Classification of Viruses

Viruses are not usually classified into conventional taxonomic groups but are usually grouped according to such properties as size, the type of nucleic acid they contain, the structure of the capsid and the number of protein subunits in it, host species, and immunological characteristics. It also means that when a new species of known virus family or genus is investigated it can be done in the context of the information that is available for other members of that group.

Without a classification scheme, each newly discovered virus would be like a black box, everything would have to be discovered and rediscovered. The development of a classification scheme is therefore an important and inevitable consequence. The current classification scheme allows most newly described viruses to be labeled. In the best cases much can be assumed about the biology of the virus. Even in the worst case a framework for investigation would be suggested. Because there are so few virus discoveries now being made which do not fit into the existing classification scheme, we can state with a degree of confidence that most of the major groupings of viruses infecting humans and domesticated animals have been identified.

How are viruses classified?

Two classification systems exist: The Hierarchical virus classification system and the Baltimore Classification System.

The Hierarchical virus classification system

In 1962 Lwoff, R. W. Horne, and P. Tournier advanced a comprehensive scheme for the classification of all viruses consisting of phylum - class - order - family - subfamily - genus - species - strain/type. The subsequently formed international committee on the nomenclature of viruses accepted many principles of this system. The most important principle embodied in this system was that viruses should be grouped according to their shared properties rather than the properties of the cells or organisms they infect. Four main characteristics are used:

1. Nature of the nucleic acid: RNA or DNA
2. Symmetry of the capsid: Icosahedral, Helical or Complex symmetry
3. Presence or absence of an envelope: Enveloped virus or Non-enveloped (naked) virus
4. Dimensions of the virion and capsid

At the moment classification is really only important from the level of families down. Members within a virus family are ordered with Genomics, the elucidation of evolutionary relationships by analyses of nucleic acid and protein sequence similarities. All Families have the suffix -viridae e.g. Caliciviridae, Picornaviridae, Reoviridae. Genera have the suffix -virus. Within the Picornaviridae there are 5 genera: enterovirus, cardiovirus, rhinovirus, apthovirus and hepatovirus.

The definition of `species' is the most important but difficult assignment to make with viruses. There is an element of subjectivity about it.

Nucleic Acid	Capsid Symmetry	Presence/ Absence of Envelope	Physical State of Nucleic Acid	Positive/ Negative Stranded	Family	Specific Pathogenic Viruses (or Disease Caused)
RNA	ICOSAHEDRAL	Naked	SS Non-segmented	+	Picorna Viridae	Polio virus Coxsackie A & B virus Hepatitis A virus Rhinovirus New enteroviruses
			SS Non-segmented	+	Calici Viridae	Norwalk virus Hepatitis E virus *
			DS Segmented (11)	DS	Reo Viridae	Rota virus (diarrhea in children)
		Enveloped	SS Non-segmented	+	Toga virus	Mosquito borne encephalitis
			SS Non-segmented	+	Flavi viridae	Yellow fever virus Dengue fever St. Louis encephalitis Japanese encephalitis Hepatitis E virus*
	HELICAL	Enveloped	SS Non-segmented	+	Corona viridae	Respiratory illness (cold)
			SS Segmented (3)	-	Bunya viridae	California encephalitis virus Rift valley fever virus Sandfly fever virus Hantavirus
			SS Segmented (8)	-	Orthomyxo viridae	Influenza virus (types A, B & C)
			SS Non-segmented	-	Paramyxo viridae	Para-influenza virus Respiratory syncytial virus Mumps virus Measles virus
			SS Non-segmented	-	Rhabdo viridae	Rabies virus
			SS Non-segmented	-	Filo viridae	Ebola virus (hemorrhagic fever) Marburg virus (hemorrhagic fev
			SS Segmented (2)	-	Arena viridae	Lymphocytic choriomeningitis vi Lassa virus
	COMPLEX	Complex Coat	SS Diploid (2 identical copies of + stranded RNA)	+ Reverse transcribe d to DNA	RETRO viridae (reverse transcriptase enzyme)	Human Immunodeficiency virus (HIV types I & II) Human T-Leukocyte Virus (HTLV types I & II)
DNA	ICOSAHEDRAL	Naked	SS linear		Parvo viridae	Erythema infectiosum Transient aplastic anemia crisis
			DS circular		Papova viridae	Human papilloma virus (cervical cancer) BK polyomavirus JC polyomavirus
			DS linear		Adeno viridae	Childhood respiratory virus (cold Epidemic keratoconjuctivitis
		Enveloped	DS linear		Herpes viridae	Herpes simplex virus (I & II) Varicella-zoster virus Cytomegalovirus Epstein-Barr virus Human herpesvirus 6 (Roseola)
			DS circular		Hepadna viridae	Hepatitis B virus
	COMPLEX	Complex	DS linear		Pox viridae	Small pox Vaccinia

The Baltimore Classification

The Baltimore system of virus classification provides a useful guide with regard to the various mechanisms of ***viral genome replication***. The central theme here is that all viruses must generate positive strand mRNAs from their genomes, in order to produce proteins and replicate themselves. The precise mechanisms whereby this is achieved differ for each virus family. These various types of virus genomes can be broken down into seven fundamentally different groups, which obviously require different basic strategies for their replication. David Baltimore, who originated the scheme, has given his name to the so-called "Baltimore Classification" of virus genomes. By convention the top strand of coding DNA written in the 5' - 3' direction is + sense. mRNA sequence is also + sense. The replication strategy of the virus depends on the nature of its genome. Viruses can be classified into seven (arbitrary) groups:

I. Double-stranded DNA (Adenoviruses; Herpesviruses; Poxviruses, Papovaviruses, etc.).
Some replicate in the nucleus e.g. adenoviruses using cellular proteins. Poxviruses replicate in the cytoplasm and make their own enzymes for nucleic acid replication.

II. Single-stranded (+)sense DNA (Parvoviruses e.g. the Rotavirus)
Replication occurs in the nucleus, involving the formation of a (-) sense strand, which serves as a template for (+) strand RNA and DNA synthesis.

III. Double-stranded RNA (Reoviruses; Birnaviruses)
These viruses have segmented genomes. Each genome segment is transcribed separately to produce monocistronic mRNAs.

IV. Single-stranded (+) sense RNA (Picornaviruses; Togaviruses, etc.)
a) Polycistronic mRNA e.g. Picornaviruses; Hepatitis A. Genome RNA = mRNA. Means naked RNA is infectious, no virion particle associated polymerase. Translation results in the formation of a polyprotein product, which is subsequently cleaved to form the mature proteins.
b) Complex Transcription e.g. Togaviruses. Two or more rounds of translation are necessary to produce the genomic RNA.

V. Single-stranded (-)sense RNA (Orthomyxoviruses, Rhabdoviruses, etc.)
Must have a virion particle RNA directed RNA polymerase.
a) Segmented e.g. Orthomyxoviruses. First step in replication is transcription of the (-) sense RNA genome by the virion RNA-dependent RNA polymerase to produce monocistronic mRNAs, which also serve as the template for genome replication.
b) Non-segmented e.g. Rhabdoviruses. Replication occurs as above and monocistronic mRNAs are produced.

VI. Single-stranded (+)sense RNA with DNA intermediate in life-cycle (Retroviruses)
Genome is (+) sense but unique among viruses in that it is DIPLOID, and does not serve as mRNA, but as a template for reverse transcription.

VII. Double-stranded DNA with RNA intermediate (Hepadnaviruses)
This group of viruses also relies on reverse transcription, but unlike the Retroviruses, this occurs inside the virus particle on maturation. On infection of a new cell, the first event to occur is repair of the gapped genome, followed by transcription.