

Ch10 Classification and Nomenclature of Viruses



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Authority: International Committee on Taxonomy of Viruses

<http://www.ncbi.nlm.nih.gov/ICTVdb/index.htm>

At a glance

Taxonomic groups: Order

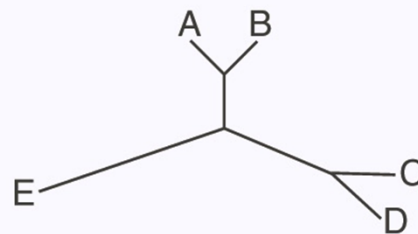
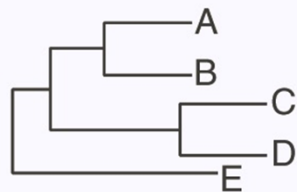
Family

Subfamily

Genus

Species

Phylogenetic trees - based on genome sequences
 - indicate relationships between viruses:



Baltimore Classification: - seven classes of viruses
 - based on genome type and transcription.

10.1 History of virus classification and nomenclature

- Some of characteristics can be used for the purposes of classification:
 - ✓ whether the nucleic acid is DNA or RNA
 - ✓ whether the nucleic acid is single stranded or double stranded
 - ✓ whether or not the genome is segmented
 - ✓ the size of the virion
 - ✓ whether the capsid has helical symmetry or icosahedral symmetry
 - ✓ whether the virion is naked or enveloped

10.1.1 International Committee on Taxonomy of Viruses (ICTV) 國際病毒分類委員會

- By 1966 it was decided that some order had to be brought to the business of naming viruses and classifying them into groups, and the International Committee on Taxonomy of Viruses (ICTV) was formed.
- The ICTV lays down the rules for the nomenclature and classification of viruses, and it considers proposals for new taxonomic groups and virus names.
- <http://ictvonline.org/index.asp>

Virus Taxonomy

North 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 · Elliot J. Lefkowitz

Springer

Virus Taxonomy

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.



The official ICTV 2011 taxonomy is now available.
Select the taxonomy menu above or click [here](#).

Year/Report	Orders	Families	Subfamilies	Genera	Species
2005 (8 th Report)	3	73	11	289	1898
2008	5	82	11	307	2078
2009 (9 th Report)	6	87	19	349	2285
2011	6	94	22	395	2480

10.2 Modern virus classification and nomenclature

- Some virus families have been grouped into orders, but higher taxonomic groupings, such as class and phylum, are not used.
- Only some virus families are divided into subfamilies.
- Each order, family, subfamily and genus is defined by viral characteristics that are necessary for membership of that group, whereas members of a species have characteristics in common but no one characteristic is essential for membership of the species.

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- Many species contain variants known as virus strains, serotypes (differences are detected by differences in antigens) or genotypes (differences are detected by differences in genome sequence).
 - Many of the early names of virus groups were used to form the names of families and genera. Ex: the picornaviruses became the family *Picornaviridae*.
 - Each taxonomic group has its own suffix and the formal names are printed in italic with the first letter in upper case, ex: the genus *Morbillivirus*.
 - When common names are used, they are not in italic and the first letter is in lower case. Ex: the morbilliviruses.

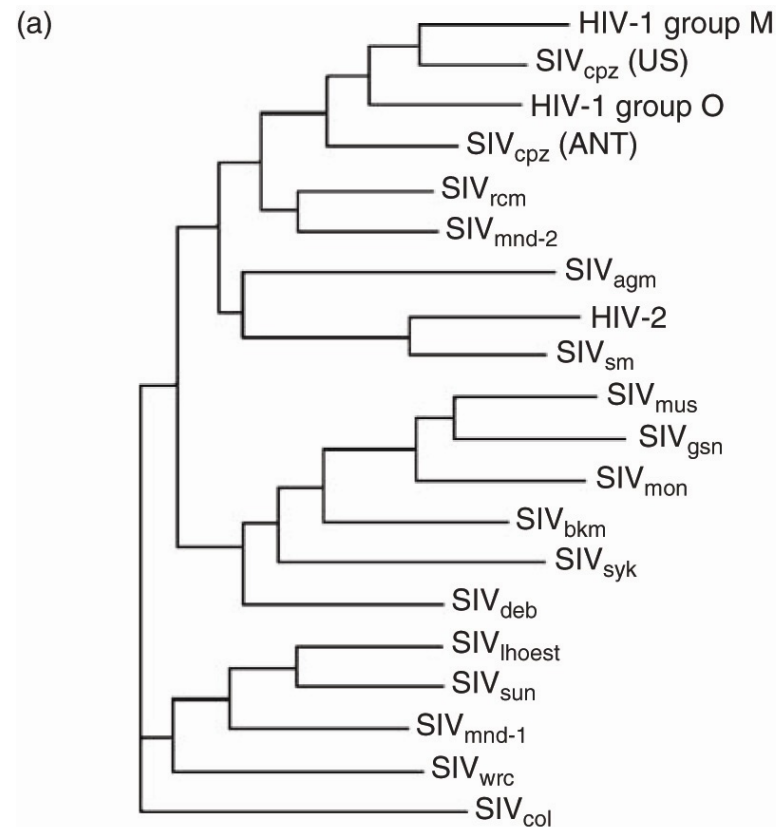
Table 10.1 Taxonomic groups of viruses

Taxonomic group	Suffix	Example 1	Example 2	Example 3
Order	<i>-virales</i>	<i>Caudovirales</i>	<i>Mononegavirales</i>	<i>Nidovirales</i>
Family	<i>-viridae</i>	<i>Myoviridae</i>	<i>Paramyxoviridae</i>	<i>Coronaviridae</i>
Subfamily	<i>-virinae</i>	–	<i>Paramyxovirinae</i>	–
Genus	<i>-virus</i>	<i>T4-like viruses</i>	<i>Morbillivirus</i>	<i>Coronavirus</i>
Species	–	<i>Enterobacteria phage T4</i>	<i>Measles virus</i>	<i>Severe acute respiratory syndrome virus</i>

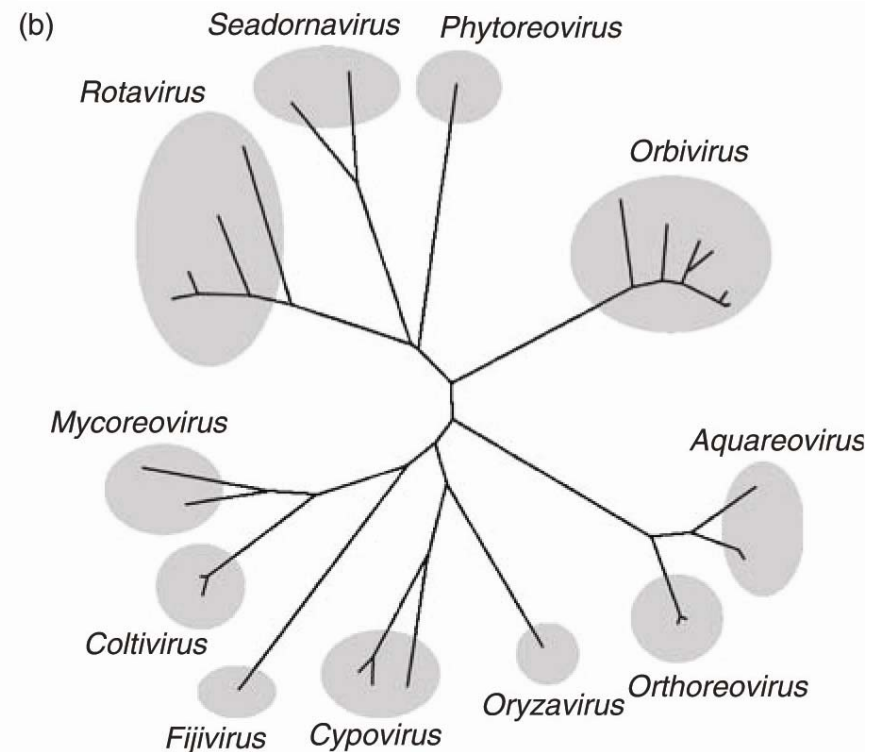
10.2.1 Classification based on genome sequences

- The modern approach to virus classification is based on comparisons of genome sequences and organizations.
- The degree of similarity between virus genomes can be assessed using computer programs, and can be represented in diagrams known as phylogenetic trees because they show the likely phylogeny (evolutionary development) of the viruses.

➤ Phylogenetic trees may be of various types:



Rooted – the tree begins at a root which is assumed to be the ancestor of the viruses in the tree. Ex: human immunodeficiency viruses (HIVs) and simian immunodeficiency viruses (SIVs) based on the RT-IN region of the *pol* gene.



Unrooted – no assumption is made about the ancestor of the viruses in the tree. Ex: the VP1 proteins of viruses in the family *Reoviridae*.

10.2.2 Nomenclature of viruses and taxonomic groups

- Viruses of humans and other vertebrates were commonly named after the diseases that they cause, ex: measles virus, smallpox virus, foot and mouth disease virus, though some were named after the city, town or river where the disease was first reported, ex: Newcastle disease virus, Norwalk virus, Ebola virus.
- Some of these original names have been adopted as the formal names of the viruses.

Table 10.2 Names of virus families and genera derived from place names

Place name	Family/genus name
Bunyamwera (Uganda)	Family <i>Bunyaviridae</i>
Ebola (river in Zaire)	Genus <i>Ebolavirus</i>
Hantaan (river in South Korea)	Genus <i>Hantavirus</i>
Hendra (Australia) and Nipah (Malaysia)	Genus <i>Henipavirus</i>
Norwalk (United States)	Genus <i>Norovirus</i>

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- Many insect viruses were named after the insect, with an indication of the effect of infection on the host.
 - ✓ Ex: a virus was isolated from *Tipula paludosa* (歐洲大蚊) larvae that were iridescent as a result of the large quantities of virions in their tissues → *Tipula* iridescent virus
 - ✓ Ex: a virus was isolated from *Autographa californica* (加州苜蓿夜蛾) larvae that had large polyhedral structures in the nuclei of infected cells → *Autographa californica* nuclear polyhedrosis virus

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- Most plant viruses were given names with two components: the host and signs of disease.
 - ✓ Ex: potato yellow dwarf virus, tobacco rattle virus
 - Some of these names have been used as the bases for family and genus names.

Table 10.3 Names of families and genera of plant viruses based on the host and signs of disease

Host and disease signs	Family/genus name
Brome mosaic	Family <i>Bromoviridae</i>
Cauliflower mosaic	Family <i>Caulimoviridae</i>
Cowpea mosaic	Family <i>Comoviridae</i>
Tobacco mosaic	Genus <i>Tobamovirus</i>
Tobacco rattle	Genus <i>Tobravirus</i>
Tomato bushy stunt	Family <i>Tombusviridae</i>

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- Many names of virus taxonomic groups are based on Latin words, while some have Greek origins.
 - We can note that both Latin and Greek translations have been used to name the viruses.
 - ✓ Ex: Latin and Greek translations of “thread” have been used to name the filoviruses and the closteroviruses, respectively.

Table 10.4 Names of virus families and genera based on Latin and Greek words

		Translation	Reason for name	Family/genus name
Latin	<i>Arena</i>	Sand	Ribosomes in virions resemble sand grains in thin section	Family <i>Arenaviridae</i>
	<i>Baculum</i>	Stick	Capsid shape	Family <i>Baculoviridae</i>
	<i>Filum</i>	Thread	Virion shape	Family <i>Filoviridae</i>
	<i>Flavus</i>	Yellow	Yellow fever virus	Family <i>Flaviviridae</i>
	<i>Luteus</i>	Yellow	Barley yellow dwarf virus	Family <i>Luteoviridae</i>
	<i>Parvus</i>	Small	Virion size	Family <i>Parvoviridae</i>
	<i>Tenuis</i>	Thin, fine	Virion shape	Genus <i>Tenuivirus</i>
	<i>Toga</i>	Cloak	Virion is enveloped	Family <i>Togaviridae</i>
Greek	<i>Kloster</i>	Thread	Virion shape	Family <i>Closteroviridae</i>
	<i>Kystis</i>	Bladder, sack	Virion is enveloped	Family <i>Cystoviridae</i>
	<i>Mikros</i>	Small	Virion size	Family <i>Microviridae</i>
	<i>Pous</i>	Foot	Phages with short tails	Family <i>Podoviridae</i>

10.3 Baltimore classification of viruses

- This approach to virus classification was first suggested by David Baltimore, after whom the scheme is named.
- An advantage of the Baltimore classification is its differentiation between plus-strand RNA viruses that do (class VI) and do not (class IV) carry out reverse transcription, and between dsDNA viruses that do (class VII) and do not (class I) carry out reverse transcription. Ref to Ch7.