ICTV EXECUTIVE COMMITTEE REPORT (2017-2020)

Andrew Davison

President

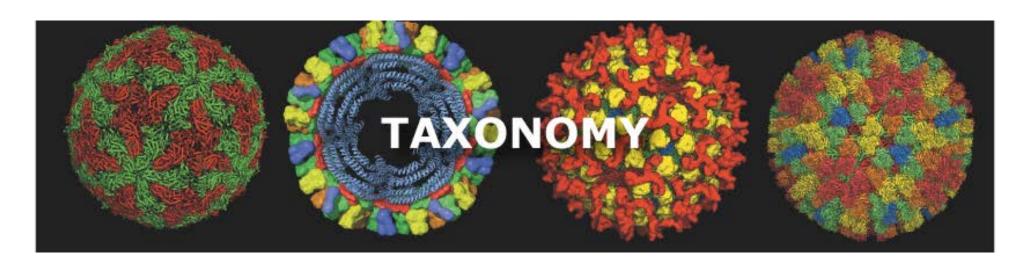


The ICTV

Committee of the Virology Division of the International Union of Microbiological Societies (IUMS)

Responsible for developing taxonomy and names of taxa

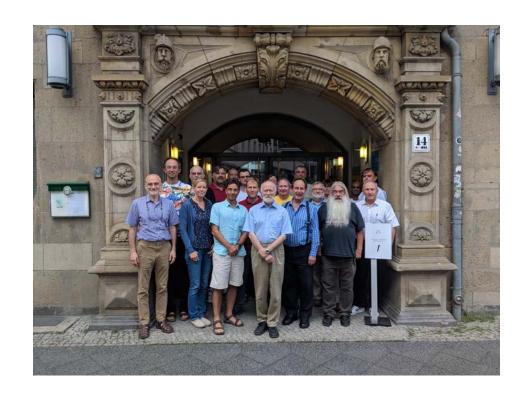
Founded 54 years ago





ICTV

Involves many virologists Any virologist can submit a proposal Study Group provides comments **Executive Committee meets annually** ICTV members vote annually Taxonomy lists updated annually New taxonomy published annually ICTV Report published online











Wellcome grant (2016-2021)



Three staff employed

Freely available online ICTV Report (editor-in-chief Stuart Siddell)

Freely available online citeable summaries published in Journal of General Virology

Freely available online resources

Focused meetings with experts

Improved connections with virologists



ICTY VIRUS TAXONOMY PROFILES

Simmonds et al., Journal of General Virology 2017;98:2-3 DOI 10.1099/jgv.0.000672



@ MICROBIOLOGY

ICTV Virus Taxonomy Profile: Flaviviridae

Peter Simmonds, 1.* Paul Becher, 2 Jens Bukh, 3 Ernest A. Gould, 4 Gregor Meyers, 5 Tom Monath, 6 Scott Muerhoff, 7 Alexander Pietney, 6 Rebecca Rico-Hesse, 9 Donald B. Smith, 10 Jack T. Stapleton 11,12 and ICTV Report Consortium

Abstract

The Flaviviridae is a family of small enveloped viruses with RNA genomes of 9000–13 000 bases. Most infect mammals and birds. Many flaviviruses are host-specific and pathogenic, such as hepatitis C virus in the genus Hepacivirus. The majority of known members in the genus Flavivirus are arthropod borne, and many are important human and veterinary pathogens (e.g. yellow fever virus, dengue virus). This is a summary of the current International Committee on Taxonomy of Viruses (ICTV) report on the taxonomy of the Flaviviridae, which is available at www.ictv.global/report/flaviviridae.

Table 1. Characteristics of the family Flaviviridae

Typical member:	yellow fever virus-D17 (X03700), species Yellow fever virus, genus Flavivirus						
Virion	Enveloped, 40-60 nm vitions with a single core protein (except for genus Pegriérus) and 2 or 3 envelope glycoproteins						
Genome	Approximately 9.0-13 kb of positive-sense, non-segmented RNA						
Replication	Cytoplasmic, in membrane vesicles derived from the endoplasmic reticulum (ER); assembled virions bud into the lumen of the ER and are secreted through the vesicle transport pathway						
Translation	Directly from genomic RNA containing a type I cap (genus Flavivirus) or an internal ribosome entry site (other genera)						
Host range	Mammala (all genera); most members of genus Flavivinus are anthropod borne						
Taxonomy	Currently four genera containing more than 60 species						

VIRION

Virions are typically spherical in shape with a lipid envelope (Table 1, Fig. 1). Virions have a single, small, basic capsid (C) protein and two (genera Flavbrirus, Hepacivirus and Pegivirus) or three (genus Pestivirus) envelope proteins.

GENOME

Virus genomes are positive-stranded, non-segmented RNA of approximately 9.2–11, 12.3–13, 8.9–10.5 and 8.9–11.3 kb for members of the genera Flawirius, Pestivirus, Hepacivirus and Pegivirus, respectively (Fig. 2). They contain a single, long ORF flanked by 5'- and 3'-terminal non-coding regions, which form specific secondary structures required for genome replication and translation. Translational initiation of genomic RNA is cap dependent in the case of members of the genus





Fig. 1. Three-dimensional cryo-electron reconstruction of immuture (left) and mature (right) particles of an isolate of dengue virus (courtesy of Richard Kuhn and Michael Rossmann). Shown is a surface rendering of immature dengue virus at 12.5 Å resolution (left) and mature dengue virus at 11.0 Å resolution (right). The viruses are depicted to scale, but not coloured to scale. Triangles outline one icosahedral unit, with the 2.4 and 5-feld was of renmetery.

Received 1 December 2016: Accepted 1 December 2016

Author affiliations: "Nuffield Expartment of Medicine, University of Dixford, Oxford O

Correspondence: Peter Simmonds, peter.simmonds@ndm.ox.ac.uk Keywords: Flaviviridae; taxonomy; ICTV Report.

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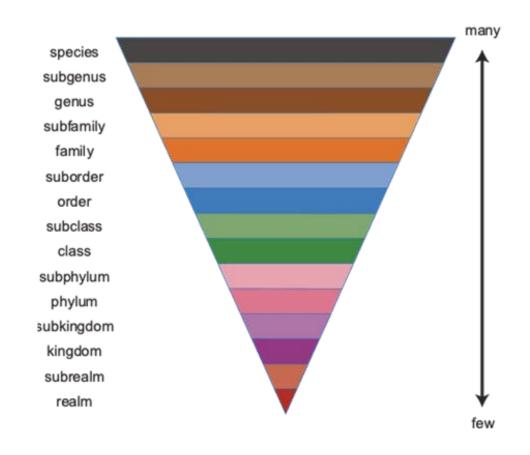


Taxonomic advances

Hundreds of proposals approved

See newsletters at
https://talk.ictvonline.org/information/
newsletters/w/newsletters
Nitus taxonomy finds its roots
ICTV ratifies expansion of the number of taxonomic ranks from 5 to 15

Executive Committee proposes uniform binomial species nomenclature for ICTV ratification



For some time, the classification of viruses by virus taxonomists has been focused on the



Executive Committee (2020-2023)

Changes to Statutes ratified by ICTV

Membership increased from 19 to 23

Online voting by ICTV members

Geographical representation improved

Gender balance greatly improved

Thanks to those leaving the Committee: Andrew Davison, Balázs Harrach, Robert Harrison, Nick Knowles and Max Nibert

Name	Affiliation	Residence
President		
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Anne-Mieke Vandamme	KU Leuven	Belgium



With thanks to all who freely give their time and talents to provide a great resource for virologists

Elliot Lefkowitz

Data Secretary



ICTV DATA SECRETARY ACTIVITIES 2017 - 2020

DATA SECRETARY ACTIVITIES



- Taxonomy Database
 - Database updated with each new taxonomy release
 - New/changed taxonomy
 - Updates to the historical taxonomy database
 - Compilation of the Master Species List
 - Updates to the Virus Metadata Resource (VMR)
- Web Site
 - Taxonomy browser updates
 - Application updates
 - News
 - Information
 - Membership lists
- Online ICTV Report



ICTV WEB SITE

http://ictv.global



Coronavirus disease 2019 (COVID-19)

WHO guidelines for naming of new human diseases can be found at "WHO issues best practices for naming new human infectious diseases" and "WHO Best Practices for the Naming of New Human Infectious Diseases" The

following article may also be of interest:

"Naming diseases: First do no harm'

Severe acute

2003

spiratory syndrome (SARS)

Middle East

2012

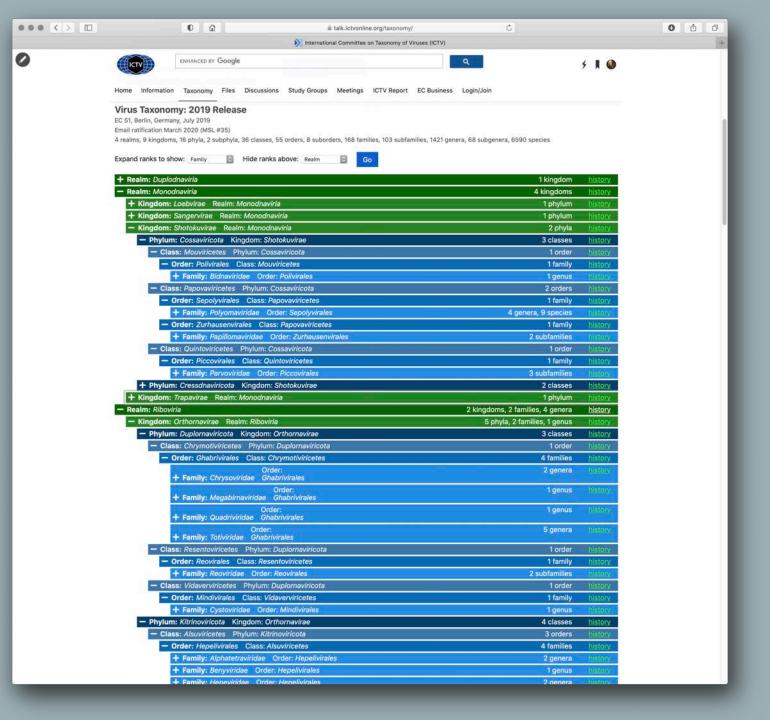
▲ First name → Name origin

spiratory syndrome (MERS)

WHO Disease



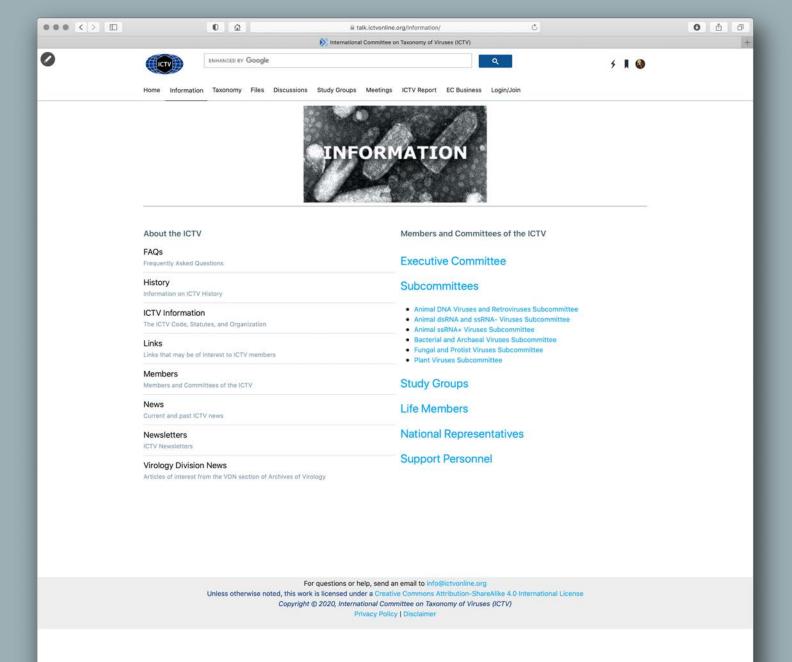
HOME PAGE https://ictv.global/





TAXONOMY BROWSER

https://ictv.global/taxonomy/

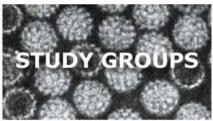




INFORMATION

https://ictv.global/information/





The ICTV maintains a Study Group for each virus family. Study Groups examine the classification and nomenclature of the viruses that are members or potential members of the family, and develop criteria (phenotypic and genotypic characters) that determine which viruses belong to a particular taxon. They also review proposals to create new taxonomy or modify existing taxonomy.

- · List of all Study Groups
- · List of Study Groups by Subcommittee

Study Group Wikis

The Links below provide information from the Study Group that help to describe and classify the viruses belonging to the indicated family.

Flaviviridae Study Group	11	Table 1 - Confirmed
Flaviviridae Study Group wiki	pages	over 1 year ago
Geminiviridae Study Group	2	Begomovirus Isolate
Geminiviridae Study Group wiki	pages	over 3 years ago
Hepeviridae Study Group	2	Proposed Orthohepe
Hepeviridae Study Group wiki	pages	3 months ago
Picornaviridae Study Group	1	Picornaviridae Study
Picornaviridae Study Group wiki	page	over 4 years ago

For questions or help, send an email to info@ictvonline.org

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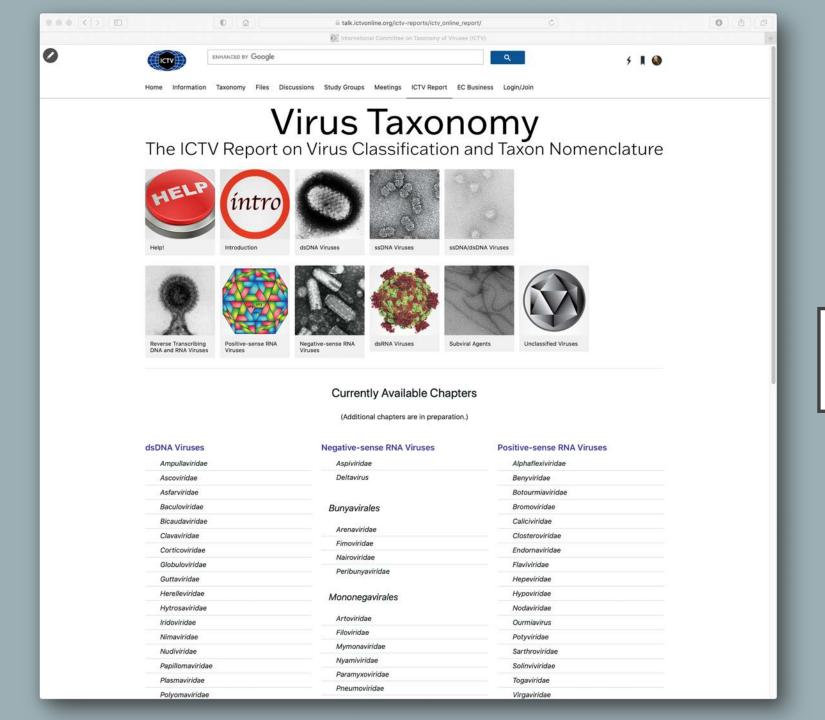
STUDY GROUP PAGES

https://ictv.global/ictv_wikis/



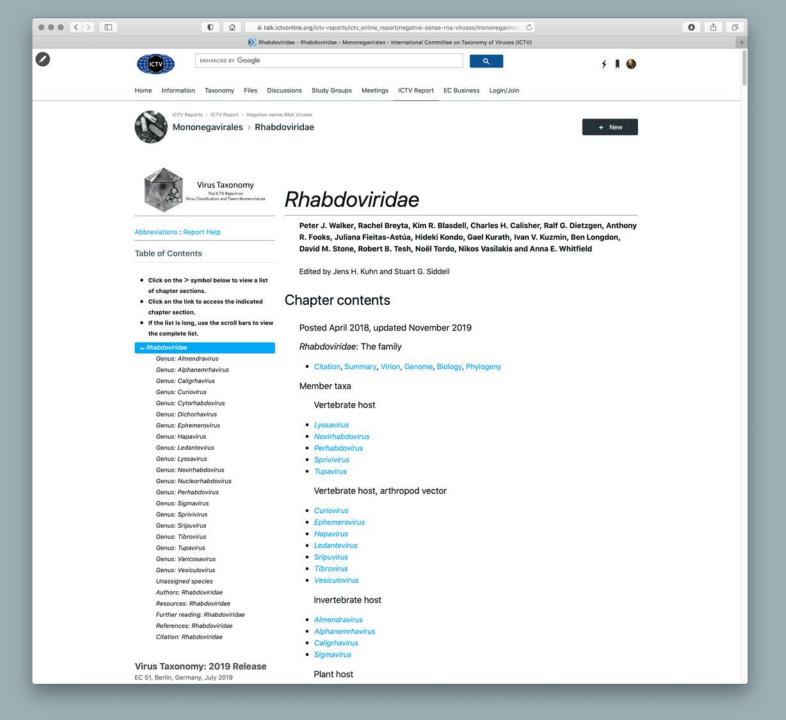
ICTV ONLINE REPORT

https://ictv.global/report



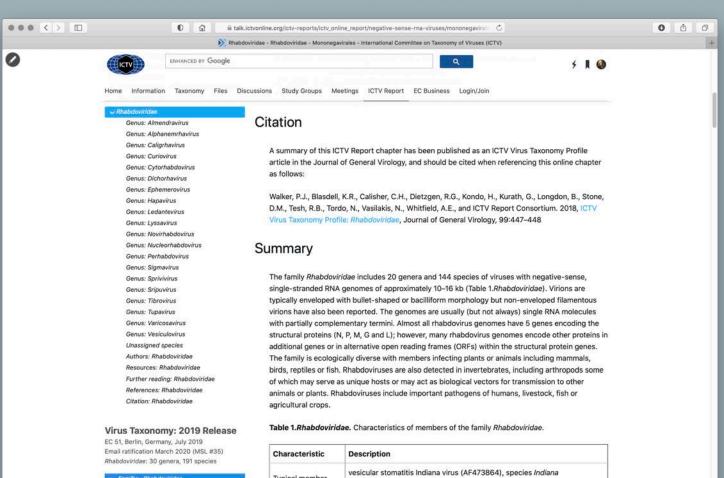


REPORT HOME https://ictv.global/report/





REPORT CHAPTER https://ictv.global/report/ rhabdoviridae/

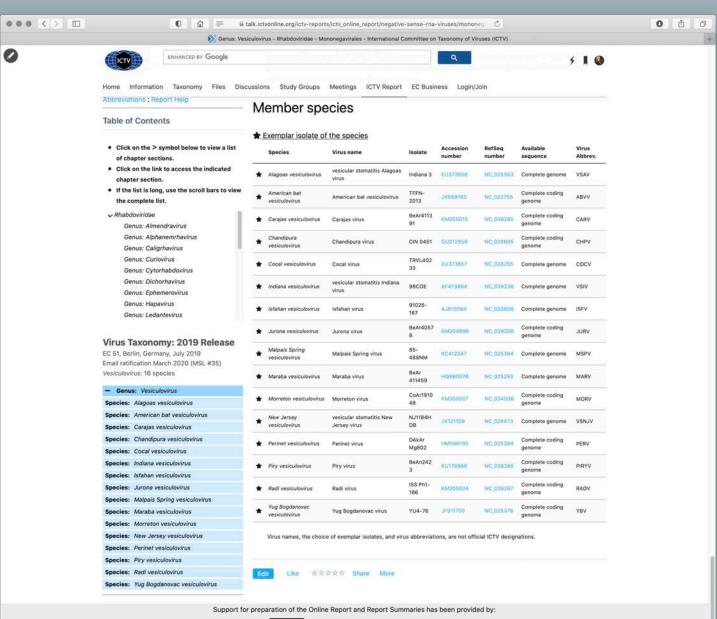


1	Family:	Rhabdoviridae
٠	Genus:	Almendravirus
۲	Genus:	Alphanemrhavirus
۲	Genus:	Alphanucleorhabdovirus
۲	Genus:	Arurhavirus
۲	Genus:	Barhavirus
۲	Genus:	Betanucleorhabdovirus
۲	Genus:	Caligrhavirus
۲	Genus:	Curiovirus
۲	Genus:	Cytorhabdovirus
۲	Genus:	Dichorhavirus
۲	Genus:	Ephemerovirus
۲	Genus:	Gammanucleorhabdovirus
۲	Genus:	Hapavirus
٠	Genus:	Ledantevirus
٠	Genus:	Lostrhavirus
۲	Genus:	Lyssavirus
_	Conunc	Mounthauteun

Characteristic	Description
Typical member	vesicular stomatitis Indiana virus (AF473864), species <i>Indiana</i> vesiculovirus, genus <i>Vesiculovirus</i>
Virion	Bullet-shaped or bacilliform particle 100–430 nm in length and 45–100 nm in diameter comprised of a helical nucleocapsid surrounded by a matrix layer and a lipid envelope. Some rhabdoviruses have non-enveloped filamentous virions.
Genome	Negative-sense, single-stranded RNA of 10.8-16.1 kb (unsegmented or bisegmented).
Replication	Ribonucleoprotein (RNP) complexes containing anti-genomic RNA are generated and serve as templates for synthesis of nascent RNP complexes containing genomic RNA.
Translation	From capped and polyadenylated mRNAs transcribed processively from each gene (3' to 5'), sometimes containing multiple ORFs.
Host Range	Vertebrates, arthropods and plants; many vertebrate and plant rhabdoviruses are arthropod-borne.



TAXON SUMMARY https://ictv.global/report/rhabdoviridae/







For questions or help, send an email to info@ictvonline.org

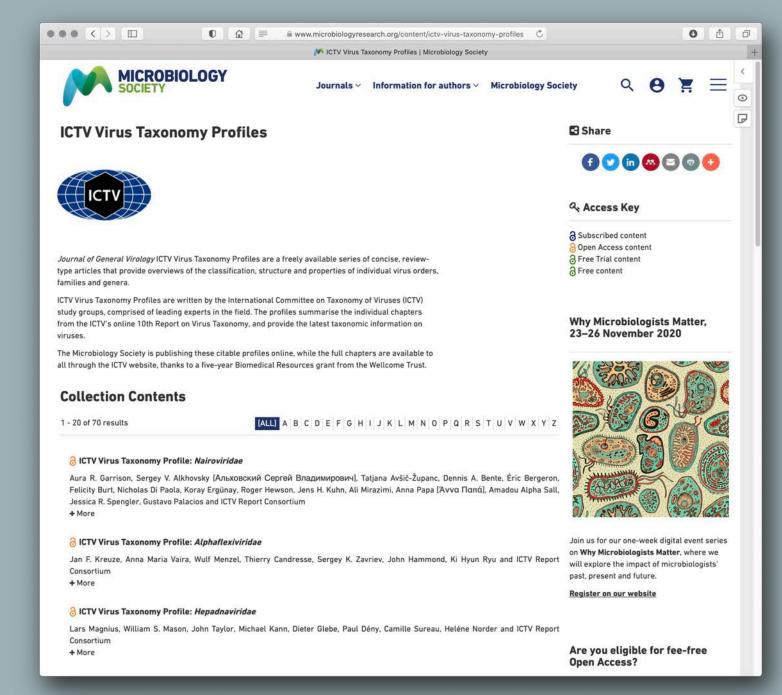
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MEMBER SPECIES TABLE



JOURNAL OF GENERAL VIROLOGY: ICTV VIRUS TAXONOMY PROFILES





JGV TAXONOMY PROFILES

https://www.microbiologyresearch.org/content/ictv-virus-taxonomy-profiles

Walker et al., Journal of General Virology 2018;99:447-448 DOI 10.1099/jgv.0.001020



∂MICROBIOLOGY

ICTV Virus Taxonomy Profile: Rhabdoviridae

Peter J. Walker, 1,* Kim R. Blasdell, 2 Charles H. Calisher, 3 Ralf G. Dietzgen, 4 Hideki Kondo, 5 Gael Kurath, 6 Ben Longdon, David M. Stone, Robert B. Tesh, Noël Tordo, Nikos Vasilakis, Anna E. Whitfield and ICTV Report Consortium

Abstract

The family Rhabdoviridae comprises viruses with negative-sense (-) single-stranded RNA genomes of 10.8-16.1 kb. Virions are typically enveloped with bullet-shaped or bacilliform morphology but can also be non-enveloped filaments. Rhabdoviruses infect plants and animals including mammals, birds, reptiles and fish, as well as arthropods which serve as single hosts or act as biological vectors for transmission to animals or plants. Rhabdoviruses include important pathogens of humans, livestock, fish and agricultural crops. This is a summary of the International Committee on Taxonomy of Viruses (ICTV) Report on the taxonomy of Rhabdoviridae, which is available at www.ictv.global/report/rhabdoviridae.

Table 1. Characteristics of the family Rhabdoviridae

Typical member:	vesicular stomatitis Indiana virus (AF473864), species Indiana vesiculovirus, genus Vesiculovirus
Virion Genome	Bullet-shaped or bacilliform particle 100-430 nm in length and 45-100 nm in diameter comprised of a nucleocapsid surrounded by a matrix layer and a lipid envelope. Some rhabdoviruses have non-enveloped filamentous virions Negative-sense, single-stranded RNA of 10.8-16.1 kb (unsegmented or bi-segmented)
Replication Translation	Ribonucleoprotein (RNP) complexes containing anti-genomic RNA are generated and serve as templates for synthesis of nascent RNP complexes containing genomic RNA Capped and polyadenylated mRNAs transcribed processively from each gene (3' to 5'), sometimes containing multiple ORFs
Host range	Vertebrates, arthropods and plants; many vertebrate and plant rhabdoviruses are arthropod-borne
Taxonomy	18 genera containing >130 species. Many rhabdoviruses remain unclassified

VIRION

Virions are usually enveloped and bullet-shaped or bacilliform (i.e. with two rounded ends) and contain five structural proteins (Table 1, Fig. 1). The nucleocapsid protein (N), the large multi-functional RNA-dependent RNA polymerase (L) and the polymerase-associated phosphoprotein (P) together with the RNA genome form the ribonucleoprotein (RNP) complex. The nucleocapsid is encased in the matrix protein (M) layer which also interacts with the envelope containing the transmembrane glycoprotein (G). Plant rhabdoviruses assigned to the genus Varicosavirus are filamentous and lack an envelope.

GENOME

Rhabdovirus negative sense (-) single-stranded RNA genomes range from 10.8 to 16.1 kb [1]. Almost all rhabdovirus genomes are unsegmented but rhabdoviruses with bi-segmented genomes are also known [2]. Terminal non-coding regions are partially complementary. Genomes usually encode five major structural proteins but may also encode additional (accessory) proteins either in additional genes or as alternative ORFs within the structural protein genes (Fig. 2) [1, 3].

REPLICATION

Rhabdovirus replication generally occurs in the cytoplasm following receptor-mediated endocytosis. Primary

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Author affiliations: 1School of Biological Sciences, University of Queensland, St. Lucia, QLD 4072, Australia; 2CSIRO Health and Biosecurity, Geelong, VIC 3220, Australia; 3Colorado State University, Fort Collins, CO 80523, USA; 4Queensland Alliance for Agriculture and Food Innovation, University of Queensland, St. Lucia, QLD 4072, Australia: Sinstitute of Plant Science and Resources, Okayama University, Kurashiki, 710-0046, Japan; Western Fisheries Research Center, Seattle, WA 98115, USA; Department of Biosciences, University of Exeter, Penryn TR10 9FE, UK; Centre for Environment, Fisheries and Aquaculture Science, Weymouth, DT4 8UB, UK; Department of Pathology and Center for Biodefense and Emerging Infectious Diseases, University of Texas Medical Branch, Galveston, TX 77555, USA; 10 Institut Pasteur de Guinée, Gamal Abdel Nasser University, Conakry, Guinea; 11 Department of Plant Pathology, Kansas State University, Manhattan KS 66506, USA.

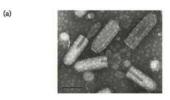
*Correspondence: Peter J. Walker, peter.walker@ug.edu.au

Keywords: Rhabdoviridae: rhabdoviruses: ICTV: Taxonomy.

Abbreviations: N, nucleocapsid protein; L, large polymerase protein; P, phosphoprotein; M, matrix protein; G, glycoprotein; RdRP, RNA-dependent RNA polymerase: RNP, ribonucleoprotein.

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Walker et al., Journal of General Virology 2018;99:447-448



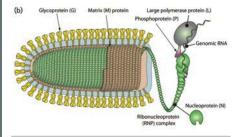


Fig. 1. (a) Negative-contrast electron micrograph of vesicular stomatitis Indiana virus particles. The bar represents 100 nm (courtesy of P. Perrin). (b) Schematic illustration of a rhabdovirus virion and ribonucleocapsid structure. Unravelling of the RNP is illustrative to show its association with L and P (courtesy of P. Le Mercier).

transcription is initiated from the incoming (-)RNP complex by the RNA-dependent RNA polymerase (RdRP). Stop-start transcription occurs 3' to 5' using gene start and gene end sequences, separated by non-transcribed intergenic sequences, to generate capped and polyadenylated mRNAs. Replication is initiated by the RdRP from a single promoter at the 3' end, ignoring gene start and end sequences to generate a (+)RNP. This is the template to generate nascent (-)RNPs which are assembled with M and G into enveloped virions. Budding can occur at either the plasma membrane or internal membranes. Some plant rhabdoviruses replicate in the nucleus.

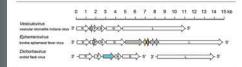


Fig. 2. Schematic representation of rhabdovirus genome organization, exemplifying variations in architecture and the number and location of accessory genes. Arrows indicate the position of long ORFs. Alternative ORFs occur within some genes; only ORFs (≥180 nt) that appear likely to be expressed are shown. ORFs encoding viroporin (yellow) and movement proteins (blue) are shown.

TAXONOMY

The Rhabdoviridae includes 18 genera and one unassigned species (Moussa virus). Viruses assigned to each genus form a monophyletic clade based on phylogenetic analyses of L protein sequences and usually have similar genome organizations, including the number and locations of accessory genes. Rhabdoviruses have been isolated from a wide range of vertebrates and plants; many have been isolated from arthropods [4, 5]. Members of the genus Lyssavirus infect only mammals, including humans in which they can cause fatal encephalitis (rabies). Members of the genera Vesiculovirus, Ephemerovirus, Tibrovirus, Hapavirus, Curiovirus, Sripuvirus and Ledantevirus infect vertebrates (mammals, birds or reptiles) and are transmitted by arthropods. Some arthropod-borne rhabdoviruses are associated with diseases of livestock; some may cause disease in humans. Members of the genus Tupavirus have only been isolated from vertebrates. Members of the genera Novirhabdovirus, Sprivivirus and Perhabdovirus infect only fish, some causing economically important diseases. Rhabdoviruses assigned to the genus Sigmavirus each infect only dipteran flies of a single species and they are transmitted vertically. Members of the genus Almendravirus replicate only in insects. Plant rhabdoviruses are assigned to the genera Cytorhabdovirus, Nucleorhabdovirus, Dichorhavirus and Varicosavirus and are transmitted by either arthropods or chytrid fungi. Many are associated with diseases of agricultural or horticultural importance.

RESOURCES

Full ICTV Online (10th) Report: www.ictv.global/report/rhabdoviridae.

Funding information

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Acknowledgements

Members of the ICTV Report Consortium are Elliot J. Lefkowitz, Andrew J. Davison, Stuart G. Siddell, Peter Simmonds, Sead Sabanadzovic, Donald B. Smith, Richard J. Orton and Jens H. Kuhn.

Conflicts of interest

The authors declare that there are no conflicts of interest.

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RHABDOVIRIDAE TAXONOMY **PROFILE**

https://www.microbiolog yresearch.org/content/ journal/jgv/I0.1099/ jgv.0.001020

Evelien Adriaenssens

Chair – Bacterial and Archaeal Viruses Subcommittee











Bacterial and Archaeal Viruses Subcommittee update

An ongoing revolution in phage taxonomy

Morphology → genome-based classification

Holistic approach at multiple ranks

Advance Access publication May 25, 2019

- DNA sequence identity for species and genus
- DNA and amino acid identity for subfamilies
- Shared (predicted) protein content and organisation at family & order level
- Supported at all ranks by phylogenies of signature genes

Syst. Biol. 69(1):110–123, 2020
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DOI:10.1093/sysbio/syz036

Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages

Jakub Barylski¹, François Enault², Bas E. Dutilh^{3,4}, Margo B.P. Schuller³, Robert A. Edwards^{5,6}, Annika Gillis⁷, Jochen Klumpp⁸, Petar Knezevic⁹, Mart Krupovic¹⁰, Jens H. Kuhn¹¹, Rob Lavigne¹², Hanna M. Oksanen¹³, Matthew B. Sullivan^{14,15}, Ho Bin Jang^{14,15}, Peter Simmonds¹⁶, Pakorn Aiewsakun^{16,17}, Johannes Wittmann¹⁸, Igor Tolstoy¹⁹, J. Rodney Brister¹⁹, Andrew M. Kropinski^{20,21}, and Evelien M. Adriaenssens^{22,23,*}

Progress of the last 3 years

Expansion in membership to be more diverse with regional representatives from across the globe Changes ratified since 2017:

- Name change of prokaryotic virus genera to be euphonious
- New and reclassified taxa:
 - 1 order
 - 12 families
 - 464 genera
 - 1084 species

New submissions in 2020:

2020	species genus	sul	ofamily family	ore	der class	ph	ylum kingdon	n re	alm
	opener general		,,				7.0		
Abolish	20	2	0	0	0	0	0	0	0
Create new	1328	781	38	20	3	1	1	1	1
Create new; assign as									
type species	737	0	0	0	0	0	0	0	0
Move	77	46	9	1	1	0	0	0	0
Move;									
rename	3	2	0	0	0	0	0	0	0
Promote	0	0	1	0	0	0	0	0	0
Rename	32	8	0	1	1	1	0	0	0

Software used by the Subcommittee

(non-exhaustive list)

GRAViTy: http://gravity.cvr.gla.ac.uk

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Jang, H. Bin et al. Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. *Nat. Biotechnol.* **37**, 632–639 (2019).

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Moraru, C., Varsani, A. & Kropinski, A. M. VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. *bioRxiv* (2020). doi:10.1101/2020.07.05.188268

VICTOR: https://ggdc.dsmz.de/victor.php (Be advised: taxonomic predictions by this tool do not always correspond with ICTV) Meier-Kolthoff, J. P. & Göker, M. VICTOR: genome-based phylogeny and classification of prokaryotic viruses. *Bioinformatics* **33**, 3396–3404 (2017).

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Balázs Harrach

Chair – Animal DNA Viruses and Retroviruses Subcommittee

Adenoviridade Ancind Varsani + 12s 12s - 6s 1g 6s streamlined 2020 revision Anelloviridae Ancind Varsani + - - 2g 8s - 17g 89s streamlined ? Asfarviridae (1 sp) Alonso Covadonga - - - - - - 2018 Asfarviridae (1 sp) Alonso Covadonga - - - - - - 2018 Baduloviridae Robert Harrison + 11s 2s 8s 8s In 1s streamlined 2020 Idualiviridae Arvind Varsani - 19s n 4s 13s 7s 8s streamlined 2017 updated 2018 Hepatitis delta virus - 19s n 4s 13s 13s 1sc 1sc <th>Animal DNA Viruses and Retroviruses</th> <th>2015</th> <th>2016</th> <th>2017</th> <th>2018</th> <th>2019</th> <th>2020</th> <th></th> <th>Report chapter</th>	Animal DNA Viruses and Retroviruses	2015	2016	2017	2018	2019	2020		Report chapter
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Boculoviridae Robert Harrison Foundation Foundat	Ascoviridae Xiao-Wen Cheng	+	rn	-	=	-	-		2017
Nudiviridae 1 sp Mart Krupovic - - - - - - - - -	Asfarviridae (1 sp) Alonso Covadonga	-	-	-	-	-	=		2018
Bidnaviridae (1 sp) Mart Krupovic - - - - - - - - -	Baculoviridae Robert Harrison	+	11s	2s	8s	8s 1rn	1 s	streamlined	2018
Circoviridae Arvind Varsani - 19s rn 4s 13s 7s 8s streamlined 2017 updated 2018 Hepadnaviridae Lars Magnius + 3s 2s 1s 3g 3s 1corr streamlined 2020 Hepatitis delta virus - 1s 18s - 4g 8s 2m streamlined 2020? Hetrpesvirides Andrew Davison + - 1s 18s - 4g 8s 2m streamlined 2020? Hytrosoviridae Gegory Chinchar + 2sf 1s 1s 1g 9s 3abo - 1g 3s streamlined 2019 Iridoviridae Gregory Chinchar + 2sf 1s 1s 1g 9s 3abo - 1g 3s streamlined 2019 2019 Paylindoviridae Gregory Chinchar + 2sf 1s 1s 1s 4s 3g 2sg - 2019 2019 Paylindoviridae Unidit Pénzes - 6s 17s 1s 1s 4s 2g 1s 2s 1s 4s	/Nudiviridae				-	-	3g 8s	streamlined	2020
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Hytrosoviridae (2 sp) Adly Abd-Alla - - - 2rn - 2019 Iridoviridae Gregory Chinchar + 25f 1s 1s 1g 9s 3abo - 1g 3s streamlined 2017 updated 18, 20 Nimaviridae (1 sp) Han-Ching Wang - - - - - - 2019 Papillomaviridae Koenraad Van Doorslaer - - - - - - 2018 Parvoviridae Judit Pénzes - 6s 17s 1s 1sf 43s 3g 20s streamlined 2019 Polyanaviridae Bernhard Ehlers + 4s 8s 10s 1rn 4s 2g 15s streamlined 2017 updated 18, 20 Poxiridae Geoffrey Smith + 1g 2s - - - - 2g 15s streamlined 2017 updated 18, 20 Poxiridae Geoffrey Smith + 1g 3s 1s 1st or 1ab - - - - 2020 under review	hepatitis delta virus				-	-	1r 1f 7g 8	S	2018
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Parvoviridae Judit Pénzes - 6s 17s 1s 1sf 43s 3g 20s streamlined 2019 Polydnaviridae (53 sp) Michael Strand - - - - - - ? Polyomaviridae Bernhard Ehlers + 4s 8s 10s 1rn 4s 2g 15s streamlined 2017 updated 18, 20 Poxviridae Geoffrey Smith + 1g 2s - - 8g 13s 1rn - ? 2020 under review Ortervirales Mart Krupovic 10 - - - 0 2020 under review Belpaoviridae (in Ortervirales SG) Carlos Llorens 1f 3s - - - 0 0 - - - 0 0 0 0 - - - 0	Nimaviridae (1 sp) Han-Ching Wang	-	-	-	-	-	-		2019
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Jens Kuhn

Chair – Animal dsRNA and ssRNA-Viruses Subcommittee

ss(-)RNA and dsRNA Virus Taxa

- Inclusion of all established taxa into a new hierarchical framework including realm, kingdom, phyla, and classes
- Expansion of non-Latinized binomial species names to all taxa except dsRNA viruses and Orthomyxoviridae (e.g., Puumala orthohantavirus)
- Adoption of first sequence-based species demarcation criteria for *Nairoviridae, Peribunyaviridae*, and *Phenuiviridae*
- Regular communication of all taxonomic changes (with exception of dsRNA viruses) via Archives of Virology Virology Division News articles

Year	Realm	Kingdom	Phyla	Classes	Orders
2017	0	0	0	0	2
2018	0	0	1	6	7
2019	1	0	1	6	8
2020	1	1	3	8	9

On the Horizon (2020 Onwards)

- Expansion and refinement/standardization of nomenclature in *Reovirales*
- Dramatic expansion and reorganization of Orthomyxoviridae and related articulavirals
- Adoption of species demarcation criteria for *Hantaviridae* and *Lispiviridae*
- Further development of the taxonomy of *Jingchuvirales*
- Adoption of a uniform species naming format for all virus species → renaming of almost all species names
- Declassification of all viruses for which coding-complete genome sequence is not available?
- Development of etymologies and pronunciation guidelines for all taxa and classified viruses
- Step-wise elimination of duplicate virus name abbreviations

Nick Knowles

Chair – Animal ssRNA+ Viruses Subcommittee



Animal ssRNA+ Viruses Subcommittee

Chair: Nick J. Knowles

The Pirbright Institute, Pirbright, Woking, Surrey, United Kingdom

Subcommittee Members

Study Group

Alpha-, Carmo-, and Permuto- tetraviridae

Arteriviridae

Astroviridae

Caliciviridae

Coronaviridae

Dicistroviridae/Iflaviridae

Flaviviridae

Hepeviridae

Mesoniviridae

Nidovirales

Nodaviridae

Picornavirales

Picornaviridae

Roniviridae

Togaviridae

Chair

Rosemary A. Dorrington,

Margo A. Brinton

Simon J. Anthony

Jan Vinjé

John Ziebuhr

Steven M. Valles

Rebecca Rico-Hesse

Michael A. Purdy

Alexander E. Gorbalenya

Alexander E. Gorbalenya

A.S. Sahul Hameed

Peter Simmonds

Roland Zell

Nick Moody/Peter Walker

Rubing Chen

Country

South Africa

USA

USA USA

Germany

USA

USA

USA

Netherlands

Netherlands

India

UK

Germany

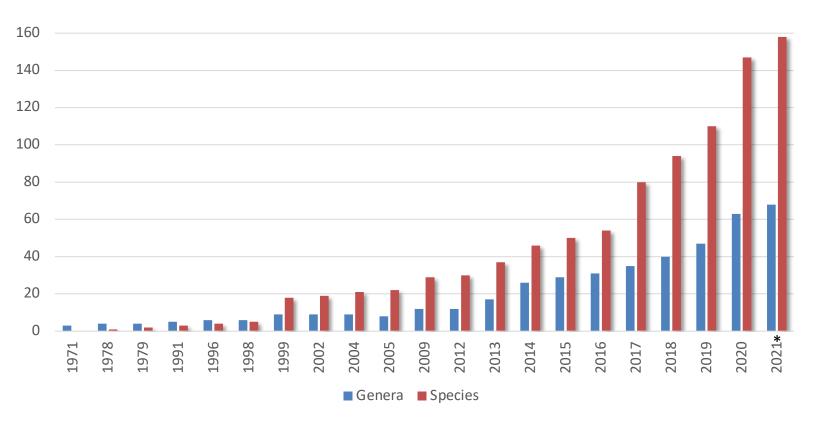
Australia

USA

Main Taxonomic Changes: 2018 to 2020

- New family, Polycipiviridae, containing 3 genera within the order Picornavirales
- Caliciviridae now included in the order Picornavirales
- 6 new genera created in the *Caliciviridae*
- Rubella virus moved from the Togaviridae and placed in a new family, Matonaviridae
- Major reorganisation of the order *Nidovirales* resulting in 14 families contain 25 subfamilies, 39 genera, 65 subgenera and 109 species
- 28 new genera containing 67 new species created in the Picornaviridae
- Taxon levels of Realm, Kingdom, Phylum and Class created for all positive-sense ssRNA animal viruses

Cumulative increase in the number of *Picornaviridae* genera & species



^{*} Includes proposed taxa

Peter Simmonds

Chair – Fungal and Protist VirusesSubcommittee

Study Groups

Current Study Groups

Family	SG Chair	Country	ICTV Report
Barnaviridae	Peter Revill	Australia	
Botourmiaviridae	Maria Ayllon	Spain	Yes
Chrysoviridae	Robert Coutts	UK	Yes
Hypoviridae	Nobuhiro Suzuki	Japan	Yes
Marnaviridae	Andrew Lang	Canada	
Marseilleviridae	Phillipe Colson	France	
Mimiviridae	Matthias Fischer	Germany	
Narnaviridae	Bradley Hillman	USA	
Partitiviridae	Eeva Vainio	Finland	Yes
Phycodnaviridae	James van Etten	USA	
Totiviridae	Max Nibert	USA	

Fungal virus families without Study Groups:

Megabirnaviridae Quadriviridae Endornaviridae Bacilladnaviridae Lavidaviridae Mycodnaviridae Botybirnaviridae

Main Taxonomic Changes: 2018 to 2020

• 2020

- Creation of the new virus family, Curvulaviridae (bipartite sdRNA)
- Expansion of the Botourmiaviridae
- Expansion of Mymonoviridae
- Classification of fungal viruses in the Genomoviridae family

2019

- Creation of new family, Polymycoviridae, 4-8 segments, dsRNA
- Expansion and reorganization of Chysoviridae and Marnaviridae

• <u>2018</u>

- Creation of new family, Ourmiaviridae, bipartite dsRNA
- Expansion and reorganization of Chysoviridae and Marnaviridae

Murilo Zerbini

Chair – Plant Viruses
Subcommittee

Update from the Plant Virus Sub-Committee 2017-2020



Plant Virus Sub-Committee (2017-2020)

Zerbini, F. Murilo	Plant Virus Subcommittee - Chair	Brazil
Kreuze, Jan	Alphaflexiviridae Study Group - Chair	Peru
Sabanadzovic, Sead	Amalgaviridae Study Group - Chair	USA
García, Maria Laura	Aspiviridae Study Group - Chair	Argentina
Di Serio, Francisco	Avsunviroidae and Pospiviroidae Study Group - Chair	Italy
Tzanetakis, Ioannis	Beta-, Gamma- and Deltaflexiviridae Study Group - Chair	USA
Gallitelli, Donato	Bromoviridae Study Group - Chair	Italy
Teycheney, Pierre-Yves	Caulimoviridae Study Group - Chair	France
Fuchs, Marc	Closteroviridae Study Group - Chair	USA
Valverde, Rodrigo	Endornaviridae Study Group - Chair	USA
Elbaino, Toufic	Fimoviridae Study Group - Chair	Italy
Fiallo-Olivé, Elvira	Geminiviridae and Tolecusatellitidae Study Group - Chair	Spain
Melzer, Michael	Kitaviridae Study Group - Chair	USA
Miller, W Allen	Luteoviridae Study Group - Chair	USA
Thomas, John E	Nanoviridae Study Group - Chair	Australia
Wylie, Steve	Potyviridae Study Group - Chair	Australia
Karasev, Alexander	Secoviridae Study Group - Chair	USA
Somera, Merike	Solemoviridae Study Group - Chair	Estonia
Sasaya, Takahide	Tenuivirus Study Group - Chair	Japan
Scheets, Kay	Tombusviridae Study Group - Chair	USA
Adkins, Scott	Tospoviridae Study Group - Chair	USA
Hammond, Rosemarie	Tymoviridae Study Group - Chair	USA
Ryu, Ki Hyun	Virgaviridae and Benyvirus Study Group - Chair	Korea

23 members

17 M

6 F

10 North Am

6 Europe

3 South Am

2 Asia

2 Australasia

Plant virus chapters of the ICTV Report

Published/updated in 2018-2020: Alphaflexiviridae

Aspiviridae

Avsunviroidae

Botourmiaviridae#

Bromoviridae

Caulimoviridae

Closteroviridae

Endornaviridae

Fimoviridae

Geminiviridae

Potyviridae

Secoviridae

To be published soon:

Nanoviridae

Pospiviroidae Solemoviridae

[#] Together with Fungal and Protis

Changes to the taxonomy since 2017

75 plant virus Taxonomy Proposals ratified in 2018, 2019, 2020

Creation of new taxa

5 families, 5 sub-families, 25 genera, 361 species

New families

Alphasatellitidae, Deltaflexiviridae, Kitaviridae, Mayoviridae, Solemoviridae

Creation of a second family of ssDNA satellites

Family Alphasatellitidae (two subfamilies, 11 genera, 71 species)

Major reorganizations/updates

Tombusviridae, Tospoviridae

All plant virus families classified in the four Realms

Only DNA satellites and viroids not classified

Proposals under consideration at EC52 (for 2021 ratification vote)

36 plant virus Taxonomy Proposals

New taxa

Family *Metaxyviridae* (one genus, one species)
Subfamily *Petromoalphasatellitinae* (four genera, seven species)
Nine new genera (*Alphasatellitidae*, *Caulimoviridae*, *Geminiviridae*)
164 new species

R.I.P. Luteoviridae

Its three genera will be reassigned to *Tombusviridae* and *Solemoviridae*

All proposals posted on the ICTV website