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Virus genomes

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Virus Classification

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- Classification on the basis of disease
- Classification on the basis of host range
- Classification on the basis of particle morphology
- Classification on the basis of viral nucleic acid

Classification on the basis of disease

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Hepatitis viruses

CNS infection: encephalitis, meningitis etc
Rabies virus, Japanese encephalitis virus, Poliovirus etc.

Respiratory tract infection : common cold, influenza
Rhinovirus, Adenovirus, Influenza virus etc

Classification on the basis of host range

Advantage: virus-host interaction

Disadvantage: difficult to designate virus based on host species

Hepatitis B virus : very restricted host, human, thus, a designation base on host is appropriate.

Poliovirus: various primates as host, designation becomes complicate.

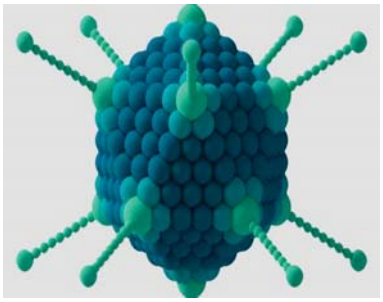
Viruses that infect plant and insect or various species of host, designation by host species is sophisticate.

Morphology of the particles

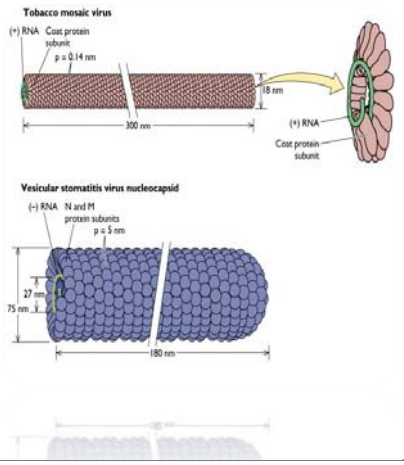
Envelope virus

Non-envelope virus

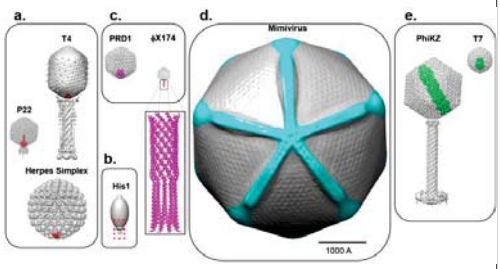
Icosahedral structure



Helical or filamentous structure

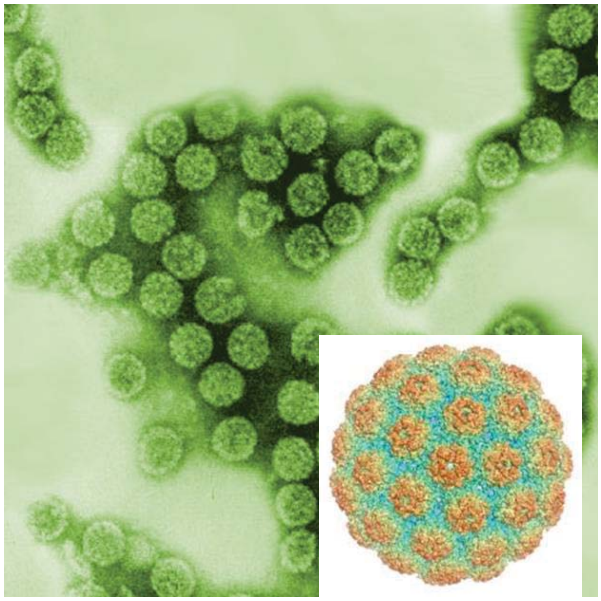


Complex structure

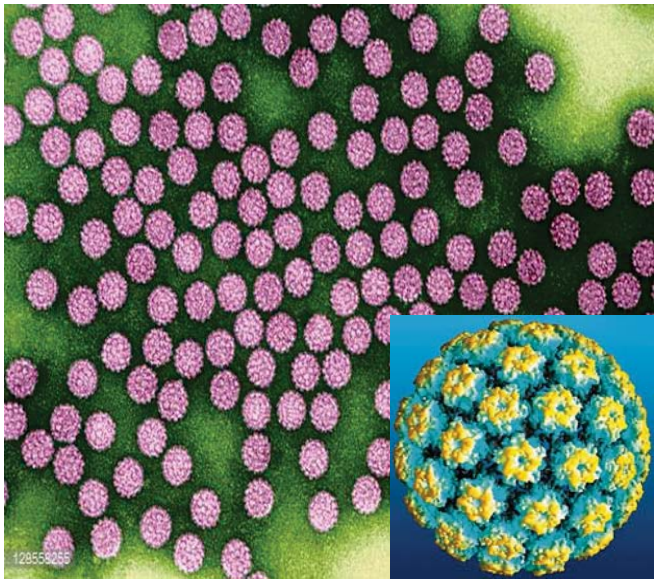


Classification on the basis of particle morphology (disadvantage)

Polyomavirus: JC virus, BK virus

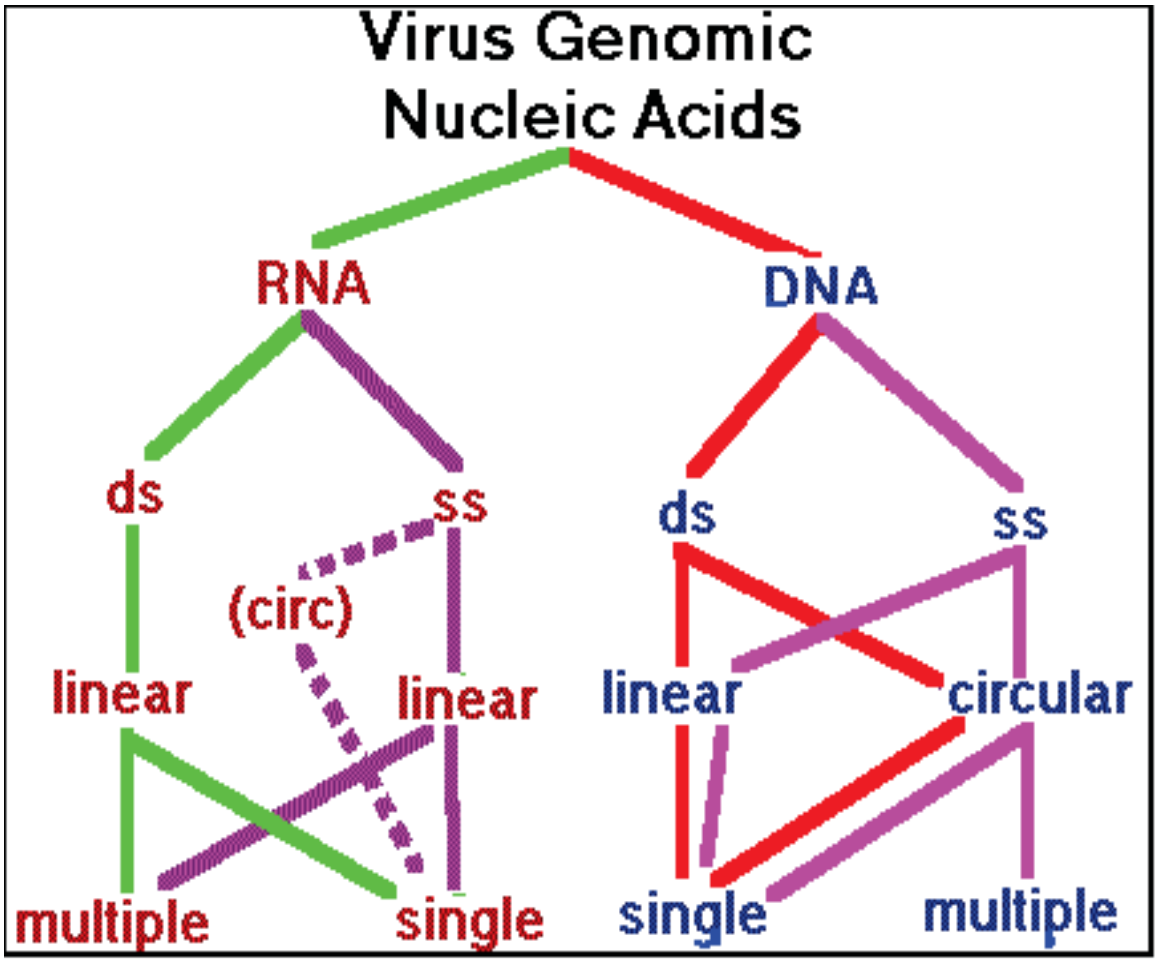


Human papillomavirus



Classification on the basis of viral nucleic acid

- Type and structure of genome
- Replication and mRNA synthesis
- Base sequence



Virus genome : RNA

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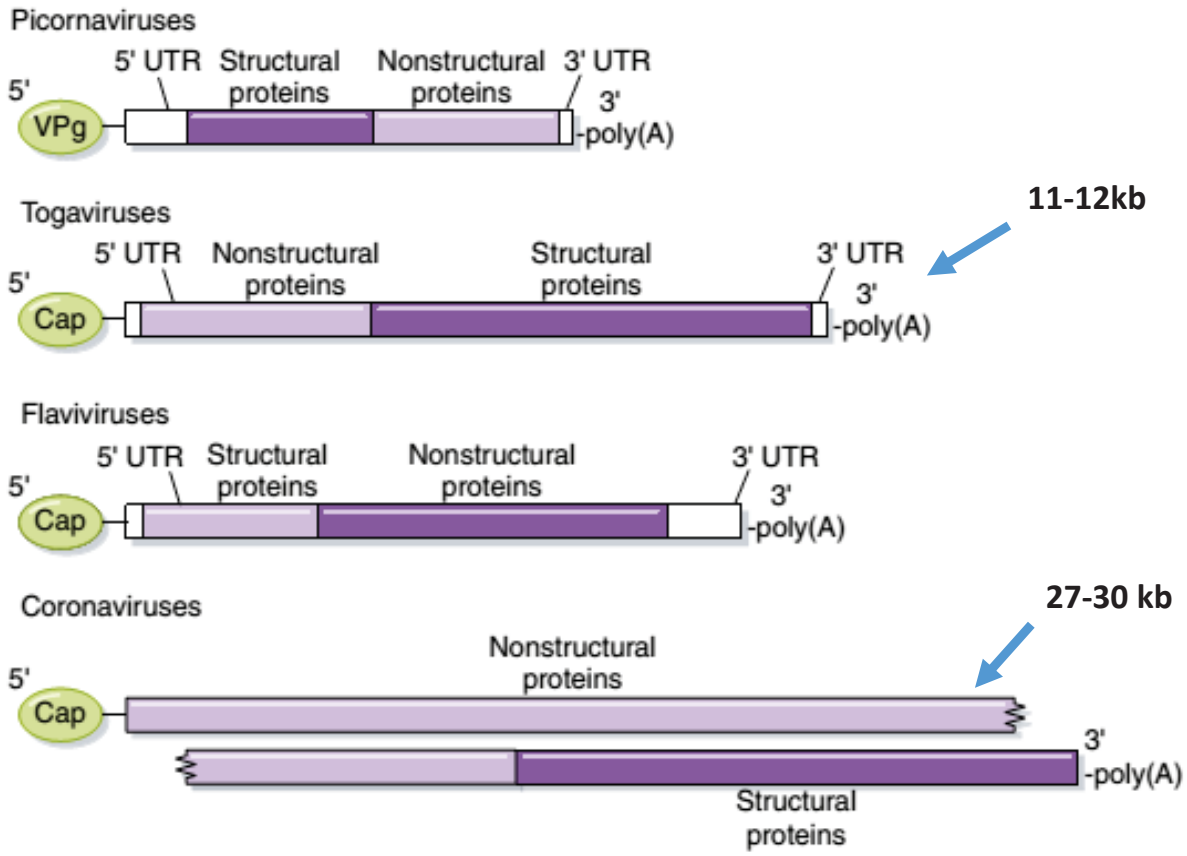
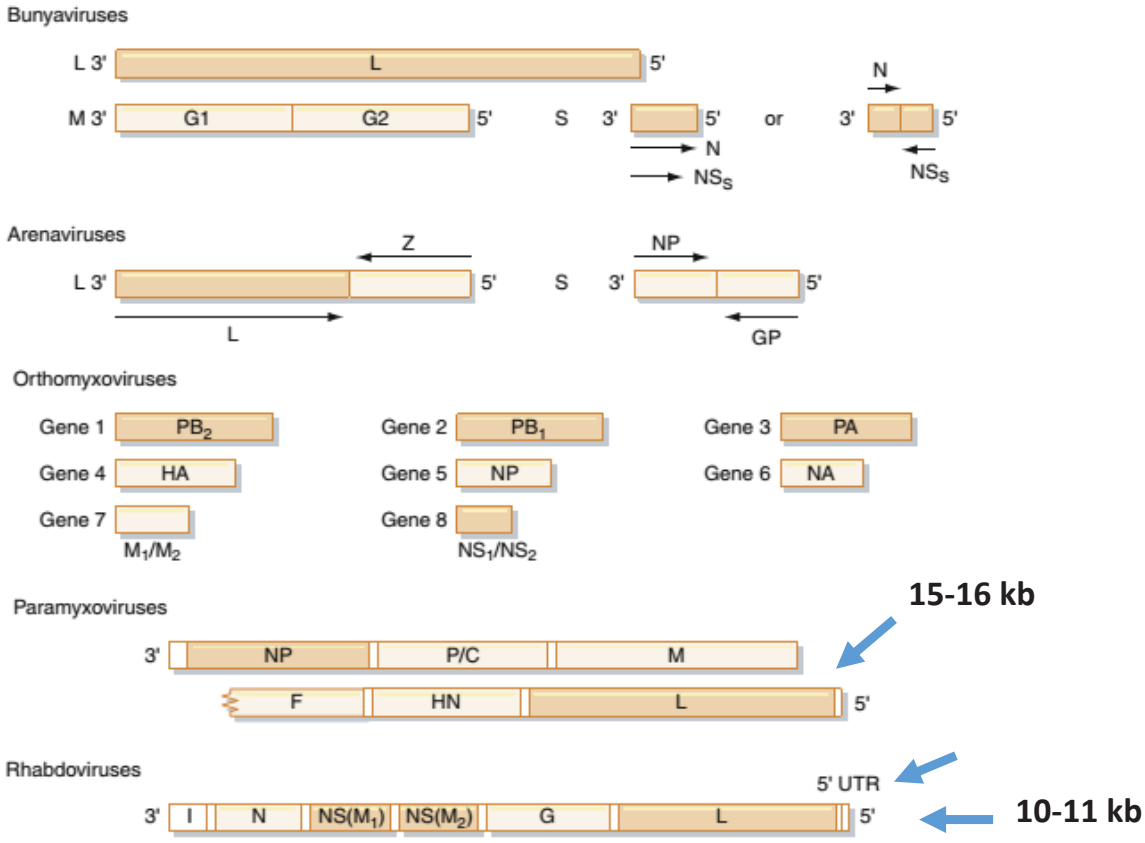
- Plus strand RNA (+ polarity RNA)
- Minus strand RNA (- polarity RNA)

Genomic organization of positive sense, single-stranded RNA viruses



Genomic organization of negative sense, single-stranded RNA viruses



What is an ambisense virus genome?

Ambisense virus genome contains at least one RNA segment that is part positive and part negative sense in the same molecule.

Arenaviruses : Both L and S genes are ambisense RNA.

Bunyaviruses : Some of Bunyaviruses have M gene as an ambisense RNA.

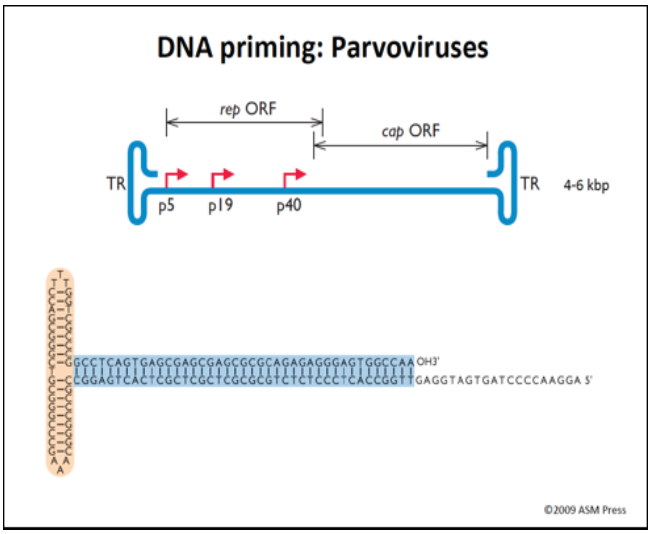
Monopartie virus genome and Multipartie virus genome

Monopartie virus genome : All viral gene segments are packaged in one particle. (Influenza virus, segmented RNA)

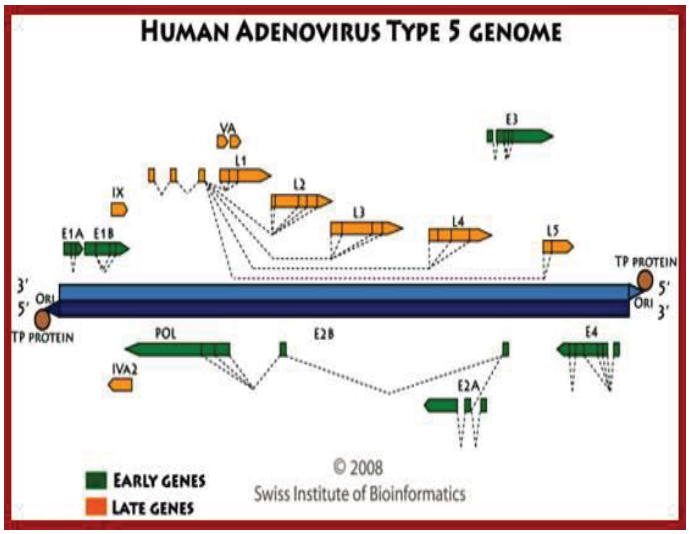
Multipartie virus genome: Separating genome segments into different particles (Geminivirus, segmented DNA, plant virus)

Organizations of DNA virus genomes : small genome

Parvovirus: single-stranded DNA, 5kbp self primers

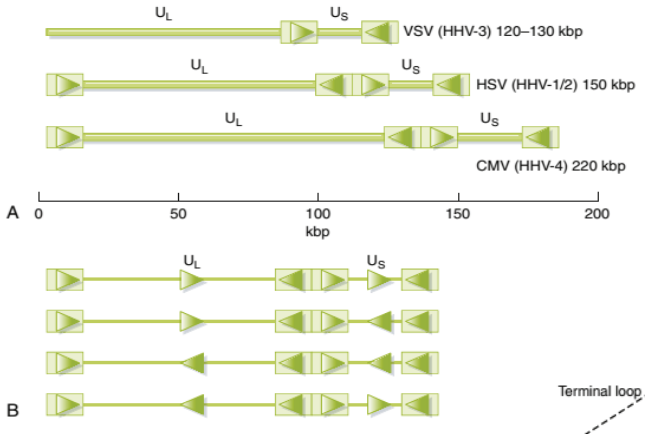


Adenovirus : double-stranded DNA, 30kbp protein primer

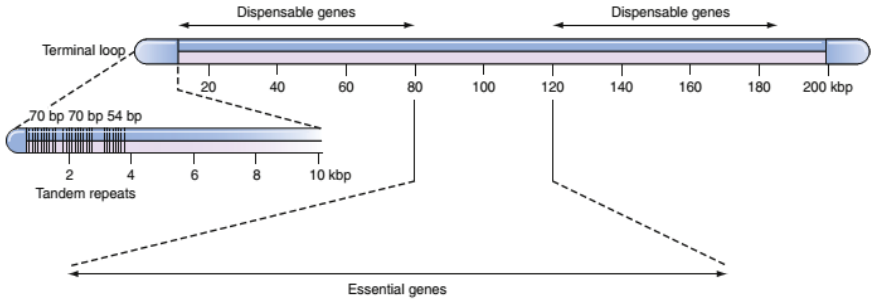


Organizations of DNA virus genomes : large genome

Herpesvirus genome: 120-240 kbp

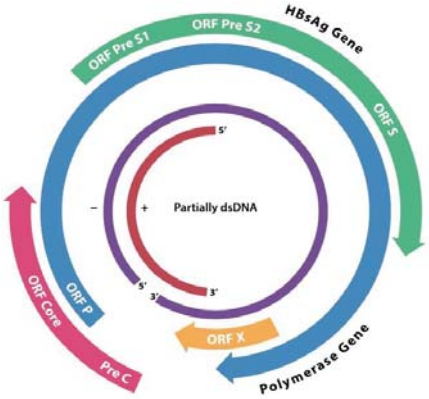


Poxvirus genome: 140-290 kbp



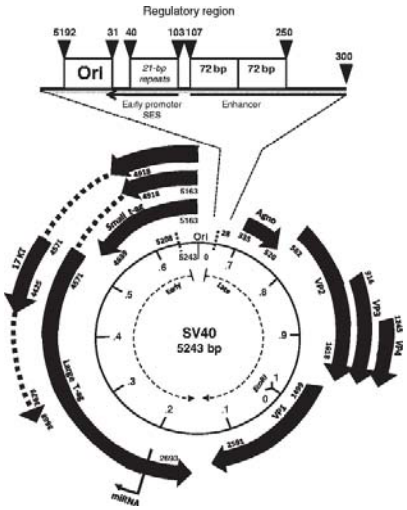
Organizations of DNA virus genomes: the circular genomes

Hepatitis B virus



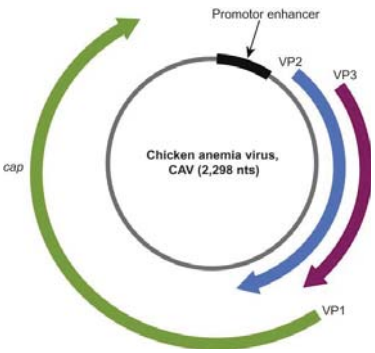
Partial double strand, circular DNA

Polyomavirus SV40



Complete close circular, double-stranded DNA

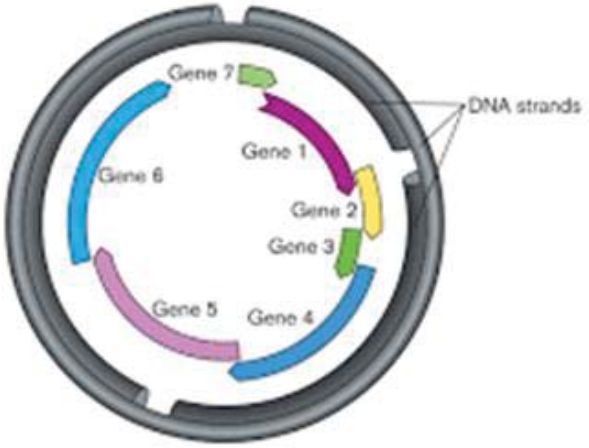
Circoviridae



Single-stranded, complete circular DNA

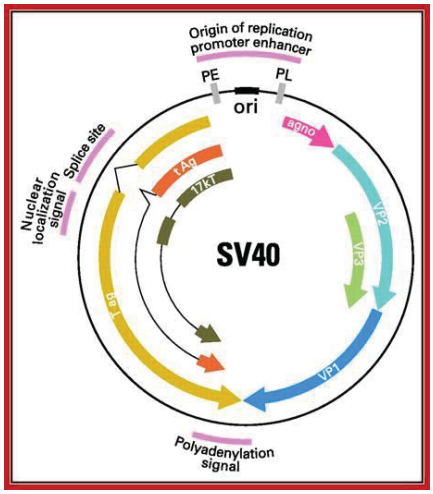
Organizations of DNA virus genomes: the circular genomes

Cauliflower mosaic virus



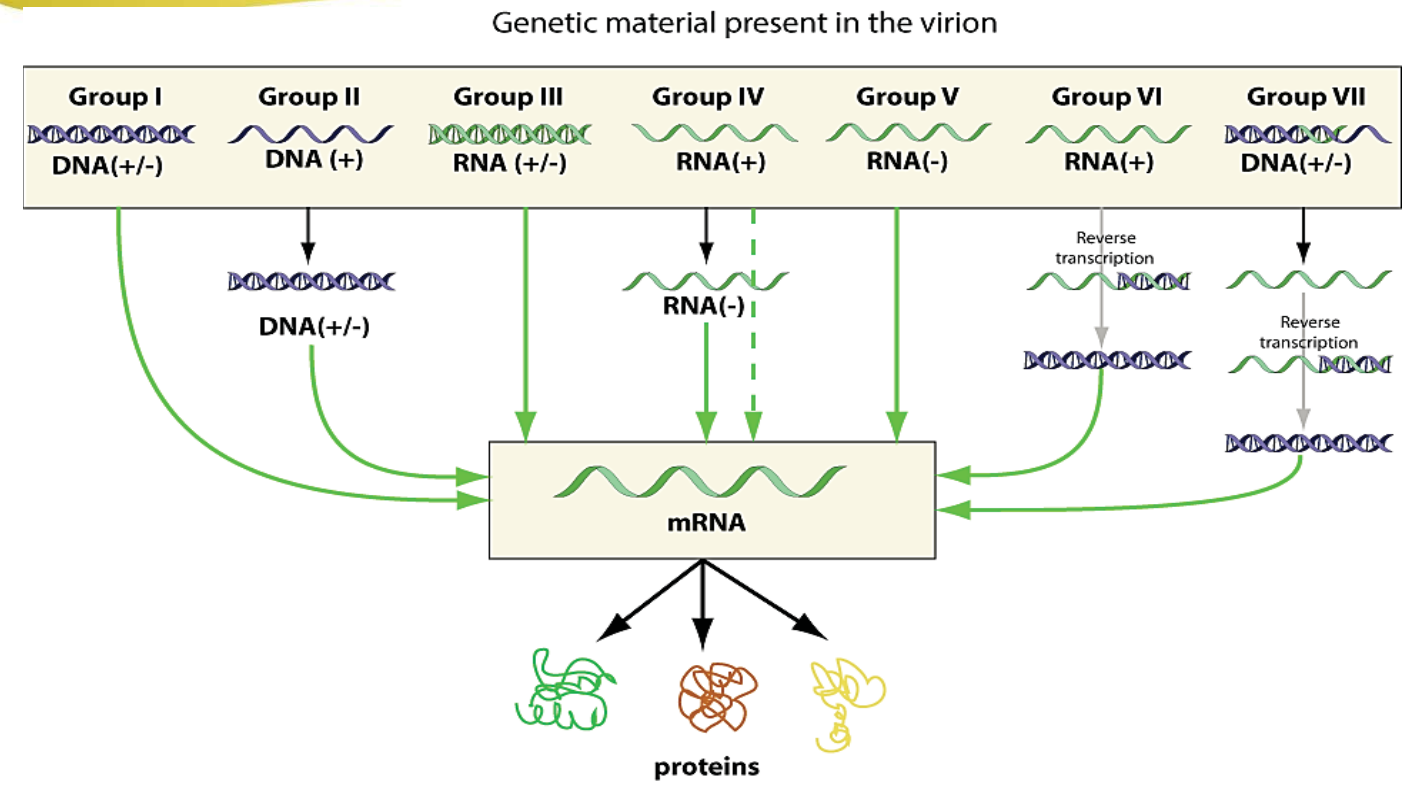
Nicked, double-stranded circular DNA

Polyomavirus SV40



Double-stranded circular DNA

Genome classification base on Replication and mRNA synthesis : The Baltimore scheme

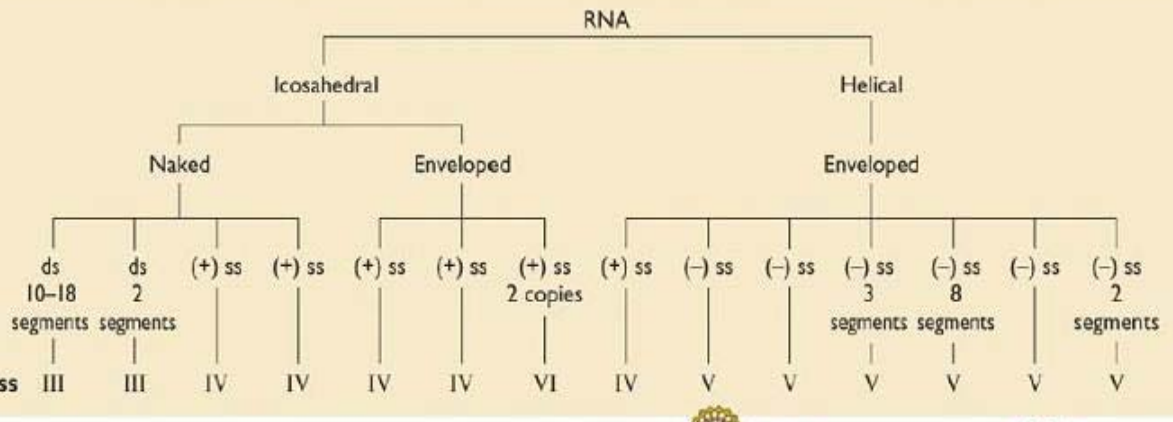


Viruses with reverse transcription

Features	Caulimoviruses	Hepadnaviruses	Retroviruses
genome	DNA(circular)	DNA(circular)	RNA
Primer for (-) strand synthesis	tRNA	protein	tRNA
Terminal repeats (LTRs)	No	No	Yes
Specific integration of virus genome	No	No	Yes

Base sequences

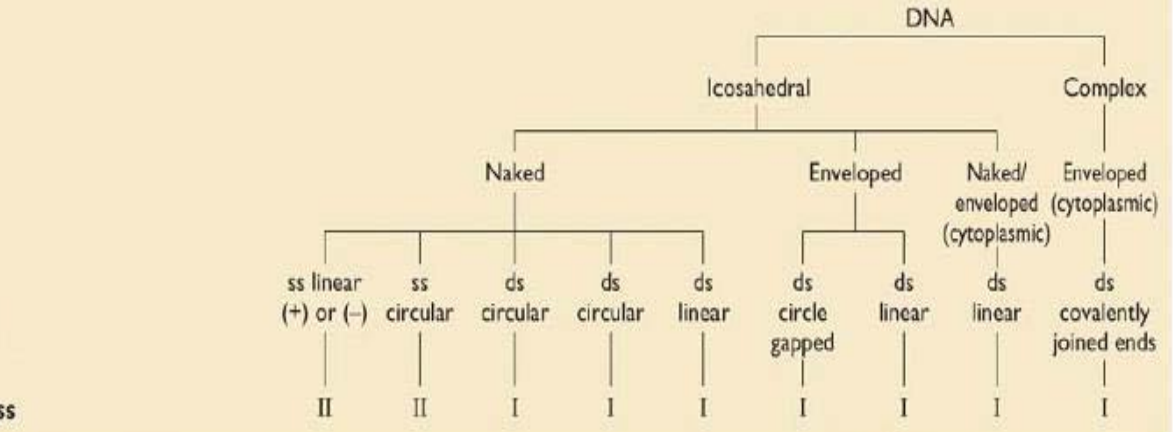
Classification criteria



Properties

Family name	Reo	Birna	Calici	Picorna	Flavi	Toga	Retro	Corona	Filo	Rhabdo	Bunya	Ortho-myxo	Para-myxo	Arena
Virion polymerase	(+)	(+)	(–)	(–)	(–)	(–)	(+)	(–)	(+)	(+)	(+)	(+)	(+)	(+)
Virion diameter (nm)	60–80	60	35–40	28–30	40–50	60–70	80–130	80–160	80 × 790–14,000	70–85 × 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

Classification criteria

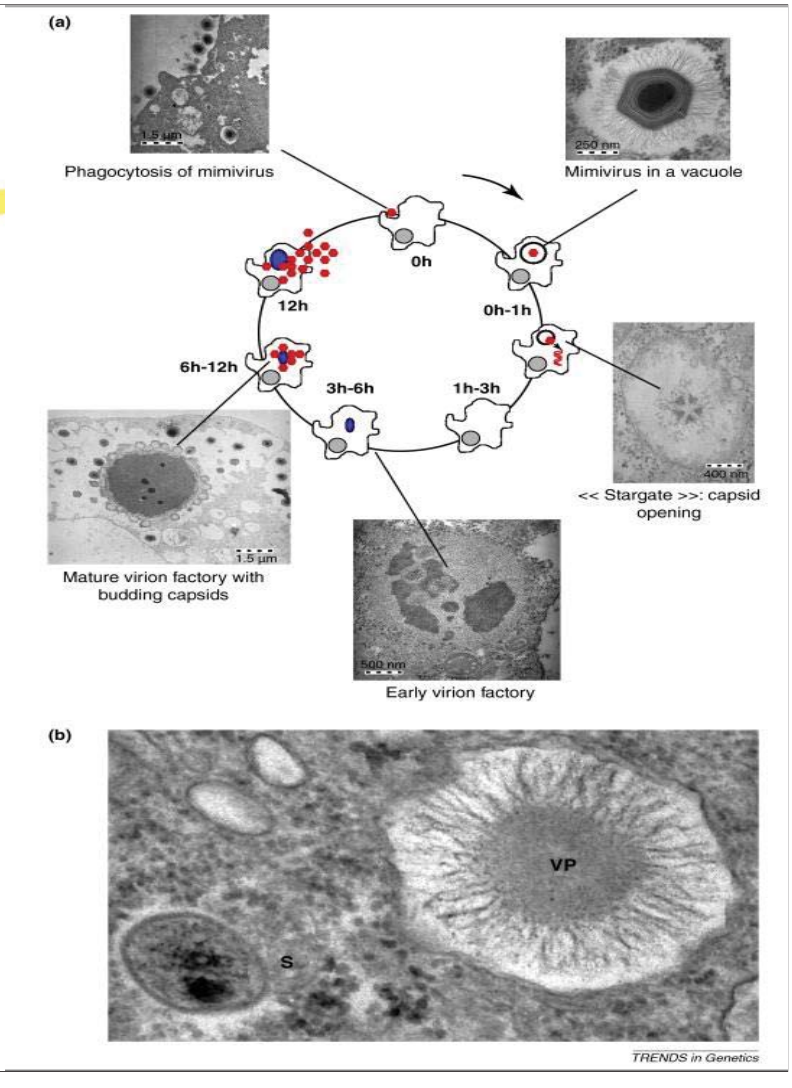


Properties

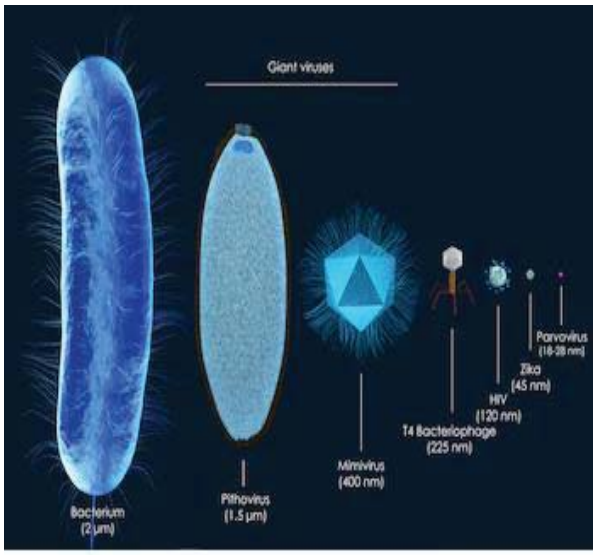
Family name	Parvo	Circo	Polyoma	Papilloma	Adeno	Hepadna	Herpes	Irido	Pox
Virion polymerase	(–)	(–)	(–)	(–)	(–)	(+)	(–)	(–)	(+)
Virion diameter (nm)	18–26	12–26	40	55	70–90	42	150–200	125–300	170–200 × 300–450
Genome size (total in kb)	5	1.8–2.3	5	7–8	36–38	3.2	120–200	150–350	130–280

The Giant Viruses

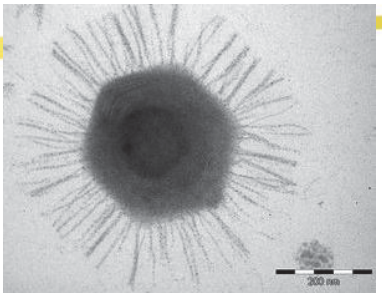
The Giant viruses



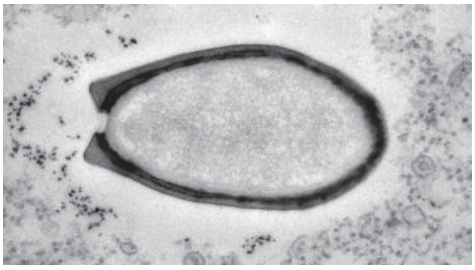
Morphology of Giant viruses



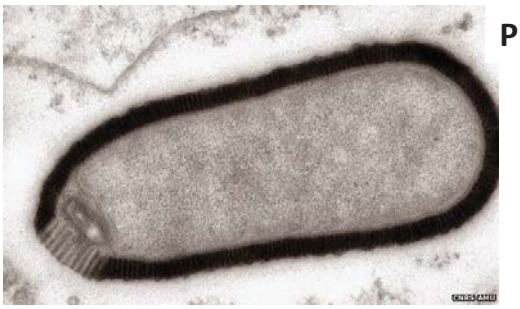
The biggest virus that have been observed.



Minivirus

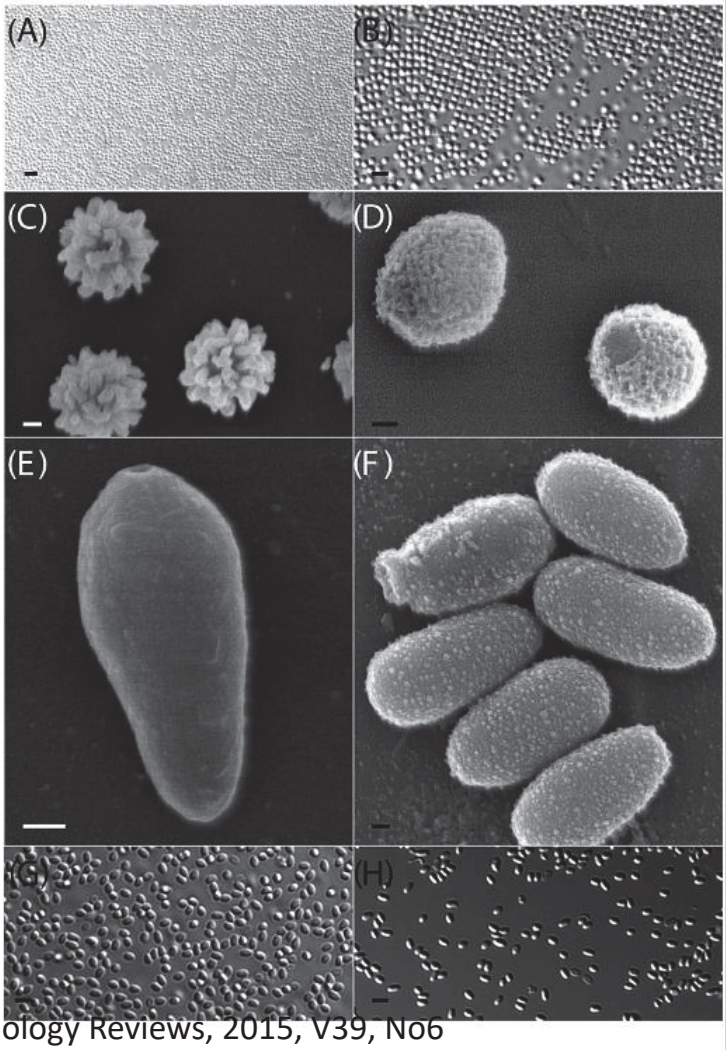


Pandoravirus

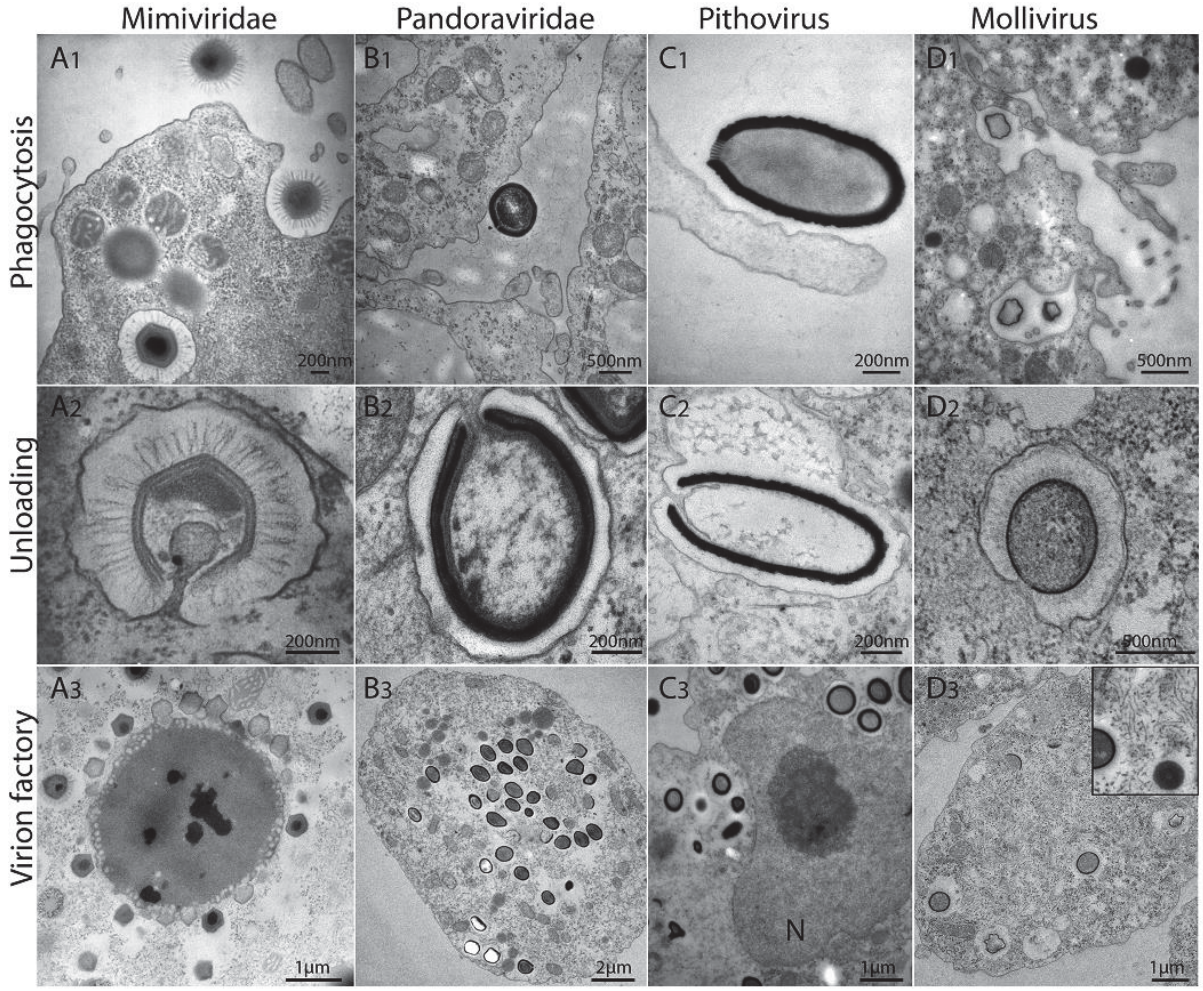


Pithovirus

It can be observed under the light microscope.

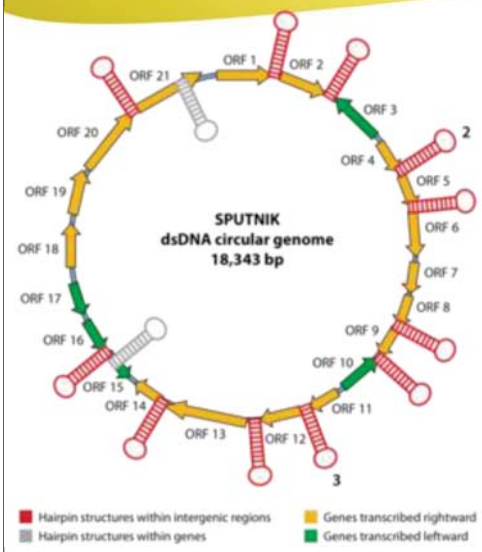


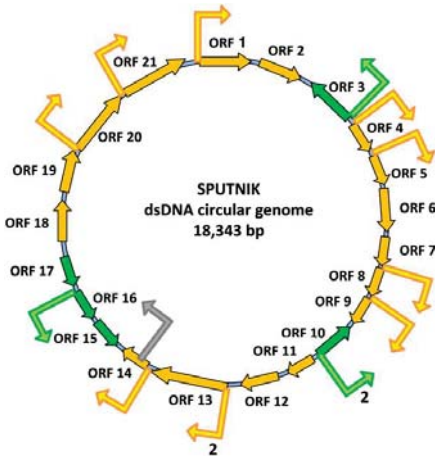
Abergel et al, FEMS Microbiology Reviews, 2015, V39, No6

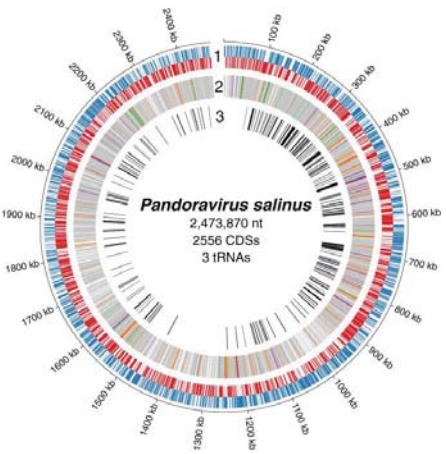


Abergel et al, FEMS Microbiology Reviews, 2015, V39, No6

Genome structure of Giant viruses







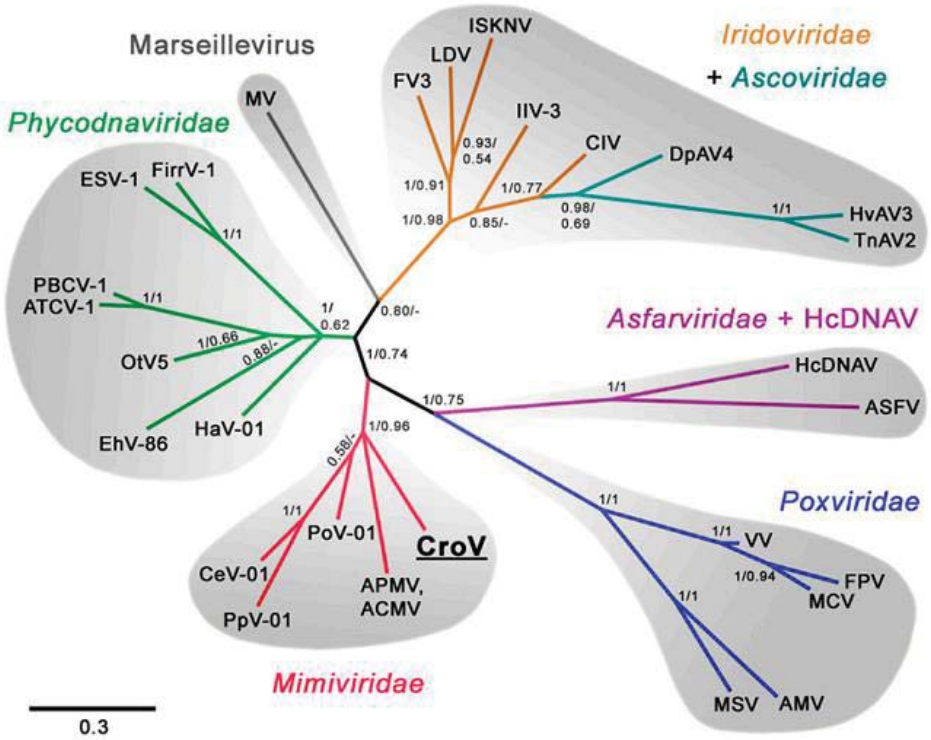
Genome **mRNA**

Table 1. Characteristics of giant viruses (grey rows) compared to other large eukaryotic viruses.

Family or genus	Name	Virion shape	Particle largest dimension (nm)	Genome max. size (kb)	G+C%	Genes	Nuclear phase	aaRS
Pandoraviridae[a]	Pandoravirus salinus	Ovoid	1200 × 500 Ø	2770	64	2556	+	Tyr Trp
Pithovirus[b]	Pithovirus sibericum	Ovoid	1500 × 500 Ø	610	36	467	–	
Mollivirus[c]	Mollivirus sibericum	Ovoid	~600 Ø	651	60	523	+	
*Mimiviridae group C[d]	Megavirus chilensis	Icosahedral	610 Ø (440 Ø)	1259	25	1123	–	Tyr Cys Arg Met Asn Trp Ile
*Mimiviridae group B[e]	Moumouvirus	Icosahedral	600 Ø (420 Ø)	1021	25	915	–	Tyr Cys Arg Asn Ile
*Mimiviridae group A[f]	Mimivirus	Icosahedral	630 Ø (390 Ø)	1182	28	1018	–	Tyr Cys Arg Met
*CroV[g]	CroV	Icosahedral	300 Ø	730 kb	23	544	–	IleRS
*PgV[h]	PgV	Icosahedral		460 kb	32	442	–	
Coccolithoviruses	EhV 86[i]	Icosahedral	180 Ø	407 kb	40	478	+	
Marseilleviridae[j]	Marseillevirus	Icosahedral	220 Ø	368 kb	45	457	–	
Poxviridae	Canarypox[k] virus	Ovoid enveloped	330 × 280 × 200 nm	365 kb	30	328	–	
Chloroviruses	PBCV-NY2A[l]	Icosahedral	200 Ø	370 kb	41	416	+	

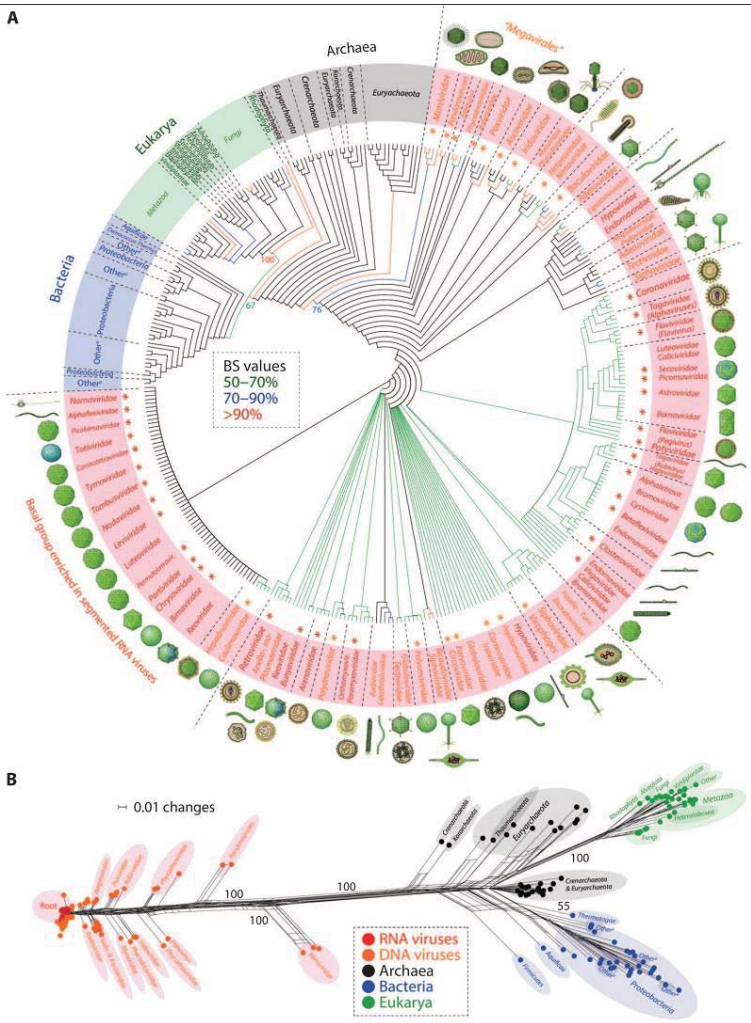
Abergel et al, FEMS Microbiology Reviews, 2015, V39, No6

Phylogenetic reconstruction of nucleocytoplasmic large DNA virus



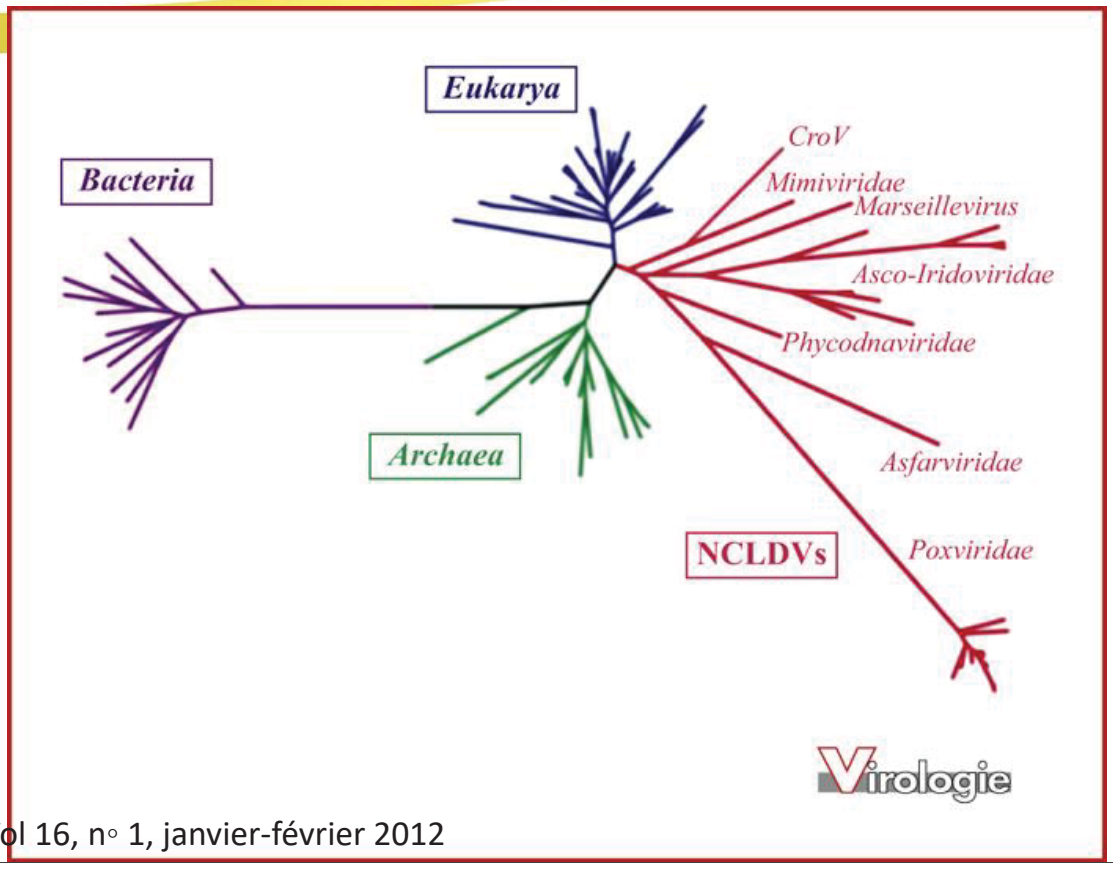
www.pnas.org/cgi/doi/10.1073/pnas.1007615107

Evolutionary relationships between viruses and cells based on proteomes tree.



Nasir and Caetano-Anollés Sci. Adv. 2015;1:e1500527

Are giant viruses a fourth domain of life?



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