

The 7th ICTV Report

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Introduction

After an unexpected and much regretted delay, the seventh Report of the International Committee on Taxonomy of Viruses (ICTV) [8] has been published. The Report is the culmination of the efforts of the many virologists who have contributed to the diverse committees and Study Groups that constitute the ICTV. Some 476 virologists from many countries have been involved in various capacities during the interval following the publication of the previous Report [5]. The size, scope and content of the 7th Report are reflections of the enormous increase in virological knowledge during the last 5 years; the Report runs to 1162 pages that describe 3 Orders, 63 Families, 240 Genera. These compare with the taxonomy described in the previous Report that comprised 1 Order, 50 Families and 164 Genera. An important development since the 6th Report was published, has been a focus on the demarcation of species within the genera [6]. Previously, many viruses were listed but it was not clear which belonged to distinct species and which were strains or other sub-specific entities within a particular species. The current taxonomy [8] lists more than 3600 viruses among 1550 species.

New features in the 7th Report

New families and genera

Fourteen new families are described in the 7th Report (Table 1). Some (e.g. *Ascoviridae*) contain new genera and others contain genera that were previously listed as “unassigned” or “floating” [5]. One family (*Papovaviridae*) described in the 6th Report has been divided into the new families *Polyomaviridae* and *Papillomaviridae* because of the profound differences between viruses in what were two genera in a single family.

The new families contain genera of viruses that have genomes of 4 of the 6 major types. Also, the classification has been extended to include viroids. These have been classified into 7 genera that are distributed among 2 families.

Other new genera have been classified into families that were already described in the 6th Report (Table 2). Some of these genera were formed by taking species out of their previous genus in recognition of its having become too diverse to be classified as one genus, some new genera were needed to classify novel virus species. Some of the genera listed in

Table 1. New families in the 7th report

Genome type	New Family	Genera	Host type
DsDNA	<i>Rudiviridae</i>	<i>Rudivirus</i>	Archaea
	<i>Ascoviridae</i>	<i>Ascovirus</i>	Invertebrates
	<i>Asfarviridae</i>	<i>Asfivirus</i>	Vertebrates
	<i>Polyomaviridae</i> ^a	<i>Polyomavirus</i>	Vertebrates
	<i>Papillomaviridae</i> ^a	<i>Papillomavirus</i>	Vertebrates
Reverse transcribing	<i>Caulimoviridae</i>	<i>Caulimovirus</i>	Plants
		PVCV-like viruses	Plants
		SCMoV-like viruses	Plants
		CVMV-like viruses	Plants
		<i>Badnavirus</i>	Plants
	<i>Pseudoviridae</i>	RTBV-like viruses	Plants
		<i>Pseudovirus</i>	Fungi/Plants
	<i>Metaviridae</i>	<i>Hemivirus</i>	Invertebrates/Fungi
		<i>Metavirus</i>	Fungi/Plants/Invertebrates
		<i>Errantivirus</i>	Invertebrates
(-) sense RNA	<i>Bornaviridae</i>	<i>Bornavirus</i>	Vertebrates
(+) sense RNA	<i>Narnaviridae</i>	<i>Narnavirus</i>	Fungi
		<i>Mitovirus</i>	Fungi
	<i>Luteoviridae</i>	<i>Luteovirus</i>	Plants
		<i>Polerovirus</i>	Plants
		<i>Enamovirus</i>	Plants
	<i>Closteroviridae</i>	<i>Closterovirus</i>	Plants
		<i>Crinivirus</i>	Plants
Viroids	<i>Pospiviroidae</i>	<i>Pospiviroid</i>	Plants
		<i>Hostuviroid</i>	Plants
		<i>Cocadviroid</i>	Plants
		<i>Apscaviroid</i>	Plants
		<i>Coleviroid</i>	Plants
	<i>Avsunviroidae</i>	<i>Avsunviroid</i>	Plants
		<i>Pelamoviroid</i>	Plants

^a Previously classified together as family *Papovaviridae*

Table 2 were already described in the 6th Report, but since then, because of new information, they have been added to previously extant families (e.g. *Tombusviridae*).

Thirteen of the new genera are currently not assigned to families, normally because it is not clear how the genera should be clustered, nor where discrete boundaries should be drawn between them. These are listed in Table 3.

New orders

Orders have only been used sparingly in virus taxonomy. Previous to the 7th Report, only the Order *Mononegavirales* had been recognised [5]. This Order brought together the families *Paramyxoviridae*, *Filoviridae* and *Rhabdoviridae*. The new Orders that have been created since then are the *Caudovirales* and the *Nidovirales*. Order *Caudovirales* contains dsDNA

Table 2. New genera in previously recognised families

Genome type	Extant family	Genus structure
dsDNA	<i>Myoviridae</i>	“T4-like viruses”
		“P1-like viruses” ^a
		“P2-like viruses” ^a
		“Mu-like viruses” ^a
	<i>Siphoviridae</i>	“SPO1-like viruses” ^a
		“φH-like viruses” ^a
		“λ-like viruses”
		“T1-like viruses” ^a
		“T5-like viruses” ^a
		“L5-like viruses” ^a
	<i>Podoviridae</i>	“c2-like viruses” ^a
		“ψM1-like viruses” ^a
		“T7-like viruses”
	<i>Phycodnaviridae</i>	“P22-like viruses” ^a
“φ29-like viruses” ^a		
<i>Chlorovirus</i> ^a <i>Prasinovirus</i> ^a <i>Prymnovirus</i> ^a		
(-) RNA	<i>Filoviridae</i>	“Marburg-like viruses” ^a
		“Ebola-like viruses” ^a
	<i>Paramyxoviridae</i>	<i>Respirovirus</i>
		<i>Rubulavirus</i>
		<i>Morbillivirus</i>
		<i>Pneumovirus</i>
		<i>Metapneumovirus</i> ^a
	<i>Rhabdoviridae</i>	<i>Vesiculovirus</i>
		<i>Lyssavirus</i>
		<i>Ephemerovirus</i>
		<i>Novirhabdovirus</i> ^a
		<i>Cytorhabdovirus</i> ^a
	<i>Orthomyxoviridae</i>	<i>Nucleorhabdovirus</i>
		<i>Influenzavirus A</i> ^a
<i>Influenzavirus B</i> ^a		
<i>Influenzavirus C</i> <i>Thogotovirus</i>		
(+) RNA	<i>Picornaviridae</i>	<i>Enterovirus</i>
		<i>Rhinovirus</i>
		<i>Cardiovirus</i>
		<i>Aphthovirus</i>
		<i>Hepatovirus</i>
		<i>Parechovirus</i> ^a
	<i>Potyviridae</i>	<i>Potyvirus</i>
		<i>Ipomovirus</i> ^a
		<i>Macluravirus</i> ^a
		<i>Rymovirus</i>
		<i>Tritimovirus</i> ^a
	<i>Nodaviridae</i>	<i>Bymovirus</i>
		<i>Alphanodavirus</i> ^a <i>Betanodavirus</i> ^a
	<i>Caliciviridae</i>	<i>Lagovirus</i> ^a

Continued

Table 2 (continued)

Genome type	Extant family	Genus structure
		“Norwalk-like viruses” ^a “Sapporo-like viruses” ^a Vesivirus ^a Aureusvirus ^a Avenavirus ^a Carmovirus Dianthovirus ^a Machlomovirus ^a Necrovirus ^a Panicovirus ^a Tombusvirus
	<i>Tombusviridae</i>	
		Alfamovirus Bromovirus Cucumovirus Ilarvirus Oleavirus ^a
	<i>Bromoviridae</i>	

^a Genera new in the 7th Report

viruses belonging to the families of “tailed phages”: *Myoviridae*, *Siphoviridae*, and *Podoviridae*. Order *Nidovirales* contains families *Coronaviridae* and *Arteriviridae* that contain positive strand RNA viruses that share a “nested set” expression strategy.

Unassigned taxa

As in the 6th Report, there is a category of taxa (usually species) that cannot be fully classified on the basis of the current state of knowledge. Some of these species are classified in genera that are not classified in a family-level taxon. This is relatively common among viruses of plants (see Table 3), although these unassigned taxa include viruses that infect all the major host types. Also, there are some species that are classified in families but for which it is not clear to which existing genus, if any, they should be assigned. These species are “Unassigned within the family”; an example is the species *Carrot red leaf virus*, which is classified as unassigned in family *Luteoviridae*. The “unassigned” category can also apply where it is unclear how a genus should fit into the subfamily structure within a family. An example is the genus “Ictalurid herpes-like viruses” in the family *Herpesviridae*.

As in the 6th Report, there are in the 7th Report brief descriptions of viruses that cannot yet be classified into species and genera because insufficient is known about them. These are listed as “Unassigned viruses” and form a target list of unclassified viruses for consideration by the ICTV Study Groups who started work in 2000.

Orthographic conventions

Another innovation in the 7th report over what has appeared before has come from revisions made to what is now known as the International Code of Virus Classification and Nomenclature [4, 8]. In previous Reports, and according to previous Rules, names of higher taxa have

Table 3. New unassigned genera

Genome	Genus	Type species	Host
ds DNA	“Sulfolobus SNDV-like viruses”	<i>Sulfolobus SNDV virus</i>	Archaea
ss DNA	<i>Nanovirus</i>	<i>Subterranean clover stunt virus</i>	Plants
ds RNA	<i>Varicosavirus</i>	<i>Lettuce big-vein virus</i>	Plants
(-) RNA	<i>Ophiovirus</i>	<i>Citrus psorosis virus</i>	Plants
(+) RNA	“Cricket paralysis-like viruses”	<i>Cricket paralysis virus</i>	Invertebrates
	“Hepatitis E-like viruses”	<i>Hepatitis E virus</i>	Vertebrates
	<i>Pomovirus</i>	<i>Potato mop-top virus</i>	Plants
	<i>Pecluvirus</i>	<i>Peanut clump virus</i>	Plants
	<i>Benyvirus</i>	<i>Beet necrotic yellow vein virus</i>	Plants
	<i>Ourmiavirus</i>	<i>Ourmia melon virus</i>	Plants
	<i>Vitivirus</i>	<i>Grapevine virus A</i>	Plants
	<i>Allexivirus</i>	<i>Shallot virus X</i>	Plants
	<i>Foveavirus</i>	<i>Apple stem pitting virus</i>	Plants

been written in italic script and with a capital initial letter. The revised Code extends this convention to the names of species as these are recognised taxa, just as are genera and families. The effect is to discriminate between species and viruses that are strains or other subspecific entities within a species. This development has met with some criticism [1, 2] and corresponding rebuttals [7, 9]. Nonetheless, the conventions are what has been approved by the ICTV and are used in the 7th Report and an increasing number of virological publications.

The future

In biology, no taxonomy is perfect as it is always an attempt to impose a discontinuous structure onto a naturally dynamic and often continuously varying natural world. The accumulation of more information will sometimes necessitate changes to existing taxa or the creation of novel taxa, in virology as in other biological disciplines. Within the ICTV structure, it is the responsibility of Study Groups to be aware of new information and to propose new structures that are implied by the new data. Even simply the recognition that a collection of virus isolates constitutes a species will require a taxonomic proposal to be made. And it is open to any virologist to make proposals concerning virus classification. The relevant Study Group would be the first point of reference for any such proposal, either directly or via the Executive Committee. The names of scientists in these committees are listed in Mayo and Fauquet [3].

ICTV will now examine the 7th Report for inaccuracies, infelicities or simply newly out-of-date information. Corrections for these will be made in the form of taxonomic proposals and will be routed *via* the appropriate subcommittee.

An important task for ICTV will be to look at the homogeneity of the criteria used in species demarcation. During the preparation of the 7th Report, each Study Group was asked to list these criteria. But often it was not possible for different Study Groups to know what other groups had produced. Although overall, there is reasonably good homogeneity among genera, in some families it looks as if virus species have been distinguished that in other families would constitute strains or isolates of one species. However, it is not simple to

harmonize species demarcation. For example, more attention is paid to discriminating among viruses that infect humans than among viruses that infect bacteria. And unevenness among the depths of knowledge of different virus types adds to the difficulties.

Another task for ICTV is to complete the list of “international names” for genera. In the 7th Report there are 28 genera that have names that include the phrase “virus-like”. Although there are fewer of these than in the 6th Report, removing such names so as to comply with the spirit of Rule 3.17 of the International Code [4, 8] is a priority.

The “bottom line” is that ICTV depends upon the participation of virologists of all specialisms and backgrounds to produce a virus taxonomy and a Report that are useful to virologists. Continuation and extension of the co-operative spirit that resulted in the 7th Report is essential if ICTV is to continue to serve virology with Reports in the future.

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