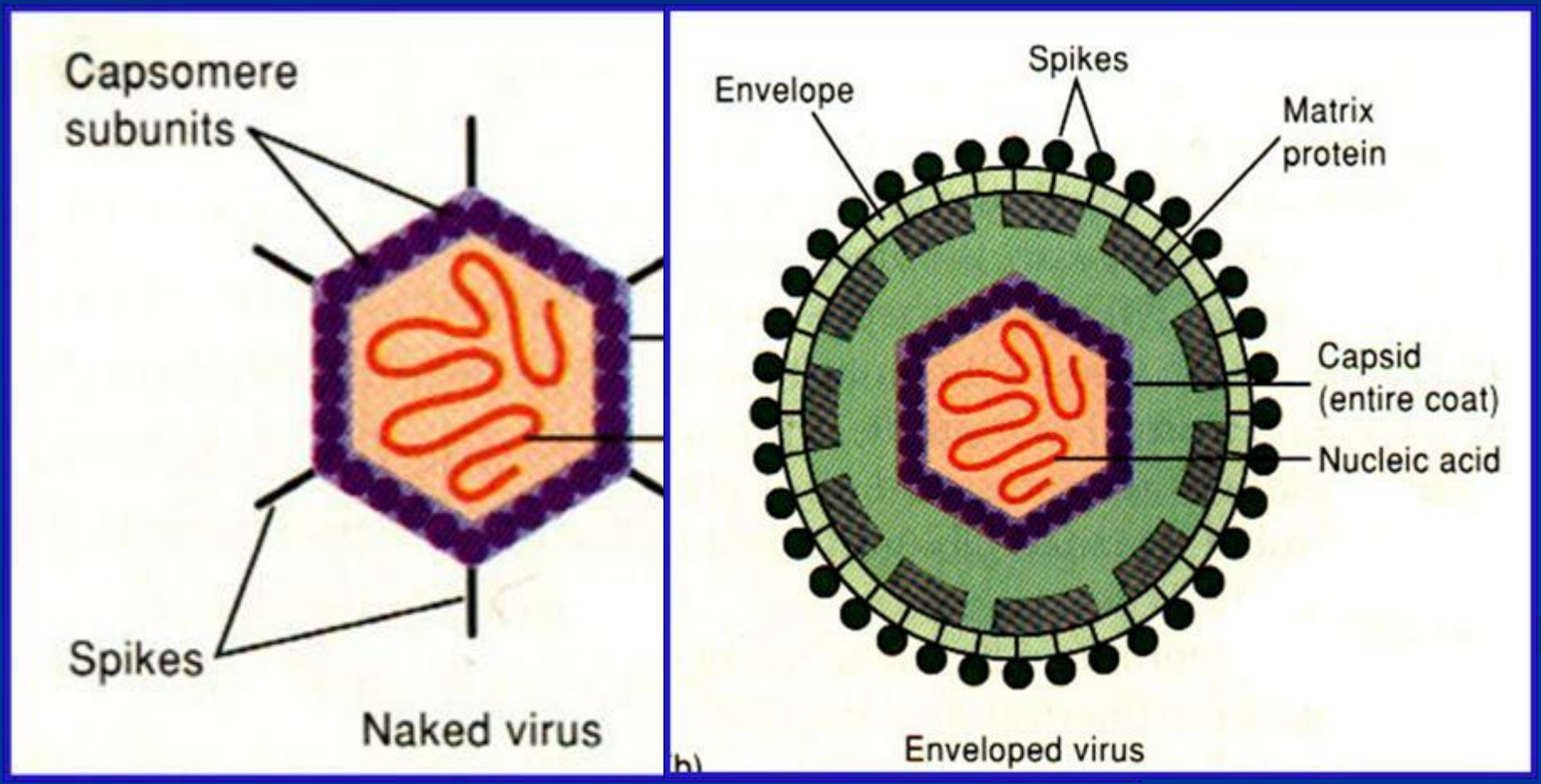
e.g. small pox virus

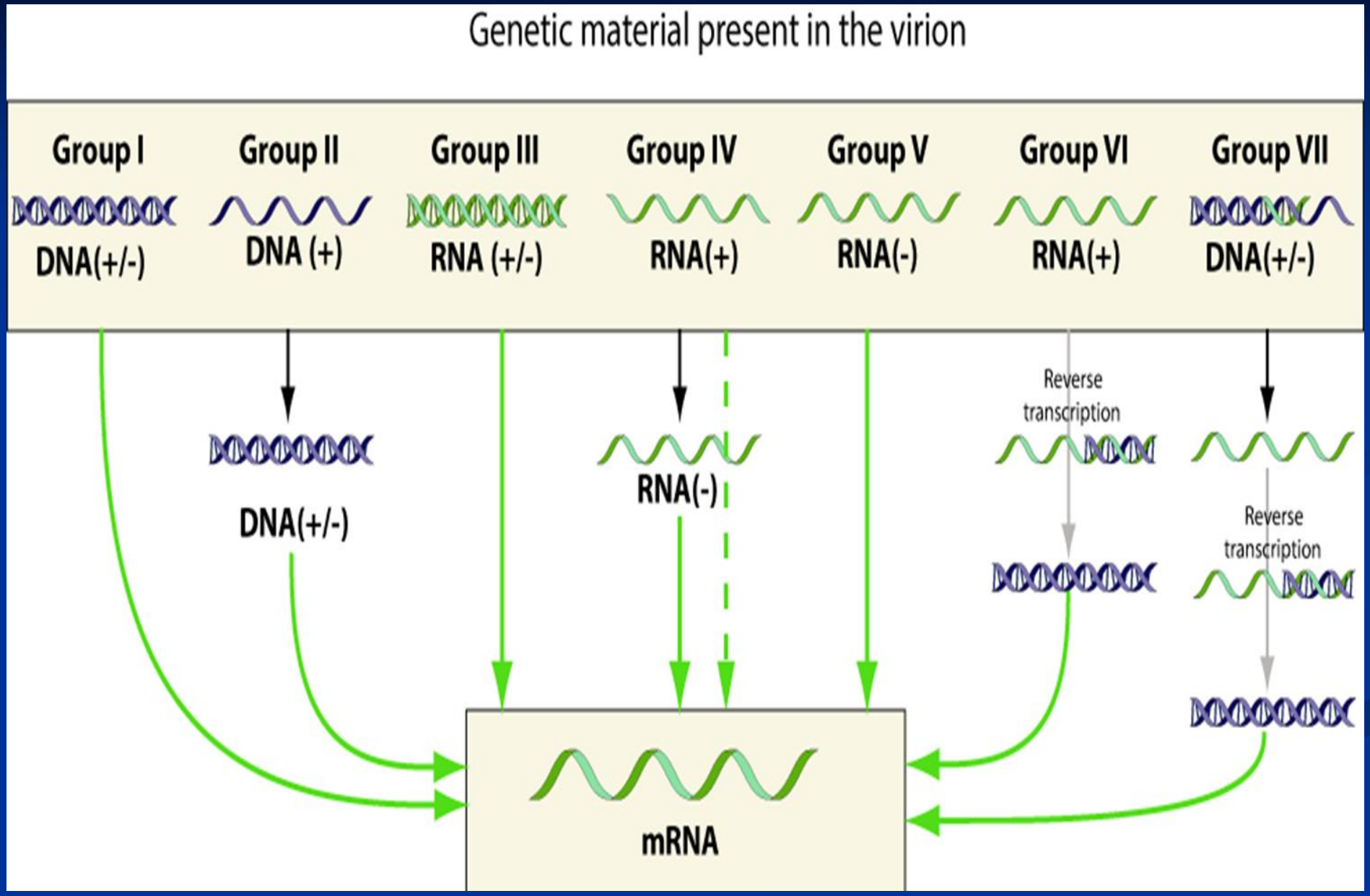


- **Both icosahedral nor helical (Binal)**

e.g. Bacteriophage

Envelope


Capsomere subunits
Spikes
Naked virus
Envelope
Spikes
Matrix protein
Capsid (entire coat)
Nucleic acid
Enveloped virus


Genetic material present in the virion
Group I
DNA(+/-)
Group II
DNA (+)
Group III
RNA (+/-)
Group IV
RNA(+)
Group V
RNA(-)
Group VI
RNA(+)
Group VII
DNA(+/-)
DNA(+/-)
RNA(-)
Reverse transcription
Reverse transcription
mRNA

ICTV

- International committee on the nomenclature of viruses (ICNV) …….. **1966**
- International committee on the taxonomy of viruses (ICTV) …….. **1973**
- Nine meetings were held to upgrade virus classification till now:

  Helsinki (Finland) 1968 …….. Leuven (Belgium) 2009

At 2016:
122 families
4404 virus

Year	Release Info	Order	Family	Subfamily	Genus	Species
2016	EC 48, Budapest, Hungary, August 2016; Email ratification 2017 (MSL #31)	8	122	35	735	4404
2015	EC 47, London, UK, July 2015; Email ratification 2016 (MSL #30)	7	111	27	609	3704
2014	EC 46, Kingston and Montreal, Canada, July 2014, Email ratification 2015 (MSL #29)	7	104	23	505	3185
2013	EC 45, Edinburgh, July 2013; Email ratification 2014 (MSL #28)	7	103	22	455	2827
2012	EC 44, Leuven, July 2012; Email ratification 2013 (MSL #27)	7	96	22	420	2617
2011	EC 42: Paris, June, 2010; EC43: Sapporo, September 2011; Email ratification 2012 (MSL #26)	6	94	22	395	2480
2009	ICTV 9th Report; EC41: Leiden, June 2009; Email ratification 2009 (MSL #25)	6	87	19	349	2285
2008	EC 39: Kingston, June, 2007; EC 40: Istanbul, August 2008; Email ratification 2008 (MSL #24)	5	82	11	307	2079
2005	ICTV 8th Report (MSL #23)	3	73	11	289	1899
2004	Postal vote 2004 (MSL #22)	3	73	11	290	1832
2002	Plenary session vote 30 July 2002 in Paris (MSL #21)	3	70	11	251	1619
2002	Postal vote spring 2002 (MSL #20)	3	70	9	247	1602
1999	Plenary session vote August 1999 in Sydney (MSL #19)	3	64	9	239	1550
1999	ICTV 7th Report (MSL #18)	3	64	9	234	1551
1998	Postal vote autumn 1998 (MSL #17)	3	63	9	233	2370
1997	Postal vote autumn 1997 (MSL #16)	2	56	9	197	2267
1996	Plenary session vote August 1996 in Jerusalem (MSL #15)	2	53	9	182	2253
1995	ICTV 6th Report (MSL #14)	1	50	9	166	2220
1993	Plenary session vote 10 August 1993 in Glasgow (MSL #13)	1	49	9	160	1700
1991	ICTV 5th Report (MSL #12)	1	40	9	142	1674
1990	Plenary session vote 29 August 1990 in Berlin (MSL #11)	1	40	9	137	1290
1987	Plenary session vote 12 August 1987 in Edmonton (MSL #10)	0	37	8	116	1275
1984	Plenary session vote 5 September 1984 in Sendai (MSL #09)	0	35	8	103	1222
1982	ICTV 4th Report (MSL #08)	0	29	8	97	1209
1981	Plenary session vote 4 August 1981 in Strasbourg (MSL #07)	0	29	8	93	1091
1979	ICTV 3rd Report (MSL #06)	0	24	8	84	1008
1978	Plenary session vote 30 August 1978 in The Hague (MSL #05)	0	24	7	76	760
1976	ICTV 2nd Report (MSL #04)	0	17	3	67	754
1975	Plenary session vote 12/16 September 1975 in Madrid (MSL #03)	0	17	1	63	309
1974	Postal vote April-May 1974 (MSL #02)	0	5	0	49	298
1971	ICTV 1st Report (MSL #01)	0	2	0	43	290

At 1971:
2 families
290 virus

Classification Methods

First classification trial:

"Based on clinical and ecological properties"

1. Common clinical and pathogenic properties
   (e.g. respiratory, nervous, digestive viruses)
2. Common organ tropism
   (e.g. liver, lung, brain, intestine)
3. Common transmission patterns
   (e.g. Arthropod-born, Air-born, vertical, venereal)

Ex. Viruses causing hepatitis (A, B, C, D,E; now belong to different families: Picorna, Hepadna, Flavi, Delta and Calici).

Classification Methods

Second classification trial:

"Based on physicochemical and antigenic properties of viruses"

1. Virion size
   (ultrafiltration - ultracentrifugation - electron microscopy)
2. Virion morphology
   (Electron microscopy)
3. Virion stability
   (pH – temperature – lipid solvents – detergents – radiation)

4- Virus antigenicity (Serological tests)

Classification Methods

Current classification trials:

"Based on virus structure and replication"

1. Hierarchical Classification System
   (Structure of virion and characteristics of virus genome)
2. Baltimore Classification System
   (Strategy of viral replication and mRNA synthesis)
3. Phylogenetic analysis/Genotyping
   (Complete or partial sequencing of viral genome)

(A) Hierarchical classification system

"Based on structure of virion and characteristics of virus genome"

1. Virus genome:

   DNA or RNA, ds or ss, + or - sense, single molecule or segmented, linear or circular, haploid or diploid.

2. Capsid:

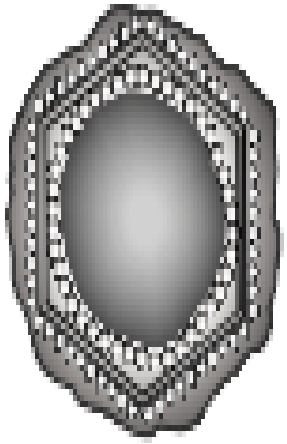
   Size and symmetry (helical, icosahedral or complex).

3. Envelope:

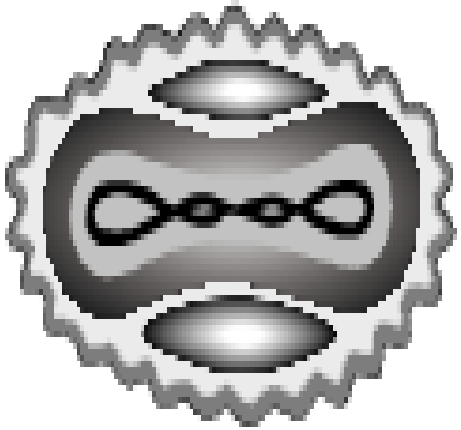
   Enveloped or naked.

DNA

dsDNA

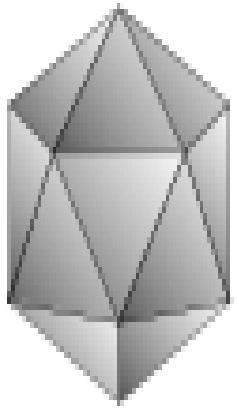


Asfarviridae



Poxviridae

Chordopoxvirinae



Iridoviridae

Ranavirus

Lymphocystivirus

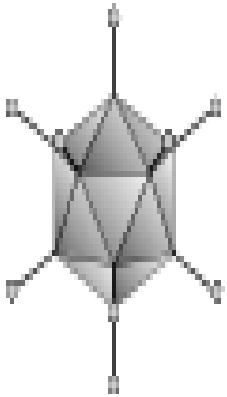
dsDNA (RT)

Hepadnaviridae

Herpesviridae

Polyomaviridae

Papillomaviridae



Adenoviridae

ssDNA

Circoviridae

Parvoviridae

Parvovirinae

RNA

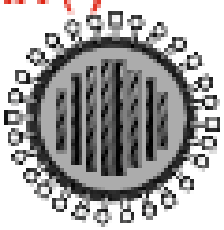
dsRNA

Reoviridae
Orthoreovirus
Orbivirus
Coltivirus
Rotavirus
Aquareovirus

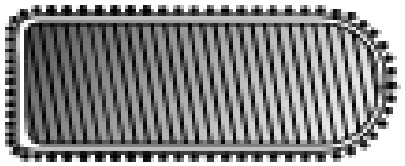
Birnaviridae
Aquabirnavirus
Avibirnavirus

100 nm

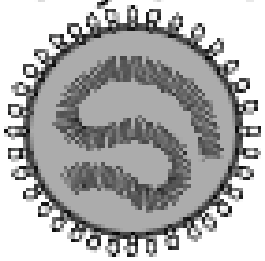
ssRNA (-)



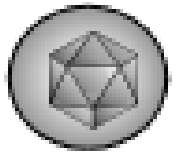
Orthomyxoviridae



Rhabdoviridae
Lyssavirus
Vesiculovirus
Ephemerovirus
Novirhabdovirus

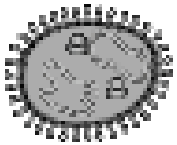


Paramyxoviridae

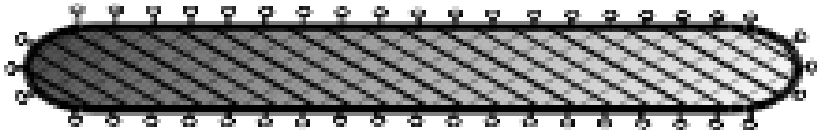


Bornaviridae

Deltavirus



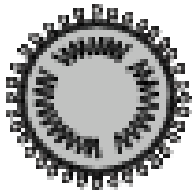
Arenaviridae



Filoviridae

ssRNA (RT)

Retroviridae



Bunyaviridae
Orthobunyavirus
Hantavirus
Nairovirus
Phlebovirus

ssRNA (+)

Caliciviridae

HEV-like

Nodaviridae
Betanodavirus

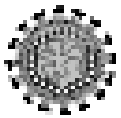
Togaviridae

Picornaviridae

Astroviridae

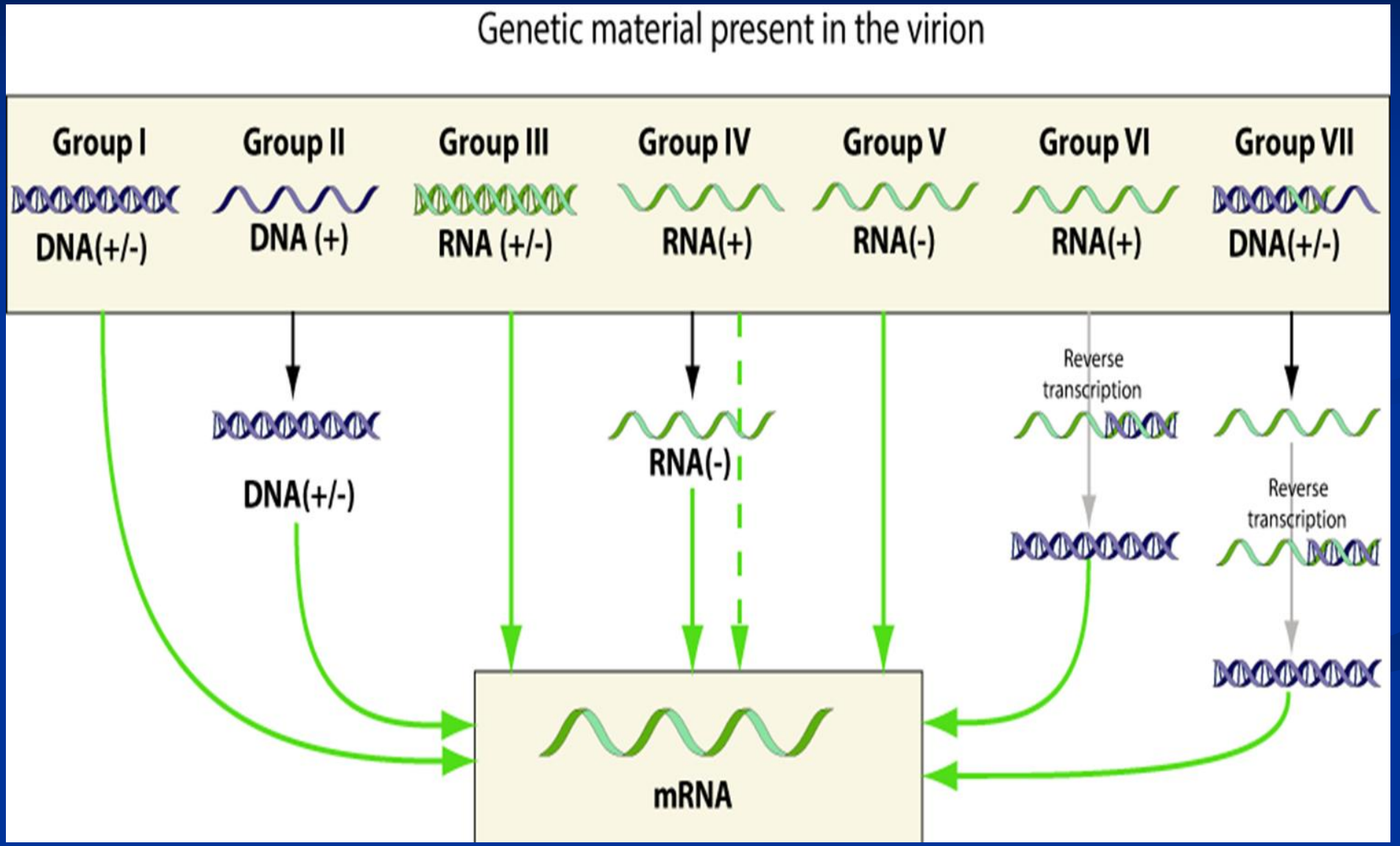
Flaviviridae

Coronaviridae



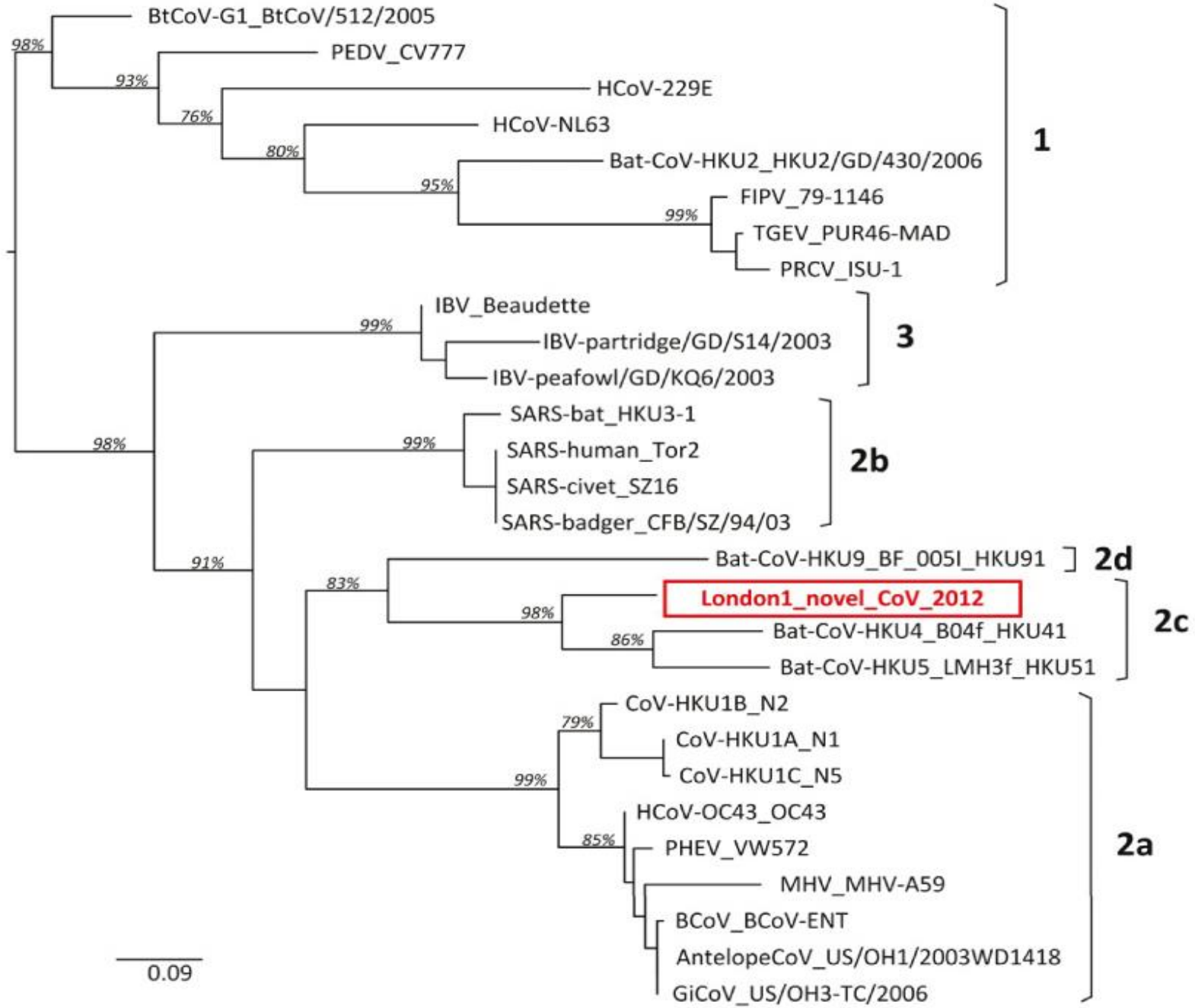
Arteriviridae

(B) Baltimore classification system



(C) Phylogenetic analysis (genotyping)

- Based on complete or partial sequencing of the viral genome.
- Comparison of the nucleotide sequence using computer softwares.
- Classify the viral strains into different lineages.
- http://www.ncbi.nlm.nih.gov


BtCoV-G1_BtCoV/512/2005
PEDV_CV777
HCoV-229E
HCoV-NL63
Bat-CoV-HKU2_HKU2/GD/430/2006
FIPV_79-1146
TGEV_PUR46-MAD
PRCV_ISU-1
IBV_Beaudette
IBV-partridge/GD/S14/2003
IBV-peafowl/GD/KQ6/2003
SARS-bat_HKU3-1
SARS-human_Tor2
SARS-civet_SZ16
SARS-badger_CFB/SZ/94/03
Bat-CoV-HKU9_BF_005I_HKU91
London1_novel_CoV_2012
Bat-CoV-HKU4_B04f_HKU41
Bat-CoV-HKU5_LMH3f_HKU51
CoV-HKU1B_N2
CoV-HKU1A_N1
CoV-HKU1C_N5
HCoV-OC43_OC43
PHEV_VW572
MHV_MHV-A59
BCoV_BCoV-ENT
AntelopeCoV_US/OH1/2003WD1418
GiCoV_US/OH3-TC/2006
98%
93%
76%
80%
95%
99%
99%
98%
99%
91%
83%
98%
86%
79%
99%
85%
1
3
2b
2d
2c
2a
0.09

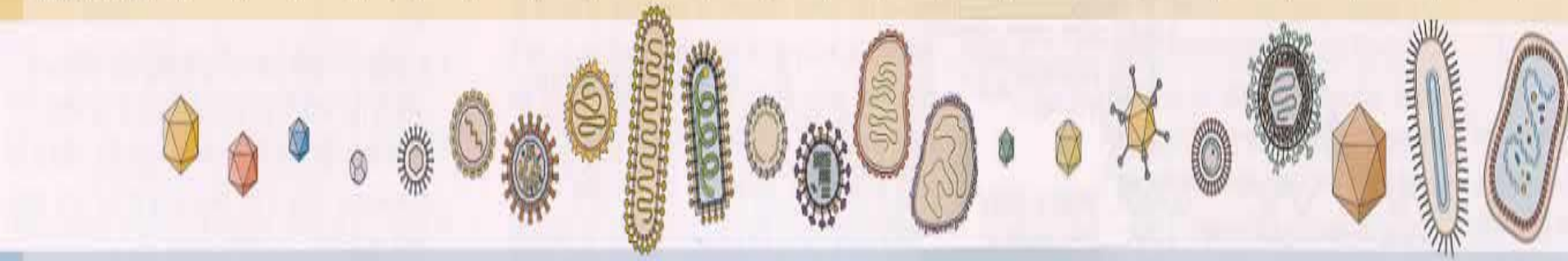
Universal system for virus taxonomy (USVT)

Established by ICTV - Based on:

1. Virion size, morphology and stability.
2. Type and characteristics of the viral genome.
3. Capsid size and symmetry.
4. Presence or absence of virus envelope.
5. Strategy of virus replication.
6. Phylogenetic analysis

Classification criteria

Nucleic acid	RNA													DNA								
Symmetry of capsid	Icosahedral							Helical						Icosahedral					Helical	Complex		
Naked or enveloped	Naked				Enveloped			Enveloped						Naked			Enveloped		Naked/Env. (cytoplasmic)	Enveloped	Enveloped (cytoplasmic)	
Genome architecture	ds 10–18 seg.	ds 2 seg.	(+) ss cont.	(+) ss cont.	(+) ss cont.	(+) ss cont.	(+) ss 2 copies	(+) ss cont.	(–) ss cont.	(–) ss cont.	(–) ss 3 seg.	(–) ss 8 seg.	(–) ss cont.	(–) ss 2 seg	ss linear (+) or (–)	ds circular	ds linear	ds circle gapped	ds linear	ds linear	ds circular	ds linear (x linked)
Baltimore class	III	III	IV	IV	IV	IV	VI	IV	V	V	V	V	V	V	II	I	I	I	I	I	I	I



Properties

Family name	Reo	Birna	Calici	Picorna	Flavi	Toga	Retro	Corona	Filo	Rhabdo	Bunya	Ortho-myxo	Para-myxo	Arena	Parvo	Papova	Adeno	Hepadna	Herpes	Irido	Baculo	Pox
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	18–26	45–55	70–90	42	150–200	125–300	60 X 300	170–200 X 300–450
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	5	5–8	36–38	3.2	120–200	150–350	100	130–280

USVT

- Order: ends with suffix (Virales)

  Order: Mononegavirales

- Family: ends with suffix (Viridae)

  Family Poxviridae - Picornaviridae

- Subfamily: ends with suffix (Virinae)

  Subfamily: Chordopoxvirinae

- Genus: ends with suffix (Virus)

  Genus: Capripoxvirus

Other terms related to virus classification

- Pathotypes:

  Variation in the virulence of virus strains.

  NDV (Lentogenic, Mesogenic and Velogenic).

- Biotypes:

  Variation in the cytopathogenisity of virus strains.

  BVD (Cytopathogenic and non-cytopathogenic).

- Serotypes:

  Variation in the antigenicity of virus strains according to serological tests.

- Genotypes:

  Variation in the genetic properties of virus strains according to molecular based techniques.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