Taxonomy Proposal Summaries for Ratification Vote, 2026

This document contains a full list of the taxonomy proposals presented for the ICTV Member ratification vote in February, 2026. These are listed by sub-committee, and a final summary of General Taxonomy proposals.

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Information provided for each proposal includes the title, authors of the submission and corresponding author, a structured summary, submission / revision dates, and a tabulated summary of the proposed changes.

Please note that these summaries are provided solely for the purposes of evaluating the proposals prior to the ratification votes. This document is confidential and should not be publicly distributed.

Similarly formatted summaries of proposals voted for by the ICTV membership will be published in the *Journal of General Virology*, and should be used for future reference.

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Animal DNA Viruses and Retroviruses Subcommittee

Contents

2025.001D.v3.Baculoviridae_4nsp_1absp

Title: Create four new species and abolish one current species in family *Baculoviridae*

Authors: Monique M van Oers, Adly M. M. Abd-Alla, Kelly S. Bateman, Jaime Bojko, Robert L. Harrison, Elisabeth A. Herniou, Johannes A. Jehle, Peter J. Krell, Bergmann M Ribeiro, Xiulian Sun

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy: There are currently 68 species in the genus *Alphabaculovirus* and 29 species in the genus *Betabaculovirus* of the family *Baculoviridae*

Proposed taxonomic change(s): We propose to create three new species in the genus *Alphabaculovirus,* create one new species in the genus *Betabaculovirus,* and abolish one species in the *genus Betabaculovirus*

Justification: Analysis of recently sequenced baculovirus genomes have identified four viruses that each represent a previously undescribed baculovirus species, in accordance with the species demarcation criteria defined for the family *Baculoviridae.* Nucleotide sequences derived from isolates of *Betabaculovirus trini* and *Betabaculovirus myunipunctae* are almost completely identical, indicating that one of these species should be abolished. We have chosen to abolish *Betabaculovirus trini* due to the significant place *that* the exemplar isolate of *Betabaculovirus myunipunctae* occupies in the history of baculovirus research.

Submitted: 26/05/2025; *Revised:* 26/05/2025

TABLE 1 - *Baculoviridae*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Alphabaculovirus calabietis*	Calliteara abietis nucleopolyhedrovirus	PP171514
New taxon	Species	*Alphabaculovirus mysequacis*	Mythimna sequax nucleopolyhedrovirus	MW380417
New taxon	Species	*Alphabaculovirus plidaeusalis*	Platynota idaeusalis nucleopolyhedrovirus	OQ658191
New taxon	Species	*Betabaculovirus plidaeusalis*	Platynota idaeusalis granulovirus	PP449363

TABLE 2 - *Baculoviridae*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	Species	*Betabaculovirus trini*

2025.002D.v4.Nudiviridae_2ng_17ns_1mvsp

Title: Addition of novel genera and species, and reclassification of some species in the *Nudiviridae*

Authors: Jamie Bojko, Jirka Petersen, Amy Burgess, Monique Van Oers, Elisabeth Herniou, Robert L. Harrison

Summary:
Taxonomic rank(s) affected:
Genus and species

Description of current taxonomy:
The current taxonomy in place includes the *Alphanudivirus* (n=7 species), *Betanudivirus* (n=1 species), *Gammanudivirus* (n=4 species), and *Deltanudivirus* (n=1 species), within *the Nudiviridae.*

Proposed taxonomic change(s):
We propose to create two new genera, move one species to a new genus, and create 17 new species.

Justification:
New discoveries of nudiviruses from crustaceans and insects (Petersen et al. 2024) have resulted in a more diverse understanding of the *Nudiviridae.* The crustacean nudiviruses split clearly into two groups, which should be considered at the genus level for this viral family. Two new genera found to infect lice are new to science and require incorporation into the nudivirus taxonomy. In addition to the genus level amendments, there are also several species that now need to be appropriately placed into the *Alphanudivirus, Gammanudivirus,* and the two new genera, *Epsilonnudivirus* and *Zetanudivirus.*

Submitted: 29/05/2025; *Revised:* —

TABLE 3 - *Nudiviridae*, 18 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Alphanudivirus apimelliferae*	Apis mellifera nudivirus	OR596894
New taxon	Species	*Gammanudivirus memercanariae*	Menippe mercenaria nudivirus	OQ725696
New taxon	Species	*Gammanudivirus casapidi*	Callinectes sapidus nudivirus	ON638996
New taxon	Species	*Gammanudivirus marosenbergii*	Macrobrachium rosenbergi nudivirus	MW484891
New taxon	Species	*Gammanudivirus arapsonii*	Aratus pisonii nudivirus	ON061174
New taxon	Species	*Gammanudivirus pevannamei*	Penaeus vannamei nudivirus	OM066077
New taxon	Genus	*Epsilonnudivirus*		
New taxon	Species	*Epsilonnudivirus dikhaemobaphes*	Dikerogammarus haemobaphes nudivirus	MT488302
New taxon	Species	*Epsilonnudivirus faxopropinqui*	Faxonius propinquus nudivirus	PP539709

New taxon	Species	*Epsilonnudivirus faxovirilis*	Faxonius virilis nudivirus	PP539710
New taxon	Species	*Epsilonnudivirus faxorustici*	Faxonius rusticus nudivirus	PP539711
New taxon	Genus	*Zetanudivirus*		
New taxon	Species	*Zetanudivirus hespinigeri*	Heterodoxus spiniger nudivirus	BK068078
New taxon	Species	*Zetanudivirus laperplexi*	Lagopoecus perplexus nudivirus	BK068079
New taxon	Species	*Zetanudivirus cucafricani*	Cuculoecus africanus nudivirus	BK068074
New taxon	Species	*Zetanudivirus echiclaytoni*	Echinophilopterus claytoni nudivirus	BK068075
New taxon	Species	*Zetanudivirus fraroseicapillae*	Franciscoloa roseicapillae nudivirus	BK068077
New taxon	Species	*Zetanudivirus myptilorhynchi*	Myrsidea ptilorhynchi nudivirus	BK068080

TABLE 4 - *Nudiviridae*, 1 move; rename taxon*

Operation	**Rank**	**New taxon name**	**Old taxon name**	**New parent taxon**	**Old parent taxon**
Move; rename taxon	Species	*Epsilonnudivirus cracrangonis*	*Gammanudivirus cracrangonis*	*Epsilonnudivirus*	*Gammanudivirus*

2025.003D.v3.Iridoviridae_1ng_1ns

Title: Creation of one new genus *(Bivalveiridovirus)* with one new species *(Bivalveiridovirus cerastoderma1)* in the subfamily *Betairidovirinae*

Authors: Chantelle Hooper, Anna M Tidy, Ron Jessop, Kelly S Bateman, Matthew J Green, Stuart H Ross, Georgia M Ward, Richard Hazelgrove, Jasmine E Hunt, Megan Parker, David Bass

Summary:Taxonomic rank(s) affected:
Formation of a novel genus within *Betairidovirinae* containing a single confirmed species.

Description of current taxonomy:
The subfamily *Betairidovirinae* currently contains four genera, with its members primarily infecting invertebrate hosts.

Proposed taxonomic change(s):
Formation of the novel genus *Bivalveiridovirus* within *Betairidovirinae* and the recognition of novel iridovirus species *Bivalveiridovirus cerastoderma1.*

Justification:
Generation of the complete genome of a novel iridovirid from cockles *(Cerastoderma edule)* and determination of its tropism within the tissues of infected animals represents the most complete description of a bivalve-infecting iridovirid to date. The genome size and G+C% content of *Bivalveiridovirus cerastoderma1* was similar to other *Betairidovirinae.* Pathology of infection with *Bivalveiridovirus cerastoderma1* in cockles was similar to that described for *Decapodiridovirus litopenaeus1* infection in shrimp tissues, and icosahedral virions, typical of iridovirids, were observed in the cytoplasm of infected cockle haemocyte cells. Comparison of the amino acid sequence from conserved iridovirid genes in *Bivalveiridovirus cerastoderma1* to other iridovirids showed 76.36% amino acid similarity to the nearest iridovirus in the major capsid protein (MCP) and 65.46% in the AAA-ATPase protein. Phylogenetically, *Bivalveiridovirus cerastoderma1* branches within

Betairidovirinae, but as a separate clade to other recognised genera.

Based on the host range, phylogenetic position, and sequence similarity of this novel virus to known iridovirids, we propose the construction of a new genus, designated *Bivalveiridovirus,* to indicate its infectivity toward a species within the Bivalvia class of animals, and that it be considered a fifth genus within the subfamily *Betairidovirinae.*

Submitted: 03/12/2025; *Revised:* —

TABLE 5 - *Iridoviridae*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Bivalveiridovirus*		
New taxon	Species	*Bivalveiridovirus cerastoderma1*	Bivalve iridovirus 1	PQ846775

2025.004D.v3.Adenoviridae_20ns

Title: Create 20 new species in the genera *Aviadenovirus, Mastadenovirus* and *Siadenovirus (Rowavirales: Adenoviridae)*

Authors: Balázs Harrach, Mária Benkő, Győző L. Kaján, Thomas S. Postler, Arvind Varsani, Márton Z. Vidovszky, ,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
125 species in 6 genera in the *family Adenoviridae.*

Proposed taxonomic change(s):
Adding 20 new species; 16 to genus *Mastadenovirus,* 3 to *Siadenovirus,* 1 to *Aviadenovirus;* correcting two minor typing errors in the names of two mastadenovirus species.

Justification:
Novel adenovirus sequences have been submitted to GenBank, reflecting very rich diversity (https: //sites.google.com/site/adenoseq). From these sequences, 20 full or almost full (coding-complete) vertebrate adenovirus genomes originating from 13 mammalian, 3 avian and 1 turtle species merit the establishment of new species for them. The phylogenetic distance of their DNA polymerase amino acid sequences shows adequate evolutionary distance to members of accepted adenovirus species (Fig. 1). A divergence in pairwise amino acid identity of the DNA polymerase sequence exceeding 15% is the main demarcation criterion. In case of 14-15% pairwise identity divergence, other criteria (e.g. different host species, genome organization or whole-genome GC% difference) and the monophyletic clustering of the available pol sequences helped to classify the adenoviruses into species.

Submitted: 06/09/2025; *Revised:* 31/08/2025

TABLE 6 - *Adenoviridae*, 20 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar

New taxon	Species	*Mastadenovirus hylobatidae*	simian adenovirus 57 (gibbon adenovirus)	OP921948
New taxon	Species	*Mastadenovirus pollicis*	simian adenovirus 58 (black-and-white colobus adenovirus 4)	PP985428
New taxon	Species	*Mastadenovirus bestiae*	simian adenovirus 60	PQ490709
New taxon	Species	*Mastadenovirus aethiopiense*	simian adenovirus 61	PQ490710
New taxon	Species	*Mastadenovirus sanguineicordis*	simian adenovirus 64	PQ490717
New taxon	Species	*Mastadenovirus geladae*	simian adenovirus 65	PQ490713
New taxon	Species	*Mastadenovirus mastomysis*	murine adenovirus 4	PQ490628
New taxon	Species	*Mastadenovirus eliomysis*	garden dormouse adenovirus 1	PQ576919
New taxon	Species	*Mastadenovirus rattasiense*	tanezumi rat adenovirus 1 (Yunan rodent adenovirus 1)	PQ678060
New taxon	Species	*Mastadenovirus eothenomysis*	Kachin red-backed vole adenovirus 1 (Yunan rodent adenovirus 2)	PQ678115; PQ678116
New taxon	Species	*Mastadenovirus kuhlii*	Kuhl's pipistrelle adenovirus MAG44	PP410068
New taxon	Species	*Mastadenovirus ferrumequini*	greater horseshoe bat adenovirus MAG47	PP410069
New taxon	Species	*Mastadenovirus noctulae*	common noctule adenovirus Quixote	PP297886
New taxon	Species	*Mastadenovirus portugalense*	bat adenovirus F45	PV383552
New taxon	Species	*Mastadenovirus himalaiense*	Himalayan wiskered bat adenovirus 1	OR998961
New taxon	Species	*Mastadenovirus arundinis*	greater bamboo bat adenovirus	OR998870
New taxon	Species	*Siadenovirus columbae*	pigeon adenovirus 4	PP999621
New taxon	Species	*Siadenovirus sulawense*	Sulawesi adenovirus 1 (Chinese soft-shelled turtle adenovirus)	PQ083072
New taxon	Species	*Siadenovirus coturnicis*	quail adenovirus 1	PV175342
New taxon	Species	*Aviadenovirus cinerei*	Timneh grey parrot adenovirus 1	OR096706

TABLE 7 - *Adenoviridae*, 2 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Species	*Mastadenovirus asiense*	*Mastadenovirus asiensse*
Rename taxon	Species	*Mastadenovirus rhinolophidae*	*Mastadenovirus rhinolopidae*

2025.005D.Ac.v4.Parvoviridae_1absf_4nsf_39ns

Title: Abolition of a subfamily, establishment of four new subfamilies and classifying 39 new species in the *Parvoviridae* family

Authors: Judit J Penzes, Marta Canuti, Maria Söderlund-Venermo, Sarah Francois, Peter Tijssen, Jianming Qiu, Anna M Eis-Hübinger,

Summary:
Taxonomic rank(s) affected:

Subfamily, genus, species

Description of current taxonomy:
The *Parvoviridae* is currently composed of three subfamilies. Two of these, the *Parvovirinae* and the *Densovirinae,* are clearly monophyletic and are united by biological synapomorphies. The subfamily *Hamaparvovirinae* was established in 2019, albeit even at that time it was regarded as an extremely heterogenous subfamily, especially in comparison to the other two subfamilies. This heterogeneity has now matured to be characterized in more detail and recognize the individual lineages it has been keeping together.

Proposed taxonomic change(s):
Here, we suggest the abolition of the subfamily *Hamaparvovirinae* and the establishment of three subfamilies in its wake, designated *Hamavirinae, Penbrevirinae,* encompassing two of the current *Hamaparvovirinae* genera each, and the monotypic *Hepanvirinae.* We also propose the elevation of the currently floating genus, *Metalloincertoparvovirus,* to the subfamily rank, with a single monotypic genus. Furthermore, we propose the establishment of two new monotypic genera within the newly founded *Hamavirinae,* which would be called *Embehamavirus* and *Coluhamavirus,* respectively. Lastly, we propose the establishment of 36 new species in the newly established *Chaphamavirus* genus and one new species within the *Diciambidensovirus* genus of the *Densovirinae* subfamily. We will also retrospectively apply the binomial nomenclature to the *Miniambidensovirus* species, containing Acheta domesticus mini ambidensovirus.

Justification:
The proposed changes will result in six monophyletic subfamilies within the *Parvoviridae,* which are also supported with biological traits, including their non-structural and structural protein sequence homology, virion surface morphology and structural protein fold. Furthermore, this classification system will create a more flexible framework, which has the capability of adopting future novel divergent entries.

Submitted: 06/07/2025; *Revised:* —

TABLE 8 - *Parvoviridae*, 46 move; rename taxa*. Table too large, see supplementary information sheet supp_info_tab_8

TABLE 9 - *Parvoviridae*, 44 new taxa*. Table too large, see supplementary information sheet supp_info_tab_9

TABLE 10 - *Parvoviridae*, 4 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Genus	*Brevipenbrevirus*	*Brevihamaparvovirus*
Rename taxon	Species	*Brevipenbrevirus dipteran1*	*Brevihamaparvovirus dipteran1*
Rename taxon	Species	*Brevipenbrevirus dipteran2*	*Brevihamaparvovirus dipteran2*
Rename taxon	Species	*Miniambidensovirus orthopteran1*	*Orthopteran miniambidensovirus 1*

TABLE 11 - *Parvoviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Subfamily	*Hamaparvovirinae*

2025.006D.v3.Bidnaviridae_1rns

Title: Rename one species in the family *Bidnaviridae*

Authors: Judit J Pénzes, Peter Tijssen, Mart Krupovic, Mylène Ogliastro, Qin Yao, Varsani Arvind, ,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Monodnaviria; Shotokuvirae; Cossaviricota; Mouviricetes; Polivirales; Bidnaviridae; Bidensovirus; Bombyx mori bidensovirus

Proposed taxonomic change(s):
One species is renamed to conform to the binomial format mandated by the ICTV.

Justification:
Bombyx mori *bidensovirus* is the only species in the genus *Bidensovirus* (family *Bidnaviridae).* This species name does not adhere to the binomial species naming format and thus here we propose to rename it to *Bidensovirus bombymori.*

Submitted: 06/11/2025; *Revised:* —

TABLE 12 - *Bidnaviridae*, 1 rename taxon*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Species	*Bidensovirus bombymori*	*Bombyx mori bidensovirus*

2025.007D.v4.Whispovirus_1nsp

Title: Creation of new species *"Whispovirus lacteolymphae"* in *Nimaviridae*

Authors: Satoshi Kawato, Tadashi Isshiki, Ikuo Hirono

Summary:Taxonomic rank(s) affected:
Species.

Description of current taxonomy:
The family *Nimaviridae* currently includes one species: *White* spot syndrome *virus,* which belongs to the *genus Whispovirus.*

Proposed taxonomic change(s):
Create *"Whispovirus lacteolymphae",* a new species within genus *Whispovirus in Nimaviridae.*

Justification:
Chionoecetes opilio bacilliform virus (CoBV), which was initially described as the causative agent of the milky hemolymph disease in the snow *crab (Chionoecetes opilio)* in the Sea of Japan (Kon et al., 2011; Motobayashi et al., 2018), has recently been characterized at the genomic level (Kawato et al., 2023). CoBV possesses a circular, double-stranded DNA genome ranging 240 kbp in size with 105

predicted protein-coding genes, including 76 WSSV orthologs (Kawato et al., 2023).
Phylogenetic analysis using conserved naldaviral core genes (Kawato et al., 2019; 2023) confirms the placement of CoBV within the family *Nimaviridae.* Nimaviral core gene phylogeny (Kawato et al., 2024) and Jaccard similarity clustering based on shared orthologs (File S1) both support a coherent grouping of CoBV with WSSV. Taken together, although CoBV is substantially divergent from WSSV (average amino acid identity: 34.7%; File S1), its position within the overall diversity of *Nimaviridae* is consistent with inclusion in the genus *Whispovirus.* Therefore, we propose the creation of a new species, *"Whispovirus lacteolymphae",* to accommodate CoBV.

Submitted: 18/06/2025; *Revised:* 26/08/2025

TABLE 13 - *Whispovirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Whispovirus lacteolymphae*	Chionoecetes opilio bacilliform virus	LC741431

2025.008D.v3.Whispovirus_1rns

Title: Rename one species in the genus *Whispovirus*

Authors: Arvind Varsani, Mart Krupovic, Sead Sabanadzovic, , , , ,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Naldaviricetes; Nimaviridae; Whispovirus; White spot syndrome virus

Proposed taxonomic change(s):
Rename one species to conform to the ICTV binomial format.

Justification:
The family *Nimaviridae* currently has one genus and withing this genus, there is a single classified species **-** *White* spot syndrome *virus.* The species name, *White* spot syndrome *virus,* is not in binomial format. Thus, we propose renaming it to *"Whispovirus xiabaidian".*

Submitted: 18/06/2025; *Revised:* —

TABLE 14 - *Whispovirus*, 1 rename taxon*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Species	*Whispovirus xiabaidian*	*White spot syndrome virus*

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Animal dsRNA and ssRNA- viruses Subcommittee

Contents

2025.001M.A.v4.Alpharhabdovirinae_2ng_14nsp

Title: Create 2 new genera and 14 new species in the subfamily *Alpharhabdovirinae,* and move 5 species from the *genus Vesiculovirus* to the new *genus* Chiroprhavirus *(Mononegavirales: Rhabdoviridae)*

Authors: Peter J Walker, Nicolas Bejerman, Kim R Blasdell , Humberto Debat , Ralf G Dietzgen , Anthony R Fooks , Juliana Freitas-Astúa , Kyle Garver, Pedro L Ramos-Gonzáles, Hideki Kondo , Robert B Tesh , Noel Tordo , Nikos Vasilakis , Anna E Whitfield

Summary:
Taxonomic rank(s) affected:
Genera and species in the subfamily *Alpharhabdovirinae, family Rhabdoviridae.*

Description of current taxonomy:
The subfamily *Alpharhabdovirinae* currently comprises 34 genera including 248 species for viruses infecting only vertebrates, only invertebrates, or vertebrate hosts and arthropod vectors.

Proposed taxonomic change(s):
Create the new genus *Chiroprhavirus* and move 5 existing species from the genus *Vesiculovirus* to the new genus.
Create the new genus *Artemrhavirus* to include 1 new species.
Create 1 new species in the genus *Ledantevirus.*
Create 1 new species in the genus *Merhavirus.*
Create 2 new species in the genus *Sigmavirus.*
Create 2 new species in the genus *Ohlsrhavirus.*
Create 2 new species in the genus *Ephemerovirus.*
Create 2 new species in the genus *Betathriprhavirus.*
Create 2 new species in the genus *Alpharicinrhavirus.*
Create 1 new species in the *genus Lyssavirus.*

Justification:
Five viruses assigned to five existing species in the genus *Vesiculovirus* are phylogenetically and ecologically distinct from all other members of the genus, justifying their re-assignment to a new genus.

A new virus detected in brine shrimp is phylogenetically and ecologically distinct from the members of other genera in the subfamily *Alpharhabdovirinae,* justifying the creation of a new genus including a single species.
Thirteen other viruses for which complete coding sequences are now available fall phylogenetically within clades representing 8 existing genera and meet demarcation criteria for the creation of new species.

Submitted: 30/05/2025; *Revised:* 19/08/2025

TABLE 1 - *Alpharhabdovirinae*, 16 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Chiroprhavirus*		
New taxon	Genus	*Artemrhavirus*		
New taxon	Species	*Artemrhavirus blanca*	brine shrimp rhabdovirus 1	OL472789
New taxon	Species	*Sigmavirus cucurbitae*	Zeugodacus cucurbitae sigmavirus 1	OR714907
New taxon	Species	*Sigmavirus bangalore*	Zeugodacus cucurbitae sigmavirus 2	OR714908
New taxon	Species	*Merhavirus corixo*	Corixo rhabdovirus	OQ968277
New taxon	Species	*Ohlsrhavirus bafoussam*	Bafoussam mosquito rhabdovirus	PP764659
New taxon	Species	*Ohlsrhavirus halifaxii*	Culex rhabdo-like virus 2	OQ067690
New taxon	Species	*Ephemerovirus hefer*	Hefer Valley virus	OQ679991
New taxon	Species	*Ephemerovirus hardee*	Hardee County ephemerovirus 1	PQ480188
New taxon	Species	*Alpharicinrhavirus marginatum*	Hyalomma marginatum rhabdovirus	PQ036169
New taxon	Species	*Alpharicinrhavirus isaaci*	Zhanhye rhabd tick virus 1	PQ754346
New taxon	Species	*Betathriprhavirus pamplona*	Orius laevigatus rhabdovirus 2	PP908636
New taxon	Species	*Betathriprhavirus oviedo*	Orius laevigatus rhabdovirus 3	PP908637
New taxon	Species	*Lyssavirus phala*	Phala bat lyssavirus	OQ970171
New taxon	Species	*Ledantevirus hipposideros*	bat ledantevirus 2	PQ541151

TABLE 2 - *Alpharhabdovirinae*, 5 move; rename taxa*

Operation	**Rank**	**New taxon name**	**Old taxon name**	**New parent taxon**	**Old parent taxon**
Move; rename taxon	Species	*Chiroprhavirus epitesicus*	*Vesiculovirus eptesicus*	*Chiroprhavirus*	*Vesiculovirus*
Move; rename taxon	Species	*Chiroprhavirus mediterranean*	*Vesiculovirus mediterranean*	*Chiroprhavirus*	*Vesiculovirus*
Move; rename taxon	Species	*Chiroprhavirus rhinolophus*	*Vesiculovirus rhinolophus*	*Chiroprhavirus*	*Vesiculovirus*
Move; rename taxon	Species	*Chiroprhavirus wufeng*	*Vesiculovirus wufeng*	*Chiroprhavirus*	*Vesiculovirus*
Move; rename taxon	Species	*Chiroprhavirus yinshui*	*Vesiculovirus yinshui*	*Chiroprhavirus*	*Vesiculovirus*

2025.002M.Ac.v4.Crustavirus_1nsp

Title: Create one new species in genus *Crustavirus (Mononegavirales: Nyamiviridae)*

Authors: Rebecca M Grimwood, Leo N Zamora, Jessica A Darnley, Lizenn Delisle , Kate S Hutson, Jemma L Geoghegan

Summary:
Taxonomic rank(s) affected: *Mononegavirales;* Nyamiviridae; *Crustavirus*

Description of current taxonomy: There are currently three recognised species in the *Crustavirus genus.*

Proposed taxonomic change(s): Establishment of one new species in the genus *Crustavirus* for Red rock lobster virus, identified in a spiny lobster *(Jasus edwardsii* (Hutton, 1875)) from New Zealand.

Justification: While there are no current species demarcation criteria for viruses from the *Nyamiviridae* beyond phylogeny and host, the divergence of the coding-complete genome sequences of Red rock lobster virus, phylogenetic placement, and the novel host of the virus suggests it to be a new species in the *Crustavirus* genus.

Submitted: 04/05/2025; *Revised:* —

TABLE 3 - *Crustavirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Crustavirus jasusedwardsii*	Red rock lobster virus	PQ440166

2025.003M.N.v2.Konkoviridae_5nsp

Title: Create five new species in the genus *Olpivirus (Hareavirales: Konkoviridae]*

Authors: Yutaro Neriya, Timo M Breit, Laura Miozzi, Anna M Vaira, Yasuhiro Tomitaka, Takahide Sasaya

Summary:Taxonomic rank(s) affected: Species

Description of current taxonomy:
Two virus species are currently classified in the genus *Olpivirus,* infect tulip and lettuce plants. The assignment of viruses to this genus is based on the placement of the viruses on a Neighbor-joining tree inferred from the complete RdRP protein sequences.

Proposed taxonomic change(s):
Classify five newly discovered konkoviruses into the new species in the *genus Olpivirus.*

Justification:
Recently, five new putative konkoviruses were discovered. We propose the creation of five new species within the genus *Olpivirus.*

Submitted: 06/05/2025; *Revised:* —

TABLE 4 - *Konkoviridae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Olpivirus freesiae*	Freesia konkovirus 1	RNA1: PQ490803; RNA2: PQ490804; RNA3: PQ490805; RNA4: PQ490806
New taxon	Species	*Olpivirus lachenaliae*	Lachenalia Phenuivirus 1	RNA1: PQ067367; RNA2: PQ067368; RNA3: PQ067369; RNA4: PQ067370
New taxon	Species	*Olpivirus soli*	soil associated konkovirus	RNA1: BK070195; RNA2: BK070196; RNA3: BK070197; RNA4: BK070198
New taxon	Species	*Olpivirus tripterocalicis*	Tripterocalyx associated konkovirus 1	RNA1: BK070397; RNA2: BK070398; RNA3: BK070399
New taxon	Species	*Olpivirus waitziae*	Waitzia associated konkovirus 1	RNA1: BK070191; RNA2: BK070192; RNA3: BK070193; RNA4: BK070194

2025.004M.A.v3.Lispiviridae_1ng_6nsp

Title: Create one new genus and six new species in the family *Lispiviridae (Mononegavirales)*

Authors: Jun-Min Li, Gong-Yin Ye, Fei Wang, Zhuang-Xin Ye,

Summary:
Taxonomic rank(s) affected:
Genus and species in the *family Lispiviridae.*

Description of current taxonomy:
Currently, the family *Lispiviridae* includes 30 genera and 45 species according to ICTV Master Species List (MSL40.v1).

Proposed taxonomic change(s):
We propose the creation of 1 new genus and 6 new species to be included in mononegaviral *family Lispiviridae.*

Justification:
Genus (and species) demarcation is proposed to be based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparisons similar to established genus/species demarcation criteria for other mononegaviral families.

Submitted: 23/05/2025; *Revised:* 18/09/2025

TABLE 5 - *Lispiviridae*, 7 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Crocevirus*		
New taxon	Species	*Crocevirus donghaiense*	Crocidura lasiura lispivirus 2	PP272508

New taxon	Species	*Coroavirus crysecense*	Cryptotermes secundus lispivirus 1	BK067115
New taxon	Species	*Copasivirus macbelense*	Macrotermes bellicosus lispivirus 1	BK067117
New taxon	Species	*Copasivirus macnatense*	Macrotermes natalensis lispivirus 1	BK067120
New taxon	Species	*Copasivirus macsubense*	Macrotermes subhyalinus lispivirus 1	BK067121
New taxon	Species	*Robevirus illinense*	Empoasca fabae lispivirus 1	PP946284

2025.005M.Ac.v3.Peropuvirus_1nsp

Title: Create a new species in genus *Peropuvirus (Mononegavirales: Artoviridae)*

Authors: Arnfinn L. Økland, Jens H. Kuhn, Gongyin Ye, Nikolaos Vasilakis

Summary:
Taxonomic rank(s) affected:
Species in the *family Artoviridae.*

Description of current taxonomy:
The family *Artoviridae* currently includes two genera, *Hexartovirus* (4 species) and *Peropuvirus* (9 species).

Proposed taxonomic change(s):
Create one new species in the *genus Peropuvirus.*

Justification:
The virus proposed to be assigned to the novel species encodes an L protein with a minimum amino acid divergence of 51.9 % compared to classified family members and occupies a distinct ecological niche.

Submitted: 19/06/2025; *Revised:* 19/08/2025

TABLE 6 - *Peropuvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Peropuvirus crocidurae*	Crocidura shantungensis peropuvirus 1	PP272484

2025.006M.Ac.v4.Phasmaviridae_4nsp

Title: Create four new species in the family *Phasmaviridae*

Authors: Matthew J Ballinger, Sandra Junglen, Lander De Coninck

Summary:
Taxonomic rank(s) affected:
Species in the *family Phasmaviridae.*

Description of current taxonomy:
The family *Phasmaviridae* includes 32 species organized across seven genera.

Proposed taxonomic change(s):
Create four new species in the family *Phasmaviridae.*

Justification:
Coding-complete virus genome sequences are available to justify creation of four new species. Each exhibits < 95% L protein amino acid sequence identity to other exemplar viruses in the family *Phasmaviridae.*

Submitted: 13/06/2025; *Revised:* 18/09/2025

TABLE 7 - *Phasmaviridae*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Wuhivirus inferensa*	Sanya sesamia inferens phasmavirus 1	L: MZ209951; M: MZ209952; S: MZ209953
New taxon	Species	*Orthophasmavirus vrasenense*	Culex orthophasmavirus 2	L: PP076545; M: PP076550; S: PP076548
New taxon	Species	*Orthophasmavirus vitinea*	Lobesia botrana phasmavirus	L: BK067724; M: BK067725; S: BK067726
New taxon	Species	*Orthophasmavirus lycotinea*	Tuta absoluta phasmavirus 1	L: PQ655392; M: PQ655393; S: PQ655394

2025.007M.Ac.v3.Phenuiviridae_1ng_3nsp

Title: Create one new genus, and three new species in the family *Phenuiviridae.*

Authors: Holly R. Hughes, Takahide Sasaya, Gustavo Palacios, Thomas Briese, Cécile Desbiez, Francesco Di Serio, Dimitre Mollov, Yutaro Neriya, Jin-Won Song, Yasuhiro Tomitaka, Massimo Turina

Summary:
Taxonomic rank(s) affected:
Genus and species in the *family Phenuiviridae.*

Description of current taxonomy:
In the family *Phenuiviridae,* there are currently 23 genera and 159 species.

Proposed taxonomic change(s):
Create one new genus *Fusavirus,* including three new species for phenuiviridis detected in fungi.

Justification:
The three viruses create a well-supported monophyletic clade separated phylogenetically from other existing genera within the family *Phenuiviridae.*

Submitted: 06/05/2025; *Revised:* 19/08/2025

TABLE 8 - *Phenuiviridae*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar

New taxon	Genus	*Fusavirus*		
New taxon	Species	*Fusavirus alternariae*	Alternaria tenuissima negative-stranded RNA virus 2	L: MK584855; M: BK061363; S: BK061364
New taxon	Species	*Fusavirus yangzi*	Fusarium asiaticum mycobunyavirus 1	L: MZ969068; M: MZ969069; S: MZ969070
New taxon	Species	*Fusavirus sclerotiniae*	Sclerotinia sclerotiorum negative-stranded RNA virus 5	L: KF913892; M: BK061361; S: BK061362

2025.008M.Ac.v4.Phenuiviridae_62nsp+1asp

Title: Establish 62 new species and abolish one species in the family *Phenuiviridae*

Authors: Yasuhiro Tomitaka, Thomas Briese, Cécile Desbiez, Francesco Di Serio, Jens H. Kuhn, Dimitre Mollov, Yutaro Neriya, Jin-Won Song, Massimo Turina, Gustavo Palacios, Takahide Sasaya

Summary:Taxonomic rank(s) affected: Species

Description of current taxonomy:
Negarnaviricota, Polyplovircotina, Bunyaviricetes, Hareavirales, *Phenuiviridae*
The family *Phenuiviridae* currently includes 23 genera and 159 species.

Proposed taxonomic change(s):
Establish 62 new species in 14 established genera in the *family Phenuiviridae* and abolish one species in *the genus Laulavirus* in the *family Phenuiviridae.*

Justification:
The 62 newly discovered phenuivirids are proposed to be classified into new species in 14 phenuivirid genera on the base of phylogenetic trees constructed from their deduced RNA-directed RNA polymerase (RdRP) amino acid sequences identities. One species was abolished due to the absence of a coding-complete genome sequence of its virus.

Submitted: 07/06/2025; *Revised:* 19/10/2025

TABLE 9 - *Phenuiviridae*, 62 new taxa*. Table too large, see supplementary information sheet supp_info_tab_9

TABLE 10 - *Phenuiviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Laulavirus wardellense*

2025.009M.Ac.v4.Rhabdoviridae_4nsp

Title: Create 2 new species in the genus *Betaplatrhavirus,* 1 new species in the genus *Alphacrustrhavirus* and 1 new species in the genus *Novirhabdovirus (Mononegavirales: Rhabdoviridae)*

Authors: Peter J Walker, Nicolas Bejerman, Kim R Blasdell , Humberto Debat , Ralf G Dietzgen , Anthony R Fooks , Juliana Freitas-Astúa , Kyle Garver, Pedro L Ramos-Gonzáles, Hideki Kondo , Robert B Tesh , Noel Tordo , Nikos Vasilakis , Anna E Whitfield

Summary:

Taxonomic rank(s) affected:

Species in the *family Rhabdoviridae.*

Description of current taxonomy:

The genus *Betaplatrhavirus* is not assigned to a subfamily. It currently includes 12 species for viruses detected in platyhelminth parasites, or in gill, gut or anal swab samples taken from vertebrates.
The subfamily *Deltarhabdovirinae* currently comprises 11 genera including 38 species for viruses detected in invertebrates. These include 2 species in the genus *Alphacrustrhavirus* for viruses detected in crustaceans.
The subfamily *Gammarhabdovirinae* currently comprises 2 genera including 4 species in the genus *Novirhabdovirus* for viruses infecting or detected in ray-finned fish and 1 species in the genus *Margarhavirus* for a virus detected in freshwater molluscs.

Proposed taxonomic change(s):

Create 2 new species in the genus *Betaplatrhavirus.*
Create 1 new species in the genus *Alphacrustrhavirus.*
Create 1 new species in the *genus Novirhabdovirus.*

Justification:

Four viruses for which complete coding sequences are now available fall phylogenetically within clades representing these three genera and meet demarcation criteria for the creation of new species.

Submitted: 30/05/2025; *Revised:* 19/08/2025

TABLE 11 - *Rhabdoviridae*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Novirhabdovirus carpione*	carpione rhabdovirus	LC630942
New taxon	Species	*Alphacrustrhavirus vison*	mink stool-associated rhabdovirus	PQ182562
New taxon	Species	*Betaplatrhavirus pipistrellus*	bat-associated rhabdovirus 1	OR951391
New taxon	Species	*Betaplatrhavirus robustula*	bat-associated rhabdovirus 3	OR951389

2025.010M.N.v3.Tupavirus_1nsp

Title: Create one new species in the genus *(Mononegavirales:)*

Authors: Oksana Vernygora, Laura Bourque, Megan EB Jones, Ole Nielsen, Carissa Embury-Hyatt, Estella Moffat, Tonya Wimmer, Oliver Lung

Summary:

Taxonomic rank(s) affected:

Create a new species in the *Tupavirus* genus *(Mononegavirales:*) based on the recently sequenced dolphin tupavirus (DTV).

Description of current taxonomy:

Currently, *Tupavirus* genus comprises nine recognized species (ICTV Master Species List 40v1, 2025) described from various terrestrial mammal and avian hosts such as bats, tree shrews, rodents, and coots.

Proposed taxonomic change(s):

We propose the creation of a new species in the *Tupavirus* genus *(Mononegavirales:)* based on the recently sequenced dolphin tupavirus (DTV). The sequence was obtained from the post-mortem brain tissue of a stranded Atlantic white-sided dolphin *(Lagenorhynchus acutus).* We suggest the species name *Tupavirus delphini* in line with the new binomial species nomenclature and the specific epithet derived from the Latin for dolphin.

Justification:
The assembled DTV genome has a typical rhabdovirus structure including the coding regions for five proteins (N, P, M, G, and L) and an additional putative small hydrophobic protein (SH). The nucleotide BLAST search showed that the closest match was the member of the *Tupavirus* genus, Wenzhou Myotis laniger tupavirus 1 (GenBank accession OM030290.1), having an overall 50.72% genome-wide nucleotide identity. Amino acid sequence divergence in the N protein between the DTV and the closest BLAST match (Wufeng bat tupavirus 2; GenBank accession OQ715690.1) was 45.12%. Amino acid sequence divergence between the DTV and the closest BLAST match was 69.38% (Wufeng bat tupavirus 2; GenBank accession OQ715690.1) and 44.64% (Klamath virus; GenBank accession KM204999.1) in the G and L proteins, respectively. Dolphin tupavirus is the first known member of the *Tupavirus* genus described from an aquatic mammal host.

Submitted: 06/06/2025; *Revised:* —

TABLE 12 - *Tupavirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Tupavirus delphini*	dolphin tupavirus	PV683224

2025.011M.Ac.v3.Xinmoviridae_5ng_5nsp

Title: Create five new genera and five new species in the family *Xinmoviridae,* order: *Mononegavirales*

Authors: Stephen R Sharpe, Binit Lamichhane, Luis Hernández-Pelegrín

Summary:Taxonomic rank(s) affected: This affects the genera and species ranks *of* the *family Xinmoviridae.*

Description of current taxonomy: The family *Xinmoviridae* is currently made up of 22 genera and 25 species.

Proposed taxonomic change(s): We propose the demarcation of 5 new genera and 5 new species within the *family Xinmoviridae.*

Justification: We have based this proposal on the current demarcation criterion for species: Members of different species within a genus have RdRP amino acid identities of 66% or less, and genus: Members of different genera have RdRP amino acid identities of 60% or less.

Thus, based on the phylogenetic analysis shown in Figure 1 and BLAST match data in Table 1, we propose the demarcation of 5 new genera and 5 new species.

Submitted: 06/09/2025; *Revised:* 19/08/2025

TABLE 13 - *Xinmoviridae*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Actovirus*		

New taxon	Species	*Actovirus hainanense*	Bactrocera dorsalis borna-like virus	MN745081
New taxon	Genus	*Yahinvirus*		
New taxon	Species	*Yahinvirus chinaense*	Guiyang xinmovirus 1	MZ209642
New taxon	Genus	*Hyatvirus*		
New taxon	Species	*Hyatvirus russiaense*	Medvezhye haematopota xinmo-like virus	OR724669
New taxon	Genus	*Opavirus*		
New taxon	Species	*Opavirus hayense*	Soldier fly-associated anphevirus	PP410010
New taxon	Genus	*Omyavirus*		
New taxon	Species	*Omyavirus bahiaense*	Forcipomyiae 1 virus	BK063245

2025.012M.Ac.v2.Spinareoviridae_1nsp

Title: Create a new species in the genus *Dinovernavirus (Reovirales: Spinareoviridae)*

Authors: Qun Wu, Fei Wang, Shunlong Wang, Zhiming Yuan, Han Xia

Summary:Taxonomic rank(s) affected:
Species in the *family Spinareoviridae.*

Description of current taxonomy:
The *Spinareoviridae* family includes nine genera: *Aquareovirus* (7 species), *Coltivirus* (5 specie), *Cypovirus* (16 species), *Dinovernavirus* (1 species), *Fijivirus* (9 species), *Idnoreovirus* (5 species), *Mycoreovirus* (3 species), *Orthoreovirus* (10 species), *Oryzavirus* (2 species).

Proposed taxonomic change(s):
We propose the creation of one new species in the *genus Dinovernavirus.*

Justification:
The proposed species is distinct based on coding-complete genome sequence analyses, phylogenetic analyses, and pairwise sequence comparisons to established species in the family *Spinareoviridae.*

Submitted: —; *Revised:* 19/08/2025

TABLE 14 - *Spinareoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Dinovernavirus albopictus*	Aedes albopictus reovirus	S1: PV842502; S2: PV842503; S3: PV842504; S4: PV842505; S5: PV842506; S6: PV842507; S7: PV842508; S8: PV842509; S9: PV842510

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Animal ssRNA+ viruses Subcommittee

Contents

2025.001S.Ac.v3.Avastrovirus_1nsp

Title: Create one new species in the genus *Avastrovirus (Stellavirales: Astroviridae)*

Authors: Daisy YM Ng, Wanying Sun, Thomas HC Sit, Christopher J Brackman, Anne CN Tse, Christine HT Bui, Amy WY Tang, Andrew NC Wonf, Andrew TL Tsang, , Joe CT Koo, Samuel MS Chang, Malik Peiris, Alex WH Chin, Leo LM Poon

Summary:

Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The current taxonomy of *Astroviridae* includes three avastrovirus species.

Proposed taxonomic change(s):
We propose the establishment of a new species in the *Avastrovirus* genus, which would include the recently sequenced duck astrovirus M (DAstV-M). We suggest the species name *Avastrovirus marecae* in line with the new binomial species nomenclature. The complete genome (6,566 nt) was sequenced from fecal swab samples collected from the host falcated duck *(Mareca falcata* (Georgi, 1775))). The resulting assembled contig was compared to publicly available sequences.

Justification:

It was found that the closest match was a avastrovirus 3 isolate MPJ1364 RdRp gene, partial cds (390bp, JX985709), which had the highest nucleotide identity (93.08%) and amino acid identity (98.46%).The nucleotide identity and amino acid identity between new species and other members of the *Avastrovirus* genus are much lower. The p-distance of ORF2 between new species and each avastrovirus species was met with ICTV classification criteria, which requires the average p-distances within 0.576 to 0.742. The results of ORF2 phylogenetic analysis and genetic distance analysis indicate that DAstV-M should be classified in a fourth species in the *Avastrovirus* genus (1).

Submitted: 19/06/2025; *Revised:* 19/09/2025

TABLE 1 - *Avastrovirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Avastrovirus marecae*	duck astrovirus M	PP623814

2025.002S.Ac.v3.Mamastrovirus_8nsp_1spren

Title: In the genus *Mamastrovirus, family Astroviridae,* rename 1 species and establish 8 new species

Authors: Yulia Aleshina, Alexander N Lukashev, Torsten Seuberlich

Summary:
Taxonomic rank(s) affected: species

Description of current taxonomy: The family *Astroviridae* includes two genera *(Mamastrovirus* and *Avastrovirus) for* viruses. The genus *Mamastrovirus* includes 19 established species.

The demarcation of species according to the 9th ICTV Report (2010) was based on analysis of ORF2 sequences with consideration of the host information. Previous species criteria were vaguely defined and did not provide unambiguous assignment of recently discovered astroviruses. A few recent publications suggested more specific criteria and several novel species; however, they have not been accommodated into the formal ICTV taxonomy.

Proposed taxonomic change(s):

To establish 8 new species:

Mamastrovirus suisencephalomyelitidis
Mamastrovirus suisvulgaris
Mamastrovirus rodentiamericaense
Mamastrovirus rattorientalis
Mamastrovirus bovisamericaense
Mamastrovirus bubali
Mamastrovirus bovisorientalis
Mamastrovirus bovisencephalitidis

To rename one species:
Rename *Mamastrovirus suis* as *Mamastrovirus suisorientalis*

Justification:
292 of the complete astrovirid genomes obtained since 2011 cannot be assigned to the established species. ORF2 amino acid sequence p-distances do not provide a threshold that could reliably distinguish several established species and is of limited use to identify distinct groups among unclassified astrovirids that were isolated recently, predominantly from cattle and pigs. A 17% nucleotide sequence distance cut-off in ORF1b clearly distinguished the established species and several groups among the unclassified viruses. Recombination at the ORF1b/ORF2 was ubiquitous within, but never between established and putative new species. As each single criterion has minor exclusions, it is suggested to use collectively ORF1b genetic distance, ORF2 phylogenetic grouping, recombination patterns, and host information to assign eight new species.

Submitted: 19/06/2025; *Revised:* 19/09/2025

TABLE 2 - *Mamastrovirus*, 8 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Mamastrovirus suisencephalomyelitidis*	mamastrovirus 22; porcine astrovirus 3 isolate US-MO123	JX556691
New taxon	Species	*Mamastrovirus suisvulgaris*	mamastrovirus 26; porcine astrovirus 4 strain 35/USA	JF713713

New taxon	Species	*Mamastrovirus rodentiamericaense*	mamastrovirus 34; rodent astrovirus isolate HK-1893F	KT946733
New taxon	Species	*Mamastrovirus rattorientalis*	mamastrovirus 35; rodent astrovirus isolate HK-22103F	KT946726
New taxon	Species	*Mamastrovirus bovisamericaense*	mamastrovirus 36; bovine astrovirus strain BoAstV10/2021/CHN	ON624260
New taxon	Species	*Mamastrovirus bubali*	mamastrovirus 37; bovine astrovirus strain BoAstV69/2021/CHN	ON885949
New taxon	Species	*Mamastrovirus bovisorientalis*	mamastrovirus 38, bovine astrovirus strain BoAstV12/2021/CHN	ON624262
New taxon	Species	*Mamastrovirus bovisencephalitidis*	mamastrovirus 39, bovine astrovirus CH13	KM035759

TABLE 3 - *Mamastrovirus*, 1 rename taxon*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Species	*Mamastrovirus suisorientalis*	*Mamastrovirus suis*

2025.003S.A.v2.Paslahepevirus_1nsp

Title: Create one new virus species in genus *Paslahepevirus,* family *Hepeviridae (Hepelivirales)*

Authors: Viola C. Haring, Rainer G. Ulrich, Florian Pfaff

Summary:Taxonomic rank(s) affected: *Paslahepevirus*

Description of current taxonomy:
Riboviria › *Orthornavirae* › *Kitrinoviricota* › *Alsuviricetes* › *Hepelivirales* › *Hepeviridae* › *Orthohepevirinae* (4 genera) › *Paslahepevirus* (2 species)

Proposed taxonomic change(s):
Add one (1) new species to genus *Paslahepevirus (“Paslahepevirus crocidurae”).*

Justification:
The proposed new species is based on two newly released genome sequences in GenBank (OR713884, OR713885) that meet the current hepevirid species demarcation criteria.

Submitted: 20/06/2025; *Revised:* —

TABLE 4 - *Paslahepevirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Paslahepevirus crocidurae*	greater white-toothed shrew hepatitis E virus	OR713884

2025.004S.A.v2.Sinaivirus_2spren

Title: Rename all species in the family to comply with the ICTV-mandated binomial

Authors: Jens H Kuhn

Summary:Taxonomic rank(s) affected: *Sinaivirus*

Description of current taxonomy: Nodamuviral family *Sinhaliviridae* currently includes a single genus, *Sinaivirus,* with two species, *Lake* Sinai virus *1* and *Lake* Sinai virus *2.*

Proposed taxonomic change(s): The sinaivirus species names *Lake* Sinai virus *1* and *Lake* Sinai virus *2* will be replaced by binomial names (see Etymology section).

Justification: In March 2021, the ICTV ratified TaxoProp 2018.001G.R.binomial_species, which requires all species names to follow a new codified rule:

"A species name shall consist of only two distinct word components separated by a space. The first word component shall begin with a capital letter and be identical in spelling to the name of the genus to which the species belongs. The second word component shall not contain any suffixes specific for taxa of higher ranks. The entire species name (both word components) shall be italicized."

This rule requires most established species names to be changed. Here, we propose to change the names of the species included in family *Sinhaliviridae* following this rule by adopting binomial names.

Submitted: 20/06/2025; *Revised:* —

TABLE 5 - *Sinaivirus*, 2 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Species	*Sinaivirus apis*	*Lake Sinai virus 1*
Rename taxon	Species	*Sinaivirus sinaiense*	*Lake Sinai virus 2*

2025.005S..v1.Pestivirus_8spren

Title: Renaming species of pestiviruses

Authors: Jens H Kuhn, Martin Beer, Peter Simmonds, Anamarija Butkovic, Jens Bukh, Jan Felix Drexler, Amit Kapoor, Volker Lohmann, Donald B Smith, Jack T Stapleton, Nikolaos Vasilakis

Summary:Taxonomic rank(s) affected: *Pestivirus*

Description of current taxonomy: Most species included in the family *Flaviviridae* have been renamed according to a Latinised binomial format. This was recommended in the recent ICTV policy change towards a more uniform format for virus species names. However, several recently described and assigned species of pestiviruses *(Pestivirus L–S)* are still named using the previous [genus name + single letter] format. This is inconsistent with intention for the species epithet to be a pronounceable word, ideally in a Latinied format that is used in the rest of biology for organism scientific names,

Proposed taxonomic change(s): The pestivirus species names *Pestivirus* L – Pestivirus *S* will be replaced with whole-word species epithets (see Etymology section).

Justification: The ICTV has promoted renaming species into a more recognizable form that matches at least in part the nomenclature used in other biological codes. Most virus species have been accordingly renamed, and the current proposals simply applies this principle to pestivirus species that were described and named after the previous pestivirus renaming proposal was adopted.

Submitted: 20/06/2025; *Revised:* —

TABLE 6 - *Pestivirus*, 8 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Species	*Pestivirus steiermarkense*	*Pestivirus L*
Rename taxon	Species	*Pestivirus phocoenae*	*Pestivirus M*
Rename taxon	Species	*Pestivirus caprinae*	*Pestivirus N*
Rename taxon	Species	*Pestivirus agnis*	*Pestivirus O*
Rename taxon	Species	*Pestivirus manidae*	*Pestivirus P*
Rename taxon	Species	*Pestivirus niviventris*	*Pestivirus Q*
Rename taxon	Species	*Pestivirus apodemuris*	*Pestivirus R*
Rename taxon	Species	*Pestivirus scotophili*	*Pestivirus S*

2025.006S.Ac.v2.Amarillovirales_3reorgfam

Title: Reorganization of *Flaviviridae* (order *Amarillovirales)* and classification of 'flavi-like' viruses into three families, 12 genera, and 3 subgenera

Authors: Peter Simmonds, Anamarija Butkovic, Joe Grove, Richard Mayne, Jon CO Mifsud, Martin Beer, Jens Bukh, Jan Felix Drexler, Amit Kapoor, Volker Lohmann, Donald B Smith, Jack T Stapleton, Nikolaos Vasilakis, Jens H Kuhn

Summary:Taxonomic rank(s) affected: *Flaviviridae, Amarillovirales*

Description of current taxonomy: *Flaviviridae* is a family for non-segmented positive-sense enveloped RNA viruses many of which are significant pathogens, including hepatitis C virus and yellow fever virus. *Flaviviridae is* the sole family included in order *Amarillovirales* and is subdivided into four genera: *Orthoflavivirus,* including 52 species into which arthropod-borne and insect-specific flavivirids are classified; *Pestivirus* (19 species), *Hepacivirus* (14 species); and *Pegivirus* (11 species).

Proposed taxonomic change(s): Recent large-scale metagenomic surveys have identified many diverse RNA viruses related to classical orthoflaviviruses and pestiviruses but possessing quite different genome lengths and configurations. They have a hugely expanded host range that spans multiple animal phyla (including mollusks, cnidarians and stramenopiles), and plants.

Phylogenetic analysis of RNA-directed RNA polymerase (RdRP) hallmark gene sequences splits flavivirid and 'flavi-like' viruses into four divergent clades and multiple lineages within them. The tree is congruent with helicase gene phylogeny, PPHMM profile comparisons, and RdRP protein structure predicted relationships predicted by AlphFold2. These results support their classification into the established order, *Amarillovirales* as three separate families *(Flaviviridae, Pestiviridae,* and *Hepaciviridae),* and a total of at least 12 genera.

Justification: Although the current classified members of the *Flaviviridae* and 'flavi-like' viruses form a monophyletic group separate from other RNA viruses, they are far more divergent from each other than other RNA virus genera, supporting their assignment as three separate families and several genera within them. ***Taxonomic*** assignments based on RdRP hallmark gene evolutionary relationships provides a stable reference for assignment of further members of this order, and a framework from which major genome re-organisational events can be understood.

Submitted: 26/06/2025; *Revised:* 17/09/2025

TABLE 7 - *Amarillovirales*, 54 move taxa***.** Table too large, see supplementary information sheet supp_info_tab_7

TABLE 8 - *Amarillovirales*, 35 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old parent taxon**	**Old taxon name**
Move; rename taxon	Genus	*Orthohepacivirus*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus*
Move; rename taxon	Species	*Orthohepacivirus bovis*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus bovis*
Move; rename taxon	Species	*Orthohepacivirus colobi*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus colobi*
Move; rename taxon	Species	*Orthohepacivirus equi*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus equi*
Move; rename taxon	Species	*Orthohepacivirus glareoli*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus glareoli*
Move; rename taxon	Species	*Orthohepacivirus hominis*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus hominis*
Move; rename taxon	Species	*Orthohepacivirus macronycteridis*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus macronycteridis*
Move; rename taxon	Species	*Orthohepacivirus myodae*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus myodae*
Move; rename taxon	Species	*Orthohepacivirus norvegici*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus norvegici*
Move; rename taxon	Species	*Orthohepacivirus otomopis*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus otomopis*
Move; rename taxon	Species	*Orthohepacivirus peromysci*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus peromysci*
Move; rename taxon	Species	*Orthohepacivirus platyrrhini*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus platyrrhini*
Move; rename taxon	Species	*Orthohepacivirus ratti*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus ratti*
Move; rename taxon	Species	*Orthohepacivirus rhabdomysis*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus rhabdomysis*
Move; rename taxon	Species	*Orthohepacivirus vittatae*	*Hepaciviridae*	*Flaviviridae*	*Hepacivirus vittatae*

Move; rename taxon	Genus	*Orthopestivirus*	*Pestiviridae*	*Flaviviridae*	*Pestivirus*
Move; rename taxon	Species	*Orthopestivirus antilocaprae*	*Pestiviridae*	*Flaviviridae*	*Pestivirus antilocaprae*
Move; rename taxon	Species	*Orthopestivirus australiaense*	*Pestiviridae*	*Flaviviridae*	*Pestivirus australiaense*
Move; rename taxon	Species	*Orthopestivirus aydinense*	*Pestiviridae*	*Flaviviridae*	*Pestivirus aydinense*
Move; rename taxon	Species	*Orthopestivirus bovis*	*Pestiviridae*	*Flaviviridae*	*Pestivirus bovis*
Move; rename taxon	Species	*Orthopestivirus brazilense*	*Pestiviridae*	*Flaviviridae*	*Pestivirus brazilense*
Move; rename taxon	Species	*Orthopestivirus giraffae*	*Pestiviridae*	*Flaviviridae*	*Pestivirus giraffae*
Move; rename taxon	Species	*Orthopestivirus L*	*Pestiviridae*	*Flaviviridae*	*Pestivirus L*
Move; rename taxon	Species	*Orthopestivirus M*	*Pestiviridae*	*Flaviviridae*	*Pestivirus M*
Move; rename taxon	Species	*Orthopestivirus N*	*Pestiviridae*	*Flaviviridae*	*Pestivirus N*
Move; rename taxon	Species	*Orthopestivirus O*	*Pestiviridae*	*Flaviviridae*	*Pestivirus O*
Move; rename taxon	Species	*Orthopestivirus ovis*	*Pestiviridae*	*Flaviviridae*	*Pestivirus ovis*
Move; rename taxon	Species	*Orthopestivirus P*	*Pestiviridae*	*Flaviviridae*	*Pestivirus P*
Move; rename taxon	Species	*Orthopestivirus Q*	*Pestiviridae*	*Flaviviridae*	*Pestivirus Q*
Move; rename taxon	Species	*Orthopestivirus R*	*Pestiviridae*	*Flaviviridae*	*Pestivirus R*
Move; rename taxon	Species	*Orthopestivirus ratti*	*Pestiviridae*	*Flaviviridae*	*Pestivirus ratti*
Move; rename taxon	Species	*Orthopestivirus S*	*Pestiviridae*	*Flaviviridae*	*Pestivirus S*
Move; rename taxon	Species	*Orthopestivirus scrofae*	*Pestiviridae*	*Flaviviridae*	*Pestivirus scrofae*
Move; rename taxon	Species	*Orthopestivirus suis*	*Pestiviridae*	*Flaviviridae*	*Pestivirus suis*

Move; rename taxon	Species	*Orthopestivirus tauri*	*Pestiviridae*	*Flaviviridae*	*Pestivirus tauri*

TABLE 9 - *Amarillovirales*, 23 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subgenus	*Crangovirus*		
New taxon	Species	*Orthoflavivirus aphei*	Crangon crangon flavivirus	MK473878
New taxon	Subgenus	*Euflavivirus*		
New taxon	Subgenus	*Fusivirus*		
New taxon	Species	*Orthoflavivirus iunctionis*	cell-fusing agent virus	KJ741267
New taxon	Genus	*Jingmenvirus*		
New taxon	Species	*Jingmenvirus rhipicephali*	Jīngmén tick virus	Seg_1: KJ001579; Seg_2: KJ001580; Seg_3: KJ001581; Seg_4: KJ001582
New taxon	Genus	*Guaicovirus*		
New taxon	Species	*Guaicovirus culicis*	Guaico Culex virus	Seg_1: KM521566; Seg_2: KM521567; Seg_3: KM521568; Seg_4: KM521569; Seg_5: KM521570
New taxon	Genus	*Tamanavirus*		
New taxon	Species	*Tamanavirus parnelli*	Tamana bat virus	AF285080
New taxon	Genus	*Termitovirus*		
New taxon	Species	*Termitovirus isopterae*	waxsystermes virus	MW052131
New taxon	Family	*Hepaciviridae*		
New taxon	Family	*Pestiviridae*		
New taxon	Genus	*Arachnivirus*		
New taxon	Species	*Arachnivirus neosconae*	Xīnzhōu spider virus 3	KR902730
New taxon	Genus	*Boletivirus*		
New taxon	Species	*Boletivirus hyalommae*	Bólè tick virus 4	KR902736
New taxon	Genus	*Chrysopivirus*		
New taxon	Species	*Chrysopivirus vittae*	Shuāngào lacewing virus 2	KR902734
New taxon	Genus	*Koshovirus*		
New taxon	Species	*Koshovirus sonchi*	Sonchus virus 1	BK062903

2025.007S.A.v3.Orthoflavivirus_2nsp_1spren

Title: Reclassification of tick-borne encephalitis *viruses (Flaviviridae: Orthoflavivirus)*

Authors: Bondaryuk AN, Andaev EI, Dzhioev YP, Zlobin VI, Tkachev SE, Kozlova IV, Pestov NB, Bukin YS

Summary:
Taxonomic rank(s) affected: *Orthoflavivirus encephalitidis*

Description of current taxonomy: Currently, the species *Orthoflavivirus encephalitidis* constitutes a paraphyletic group including at least four subtypes of tick-borne encephalitis virus (TBEV) and excluding louping ill virus (LIV). Besides, there are four unclassified isolates which are phylogenetically close to LIV: Spanish sheep encephalitis virus (SSEV), Spanish goat encephalitis virus (SGEV), Turkish sheep encephalitis virus (TSEV) and Greek goat encephalitis virus (GGEV).

Proposed taxonomic change(s): To resolve the paraphyletic issue, we propose to rename *Orthoflavivirus encephalitidis* as *Orthoflavivirus* zilberi *and* to create a new species, *Orthoflavivirus neudoerflense.* According to our proposal, the demarcation threshold runs between the European subtype of TBEV *(TBEV-EU) (Orthoflavivirus neudoerflense)* and the other TBEV subtypes *(Orthoflavivirus zilberi).* Considering unclassified LIV-like isolates, we propose to fuse LIV, SSEV, SGEV in a single species, and TSEV together with GGEV should also be assigned as the separate species, *Orthoflavivirus mediterranense* to keep monophyly within the clade of TBEV+LIV+TSEV+GGEV.

Justification: Ee provided species delimitation analysis (278 complete open reading frame (ORF) amino acid sequences) and compared evolutionary protein distances of the surface antigenic determinants of the TBEV and LIV E gene (812 sequences) *in silico.* The results of both analyses show that TBEV-EU is significantly different from the other TBEV subtypes and LIV.
Our conclusion is also supported by the other species demarcation criteria for the genus *Orthoflavivirus:* disease associations (as well as tissue tropism, disease course, case fatality rate, pathogenicity for humans and animals), antigenic characteristics, geographic association, vector association and ecological characteristics.

Submitted: 02/04/2025; *Revised:* 17/09/2025

TABLE 10 - *Orthoflavivirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Orthoflavivirus neudoerflense*	tick-borne encephalitis virus 2 (tentative)	U27495
New taxon	Species	*Orthoflavivirus mediterranense*	Turkish sheep encephalitis virus	DQ235151

TABLE 11 - *Orthoflavivirus*, 1 rename taxon*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Species	*Orthoflavivirus zilberi*	*Orthoflavivirus encephalitidis*

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Archaeal viruses Subcommittee

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2025.001A.Ac.v3.crust_viruses_6nf

Title: Create 6 new families and 1 new species of viruses infecting archaea found in basalt-hosted crustal fluid

Authors: Cherise R Spotkaeff, Michael S Rappe, Grieg Steward, Olivia D Nigro

Summary:
Taxonomic rank(s) affected:
Families, genera, species

Description of current taxonomy:
Currently, there are 34 families in the class *Caudoviricetes* of archaea-infecting viruses, one representative in the genus *Yumkaaxvirus* and eight defined families of spindle-shaped viruses.

Proposed taxonomic change(s):
Create 6 new families and 1 new species for archaea-infecting viruses with predicted spindle, rod (realm: *Adnaviria),* and head-tail like (realm: *Duplodnaviria)* morphologies, identified in pristine crustal fluid collected from CORKs (Circulation Obviation Retrofit Kits).

Justification:
Though the proposed viruses share hallmark genes of their characterized taxa, they share little other genomic similarity with classified viruses. Through a combination of methods including gene-sharing network construction, analysis of gene synteny, VIPTree proteomic analysis, terminase and PolB phylogenetic reconstruction, and previously established demarcation criteria for prokaryotic viruses (specifically, for archaeal tailed viruses), we propose the classification of 11 archaea-infecting viruses for which complete genome sequences are available.

Submitted: 17/06/2025; *Revised:* 24/08/2025

TABLE 1 – *crust viruses*, 23 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Basaltiviridae*		
New taxon	Genus	*Tsigisvirus*		
New taxon	Species	*Tsigisvirus beckeri*	Bathyarchaeota virus JdFR006	PQ111734
New taxon	Species	*Tsigisvirus orcuttae*	Archaeal virus JdFR013	PQ111735
New taxon	Species	*Yumkaaxvirus juandefucaense*	Archaeal virus JdFR077	PQ111746
New taxon	Family	*Seadebiviridae*		
New taxon	Genus	*Hacxwiqakvirus*		

New taxon	Species	*Hacxwiqakvirus coweni*	Archaeal virus JdFR009	PQ111736
New taxon	Species	*Hacxwiqakvirus wheati*	Bathyarchaeota virus JdFR012	PQ111737
New taxon	Species	*Hacxwiqakvirus orphanae*	Archaeal virus JdFR114	PQ111738
New taxon	Family	*Altumviridae*		
New taxon	Genus	*Calorvirus*		
New taxon	Species	*Calorvirus huberae*	Archaeoglobus virus JdFR416	PQ111739
New taxon	Species	*Calorvirus bachi*	Uncultured archaeal virus isolate JdFR1000234	KY229235
New taxon	Family	*Jasonviridae*		
New taxon	Genus	*Obscurovirus*		
New taxon	Species	*Obscurovirus verheini*	Archaeal virus JdFR019	PQ111740
New taxon	Family	*Infernusviridae*		
New taxon	Genus	*Tanggwanvirus*		
New taxon	Species	*Tanggwanvirus davisi*	Archaeal virus JdFR002	PQ111741
New taxon	Family	*Tenebraviridae*		
New taxon	Genus	*Caldusvirus*		
New taxon	Species	*Caldusvirus fisheri*	Archaeoglobus virus JdFR005	PQ111742

2025.002A.Ac.v3.Archaeal_Caudoviricetes_8nf

Title: Eight new families of archaeal viruses within the class *Caudoviricetes*

Authors: Yifan Zhou, Ana Gutiérrez-Preciado, David Moreira, Michail M. Yakimov, Purificación López-García, Mart Krupovic

Summary:
Taxonomic rank(s) affected:
Families, genera, species

Description of current taxonomy:
Head-tailed viruses infecting halophilic archaea (class Halobacteria) are currently classified into 12 families within class *Caudoviricetes,* whereas viruses infecting nanohaloarchaeal hosts (candidate phylum Nanohaloarchaeota) remain unclassified.

Proposed taxonomic change(s):
We propose classifying 14 head-tailed viruses associated with haloarchaeal and nanohaloarchaeal hosts into 14 new species within 13 new genera, which are assigned to 8 new families and 3 existing families within the class *Caudoviricetes.*

Justification:
The classification is based on the proteome-wide phylogenomic analysis implemented in VipTree and further supported by comparative genomics analysis.

Submitted: 20/06/2025; *Revised:* 24/08/2025

TABLE 2 – *Archaeal viruses*, 35 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Danacaviridae*		
New taxon	Genus	*Gablavirus*		
New taxon	Species	*Gablavirus danakilense*	Danakil Halobacteriales tailed virus 1	PQ827553

New taxon	Family	*Dallocaviridae*		
New taxon	Genus	*Kalovirus*		
New taxon	Species	*Kalovirus danakilense*	Danakil Halobacteriales tailed virus 2	PQ827554
New taxon	Family	*Assalcaviridae*		
New taxon	Genus	*Karumvirus*		
New taxon	Species	*Karumvirus danakilense*	Danakil Halobacteriales tailed virus 6	PQ827558
New taxon	Family	*Quasboviridae*		
New taxon	Genus	*Cusbovirus*		
New taxon	Species	*Cusbovirus danakilense*	Danakil Halobacteriales tailed virus 8	PQ827560
New taxon	Family	*Gulliviridae*		
New taxon	Genus	*Lemuelvirus*		
New taxon	Species	*Lemuelvirus danakilense*	Danakil Nanohaloarchaeota tailed virus 1	PQ827565
New taxon	Genus	*Latyvirus*		
New taxon	Species	*Latyvirus nanohalovivens*	Lake Tyrrell virus 2	AKVG01000002
New taxon	Family	*Lilliviridae*		
New taxon	Genus	*Mildendovirus*		
New taxon	Species	*Mildendovirus danakilense*	Danakil Nanohaloarchaeota tailed virus 2	PQ827566
New taxon	Family	*Blefusviridae*		
New taxon	Genus	*Wecalvirus*		
New taxon	Species	*Wecalvirus danakilense*	Danakil Nanohaloarchaeota tailed virus 3	PQ827567
New taxon	Family	*Saladoviridae*		
New taxon	Genus	*Crypovirus*		
New taxon	Species	*Crypovirus alicantense*	environmental halophage eHP-23	JQ807243
New taxon	Species	*Crypovirus chilense*	Grande Nanohaloarchaeota tailed virus 1	LMAX01000001
New taxon	Genus	*Morpovirus*		
New taxon	Species	*Morpovirus danakilense*	Danakil Halobacteriales tailed virus 4	PQ827556
New taxon	Genus	*Traglyvirus*		
New taxon	Species	*Traglyvirus danakilense*	Danakil Halobacteriales tailed virus 5	PQ827557
New taxon	Genus	*Haroovirus*		
New taxon	Species	*Haroovirus danakilense*	Danakil Halobacteriales tailed virus 7	PQ827559
New taxon	Genus	*Ethicavirus*		
New taxon	Species	*Ethicavirus danakilense*	Danakil Halobacteriales tailed virus 3	PQ827555

2025.003A.Ac.v3.Tailless_icosahedral_2nf

Title: Two new families of tailless icosahedral archaeal viruses

Authors: Yifan Zhou, Ana Gutiérrez-Preciado, David Moreira, Michail M. Yakimov, Purificación López-García, Mart Krupovic

Summary:

Taxonomic rank(s) affected:
Orders, families, genera, species

Description of current taxonomy:
Class *Laserviricetes* currently includes one order, *Halopanivirales,* with 3 families of viruses infecting halophilic archaea of the class Halobacteria *(Simuloviridae* and *Sphaerolipoviridae)* and thermophilic bacteria of the genus *Thermus (Matsushitaviridae).*

Proposed taxonomic change(s):
Create two new monotypic orders, *"Salinicovirales"* and *"Ducavirales",* for classification of viruses associated with haloarchaea (new family *"Halicoviridae")* and nanohaloarchaea (new family *"Nanicoviridae"),* respectively.

Justification:
The two recently discovered viruses encode divergent single jelly-roll major capsid proteins, justifying their inclusion in the *Singelaviria* realm. However, their relationship to each other as well as to currently known members of the order *Halopanivirales* is very distant, detectable only through sensitive profile-profile comparisons and structure-based searches. Consistently, VipTree analysis showed that both viruses form distinct branches in the proteome-wide phylogenomic tree.

Submitted: 20/06/2025; *Revised:* 24/08/2025

TABLE 3 – *Tailless viruses*, 8 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Order	*Salinicovirales*		
New taxon	Family	*Halicoviridae*		
New taxon	Genus	*Ertavirus*		
New taxon	Species	*Ertavirus danakilense*	Danakil Halobacteriales icosahedral virus 1	PQ827550
New taxon	Order	*Ducavirales*		
New taxon	Family	*Nanicoviridae*		
New taxon	Genus	*Alevirus*		
New taxon	Species	*Alevirus danakilense*	Danakil Nanohaloarchaeota icosahedral virus 1	PQ827561

2025.004A.Ac.v3.Pleomorphic_1nf_2ns

Title: Create one new family and two new species within order *Haloruvirales*

Authors: Yifan Zhou, Ana Gutiérrez-Preciado, David Moreira, Michail M. Yakimov, Purificación López-García, Mart Krupovic

Summary:

Taxonomic rank(s) affected:
Families, genera, species

Description of current taxonomy:
Monodnavirian kingdom *Trapavirae* currently comprises two families, *Pleolipoviridae* (phylum *Saleviricota,* class *Huolimaviricetes,* order *Haloruvirales)* (Liu et al., 2022), which includes haloarchaeal viruses with enveloped pleomorphic virions and single-stranded (ss) or double-stranded (ds) DNA genomes, and *Thalassapleoviridae* (phylum *Calorviricota,* class *Caminiviricetes,*

order *Ageovirales)* (Baquero et al., 2024), which contains pleomorphic viruses infecting hyperthermophilic anaerobic archaea of the class Archaeoglobi. Both families comprise three genera.

Proposed taxonomic change(s):
We propose creating one new species within genus *Betapleolipovirus* (family *Pleolipoviridae)* and one new family, *"Nanopleoviridae"*, within the order *Haloruvirales,* for classification of viruses associated with archaea of the candidate phylum Nanohaloarchaeota.

Justification:
Previously established demarcation criteria for the family *Pleolipoviridae* suggested that Danakil Halobacteriales pleomorphic virus 1 should be placed within genus *Betapleolipovirus.* By contrast, Danakil Nanohaloarchaeota pleomorphic virus 1 branched outside of the *Pleolipoviridae,* suggesting that it represents a separate virus family.

Submitted: 20/06/2025; *Revised:* 24/08/2025

TABLE 4 - *Pleomorphic*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Betapleolipovirus danakilense*	Danakil Halobacteriales pleomorphic virus 1	PQ827551
New taxon	Family	*Nanopleoviridae*		
New taxon	Genus	*Milaagivirus*		
New taxon	Species	*Milaagivirus danakilense*	Danakil Nanohaloarchaeota pleomorphic virus 1	PQ827562

2025.005A.Ac.v3.Spindle-shaped_viruses_2nf_3ns

Title: Create 2 new families of spindle-shaped archaeal viruses

Authors: Yifan Zhou, Ana Gutiérrez-Preciado, David Moreira, Michail M. Yakimov, Purificación López-García, Mart Krupovic

Summary:
Taxonomic rank(s) affected:
Families, genera, species

Description of current taxonomy:
Spindle-shaped viruses of halophilic archaea are currently classified into the family *Halspiviridae,* which includes a single species, *Salterprovirus australiense.* Spindle-shaped archaeal viruses have not been assigned to any higher-level taxonomic rank.

Proposed taxonomic change(s):
We propose creating two new families for the classification of spindle-shaped viruses associated with haloarchaeal and nanohaloarchaeal hosts. The family *"Xigoviridae"* will include a single species, *"Ispindelvirus danakilense"*, whereas family *"Lomiviridae"* will include two species, *"Gomizavirus danakilense"* and *"Gomizavirus assalense".*

Justification:
Members of the proposed families *"Xigoviridae"* and *"Lomiviridae"* are not closely related to each other or to previously characterized and classified viruses, justifying the creation of the new families. This conclusion is consistent with VipTree analysis in which the two groups of viruses clustered

separately.

Submitted: 20/06/2025; *Revised:* 24/08/2025

TABLE 5 - *Spindle-shaped viruses*, 7 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Xigoviridae*		
New taxon	Genus	*Ispindelvirus*		
New taxon	Species	*Ispindelvirus danakilense*	Danakil Halobacteriales spindle-shaped virus 1	PQ827552
New taxon	Family	*Lomiviridae*		
New taxon	Genus	*Gomizavirus*		
New taxon	Species	*Gomizavirus danakilense*	Danakil Nanohaloarchaeota spindle-shaped virus 1	PQ827563
New taxon	Species	*Gomizavirus assalense*	Danakil Nanohaloarchaeota spindle-shaped virus 2	PQ827564

2025.006A.Ac.v3.Yamazakiviridae_1nf

Title: Create a new family for classification of a spindle-shaped virus infecting a hyperthermophilic archaeon *Aeropyrum pernix*

Authors: Tomohiro Mochizuki, David Prangishvili, Mart Krupovic

Summary:Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
Viruses with spindle-shaped virions are classified into 8 families, none of which has been assigned to higher-level taxonomic ranks.

Proposed taxonomic change(s):
We propose classifying Aeropyrum pernix spindle-shaped virus 1 (APSV1) into a new species within a new genus and a new *family, "Yamazakiviridae".*

Justification:
APSV1 is not closely related to other spindle-shaped viruses and in the VipTree proteomic tree the virus formed a separate branch.

Submitted: 25/06/2025; *Revised:* 24/08/2025

TABLE 6 - *Yamazakiviridae*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Yamazakiviridae*		
New taxon	Genus	*Kodayamazakivirus*		
New taxon	Species	*Kodayamazakivirus kyodaii*	Aeropyrum pernix spindle-shaped virus 1	HE580238

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Bacterial viruses Subcommittee

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2025.078B.Ac.v3.Vibrio_phages_2ng_3ns
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2025.081B.Ac.v3.Yuavirus_12ns
2025.082B.A.v2.Yuavirus_2ns
2025.083B.Uc.v3.Zimmerviridae_1nf_3nsf_4ng_9ns
2025.084B.Ac.v3.Zizhuyuanvirus_1ng_1ns
2025.085B.A.v2.Friunavirus_32ns
2025.086B.Uc.v3.Luriaviridae_1nf_3ng_1mg_12ns
2025.088B.Uc.v3.Caudoviricetes_2ng_2ns
2025.089B.Ac.v3.Acarajevirus_1ng_1ns
2025.090B.Ac.v3.Anamaviridae_1nf

2024.035B.Uc.v3.Tubulavirales_34ng_49ns

Title: Create new genera and species in order *Tubulavirales* – 34 genera and 48 species in the family *Inoviridae* and 1 species in the family *Paulinoviridae*

Authors: Petar Knezevic, Damir Gavric, , Rob Lavigne , Andrew M Kropinski , Dann Turner

Summary:Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The order *Tubulavirales* currently comprise families *Inoviridae* with 26 genera; *Plectroviridae* with four genera and *Paulinoviridae* with two genera

Proposed taxonomic change(s):
Create 38 new genera and 48 new species in the family *Inoviridae.*
Create one new species in the *family Paulinoviridae*

Justification:

Based on the indicated demarcation criteria, all new genera and species fulfil criteria for proposed classification, as shown in supplementary tables and figures. These classifications are supported by data from BLASTn, BLASTp, VIRIDIC, CoreGenes3.5 and by phylogenetic analysis of the Zot and CoaB proteins.

Submitted: 18/07/2024; *Revised:* 26/08/2025

TABLE 1 - *Tubulavirales*, 83 new taxa*. Table too large, see supplementary information sheet supp_info_tab_1

2025.001B.Ac.v3.Alphabravovirinae_1nsf_2ng_2ns

Title: Create a new subfamily *Alphabravovirinae* containing two new genera, *Siouxcentervirus and Merionvirus* and the existing genus *Mapvirus (Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The genus *Mapvirus* was originally established under the name Ff47virus in 2015 (proposal) and renamed in 2018 (proposal 2018.007B.A.v4.rename137gen6sp). The genus is currently comprised of two species. The other viruses described in this proposal are unclassified lytic siphoviruses which are related to phages of the *genus Mapvirus*

Proposed taxonomic change(s):
Create two new genera *(Siouxcentervirus, Merionvirus)* and assign these genera and *Mapvirus* to a new *subfamily, Alphabravovirinae.*

Justification: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses this proposal is in accord with the demarcation of a subfamily [8].

Submitted: —; *Revised:* 19/08/2025

TABLE 2 - *Alphabravovirinae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Alphabravovirinae*		
New taxon	Genus	*Siouxcentervirus*		
New taxon	Species	*Siouxcentervirus jacoren57*	Mycobacterium phage JacoRen57	MK279840
New taxon	Genus	*Merionvirus*		
New taxon	Species	*Merionvirus boshow*	Mycobacterium phage NoShow	ON108645

TABLE 3 - *Alphabravovirinae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Mapvirus*	*Alphabravovirinae*

2025.002B.Ac.v3.Alvaradovirinae_1nsf_3ng_10ns

Title: Create a new subfamily, *Alvaradovirinae,* with three genera in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru, Anca M. Segall, Johannes Wittmann

Summary:

Taxonomic rank(s) affected:
Subfamily, genus and species

Description of current taxonomy:
Achromobacter phage JWX belongs to the genus *Steinhofvirus* which was created via Taxonomy Proposals 2018.007B.A.v4.rename137gen6sp and 2016.020a-dB.A.v1.Jwxvirus. This genus currently contains two species: *Steinhofvirus JWX* and *Steinhofvirus sv8324*

Proposed taxonomic change(s):
To create a new subfamily *"Alvaradovirinae"* with three genera *"Steinhofvirus", "Amaduovirus" and "Nyaakvirus";* and move *Steinhofvirus sv8324* to the *genus "Amaduovirus"*

Justification: In keeping with the criteria established [3] and supported by VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses we have sufficient evidence to support the creation of this new subfamily, genera and associated species

Submitted: 15/06/2025; *Revised:* 28/08/2025

TABLE 4 - *Alvaradovirinae*, 14 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Alvaradovirinae*		
New taxon	Species	*Steinhofvirus SE2*	Achromobacter phage SE2	OQ817844
New taxon	Genus	*Amaduovirus*		
New taxon	Species	*Amaduovirus AMA2*	Achromobacter phage AMA2	MT241607
New taxon	Genus	*Nyaakvirus*		
New taxon	Species	*Nyaakvirus tuull*	Achromobacter phage tuull	OR396896
New taxon	Species	*Nyaakvirus Axy06*	Achromobacter phage vB_AxyS_19-32_Axy06	MK962627
New taxon	Species	*Nyaakvirus ehaak*	Achromobacter phage ehaak_LB5	OQ817833
New taxon	Species	*Nyaakvirus emuu*	Achromobacter phage emuu_LB7	OQ817834
New taxon	Species	*Nyaakvirus ama1*	Achromobacter phage AMA1	MT241605
New taxon	Species	*Nyaakvirus maay*	Achromobacter phage maay_LB1	OQ817838
New taxon	Species	*Nyaakvirus Axy14*	Achromobacter phage vB_AxyS_19-32_Axy14	MK962633
New taxon	Species	*Nyaakvirus nyaak*	Achromobacter phage nyaak_TL1	OQ817839
New taxon	Species	*Nyaakvirus ART*	Achromobacter phage vB_Ade_ART	MH746817

TABLE 5 - *Alvaradovirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Steinhofvirus*	*Alvaradovirinae*

TABLE 6 - *Alvaradovirinae*, 1 move; rename taxon*

Operation	Rank	New taxon name	New parent taxon	Old taxon name

Move; rename taxon	Species	*Amaduovirus sv8324*	*Alvaradovirinae*	*Steinhofvirus sv8324*

2025.004B.Ac.v3.Shangdongvirus_3ns

Title: To create three new species, in the genus *Shangdongvirus* (class *Caudoviricetes)*

Authors: Sezin Ünlü, Aylin Üsküdar Güçlü

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The virus classified in this proposal does not have a current taxonomic assignment. The *genus Shangdongvirus was* created in 2023 and currently includes a single species (

Proposed taxonomic change(s):
We propose three new species in the genus *Shandongvirus*

Justification:
Phylogenetic, VIRIDIC, and vConTACT2 analysis of a newly isolated phage Baskent_P4_1 infecting *Pseudomonas aeruginosa* suggests that this phage is related to three other bacterial viruses; *Pseudomonas* phage PSASB_03, *Stenotrophomonas* phage vB_SM_ytsc_ply2008005c and *Stenotrophomonas* vB_SmaS_Bhz54. Analysis of genome similarity, TBLASTX distances and phylogeny of the major capsid protein supports its inclusion as new species in the genus *Shangdongvirus.*

Submitted: 14/04/2025; *Revised:* 18/08/2025

TABLE 7 - *Shangdongvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Shangdongvirus baskent*	Pseudomonas phage Baskent_P4_1	PP992516
New taxon	Species	*Shangdongvirus kolkata*	Pseudomonas phage PSASB_03	PQ621116
New taxon	Species	*Shangdongvirus braunschweig*	Stenotrophomonas phage vB_SmaS_Bhz54	OR797041

2025.005B.Ac.v3.Aussievirus_1ng_2ns

Title: Create one new genus *Aussievirus* with two species (class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes*

Description of current taxonomy:
The viruses described in this proposal are unclassified.

Proposed taxonomic change(s):
To create a new genus, *"Aussievirus"*, with two new species

Justification:
On the basis of VIRIDIC and ViPTree analysis and in keeping with the demarcation criteria described below we have created a new genus for two temperate phages of *Sinorhizobium meliloti.*

Submitted: —; *Revised:* 19/08/2025

TABLE 8 - *Aussievirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Aussievirus*		
New taxon	Species	*Aussievirus aussie*	Sinorhizobium phage Aussie	OR786373
New taxon	Species	*Aussievirus stopsmel*	Sinorhizobium phage StopSmel	OR786374

2025.006B.Uc.v3.Buchnerviridae_1nf_6ng_1mg_1mrs_13ns

Title: Create a new family *(Buchnerviridae)* with seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus)* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
According to the current taxonomy, the genus *Vieuvirus* has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Vieuvirus* genus includes two species: *Vieuvirus R3177* and *Vieuvirus B1251.*

Proposed taxonomic change(s):
Create new family *(Buchnerviridae)* with seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus)* for a group of *Acinetobacter-specific* phages (realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Vieuvirus.* Based on our analysis, we propose the creation of a family for these phages along with seven distinct genera.

To create a new family, *Buchnerviridae,* with seven genera.
To create a new single species genus, *Slezavirus.*
To create a new genus *Olaviavirus,* with six species.
To create a new single species genus, *Valdenburkvirus.*
To create a new genus *Svidnicavirus,* with two species.
To create a new single species genus, *Lubinvirus.*
To move the genus *Vieuvirus* to new family, *Buchnerviridae.*
To move *Vieuvirus R3177* from *Vieuvirus* genus and rename to new *Jauervirus* genus with one species

(Jauervirus R3177).
To create one new species in *genus Vieuvirus.*

Justification:
After examination of 20 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Buchnerviridae,* to accommodate seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 24/03/2025; *Revised:* 22/10/2025

TABLE 9 - *Buchnerviridae*, 19 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Buchnerviridae*		
New taxon	Genus	*Slezavirus*		
New taxon	Species	*Slezavirus Ab1052phi*	Acinetobacter phage Ab105-2phi	KT588075
New taxon	Genus	*Olaviavirus*		
New taxon	Species	*Olaviavirus phi5013M1*	Acinetobacter phage phi5013-M1	PQ432284
New taxon	Species	*Olaviavirus phi4197*	Acinetobacter phage phi4197	PQ432283
New taxon	Species	*Olaviavirus phi5013M2*	Acinetobacter phage phi5013-M2	PQ432285
New taxon	Species	*Olaviavirus Ab11510phi*	Acinetobacter phage Ab11510-phi	MT361972
New taxon	Species	*Olaviavirus phi503811536*	Acinetobacter phage phi5038-11536	PQ432286
New taxon	Species	*Olaviavirus phi503811551*	Acinetobacter phage phi5038-11551	PQ432288
New taxon	Genus	*Valdenburkvirus*		
New taxon	Species	*Valdenburkvirus Acba23*	Acinetobacter phage Acba_23	PV067694
New taxon	Genus	*Svidnicavirus*		
New taxon	Species	*Svidnicavirus Ftm*	Acinetobacter phage vB_AbaS_Ftm	PP236950
New taxon	Species	*Svidnicavirus Eva*	Acinetobacter phage vB_AbaS_Eva	PP236951
New taxon	Genus	*Lubinvirus*		
New taxon	Species	*Lubinvirus Ab16562*	Acinetobacter phage Ab1656-2	MZ675741
New taxon	Species	*Vieuvirus A24903*	Acinetobacter phage A2490.3	OR180313
New taxon	Genus	*Jauervirus*		

TABLE 10 - *Buchnerviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Vieuvirus*	*Buchnerviridae*

TABLE 11 - *Buchnerviridae*, 1 move; rename taxon*

Operation	Rank	New taxon name	New parent taxon	Old taxon name
Move; rename taxon	Species	*Jauervirus R3177*	*Buchnerviridae*	*Vieuvirus R3177*

2025.007B.Ac.v3.Cardingvirinae_1nsf_2ng_18ns

Title: Create a new subfamily *(Cardingvirinae)* with two genera and 18 species *(Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Nina Chanisvili

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
There is no current taxonomy for these lytic phages isolated against *Bacteroides fragilis*

Proposed taxonomic change(s):
Add two new genera, *"Kherlenvirus"* and *"Gotuavirus",* and 18 new species to a new *subfamily "Cardingvirinae"*

Justification: On the basis of VIRIDIC, CoreGenes and phylogenetic analyses and in keeping with the criteria which we have established for creation of new species, genera and subfamilies these previously unclassified Bacteroides lytic siphoviruses belong to two genera in a new subfamily [8].

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 12 - *Cardingvirinae*, 21 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Cardingvirinae*		
New taxon	Genus	*Kherlenvirus*		
New taxon	Species	*Kherlenvirus BF486P1*	Bacteroides phage BF486P1	OP172666
New taxon	Species	*Kherlenvirus BK649P1*	Bacteroides phage BK649P1	OP172680
New taxon	Species	*Kherlenvirus BF695P2*	Bacteroides phage BF695P2	OP172673
New taxon	Species	*Kherlenvirus BF698P1*	Bacteroides phage BF698P1	OP172675
New taxon	Species	*Kherlenvirus BF698P3*	Bacteroides phage BF698P3	OP172676
New taxon	Genus	*Gotuavirus*		
New taxon	Species	*Gotuavirus B408*	Bacteroides phage B40-8	FJ008913
New taxon	Species	*Gotuavirus BF10P2*	Bacteroides phage BF10P2	OP172663
New taxon	Species	*Gotuavirus BF10P3*	Bacteroides phage BF10P3	OP172664
New taxon	Species	*Gotuavirus BF766P1*	Bacteroides phage BF766P1	OP172678
New taxon	Species	*Gotuavirus VA7*	Bacteroides phage GEC_vB_Bfr_VA7	MW916539
New taxon	Species	*Gotuavirus Barc2635*	Bacteroides phage Barc2635	MN078104
New taxon	Species	*Gotuavirus NCTC*	Bacteroides phage vB_BfraS_NCTC	MW314138
New taxon	Species	*Gotuavirus BF344P1*	Bacteroides phage BF344P1	OP172665
New taxon	Species	*Gotuavirus BF766P4*	Bacteroides phage BF766P4	OP172679
New taxon	Species	*Gotuavirus BF702P1*	Bacteroides phage BF702P1	OP172677
New taxon	Species	*Gotuavirus B12414*	Bacteroides phage B124-14	HE608841
New taxon	Species	*Gotuavirus gv23*	Bacteroides phage vB_BfrS_23	MT630433
New taxon	Species	*Gotuavirus UZM3*	Bacteroides phage vB_BfrS_UZM3	OQ116603

2025.008B.Ac.v2.Caudoviricetes_11ns

Title: To create eleven new species in the Class *Caudoviricetes*

Authors: Andrew D. Millard, Andrew M. Kropinski, , , , , ,

Summary:Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses detailed in this proposal are currently unclassified.

Proposed taxonomic change(s):
Add one new species to the genus *Maaswegvirus*
Add one new species to the genus *Efquatrovirus*
Add one new species to the genus *Kuravirus*
Add one new species to the genus *Gilesvirus*
Add one new species to the genus *Karamvirus*
Add one new species to the genus Nanditavirus
Add one new species to the genus Corndogvirus
Add one new species to the genus Birdsnestvirus
Add one new species to the genus Przondovirus
Add one new species to the genus Rosenblumvirus
Add one new species to the genus Tequatrovirus

Justification:
These new taxa were identified using taxMyPhage which shows 96.7% accuracy at the genus level and 97.9% accuracy at the species level. The system also detects inconsistencies in current ICTV classifications, identifying cases where genera did not adhere to ICTV's 70% inter-genomic similarity threshold for genus classification or 95% similarity for species. Each of the bacteriophages detailed in this proposal fall within the demarcation criteria for inclusion as new species in existing genera within the class *Caudoviricetes.*

Submitted: 05/06/2025; *Revised:* 26/08/2025

TABLE 13 - *Caudoviricetes*, 11 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Maaswegvirus centimanus*	Klebsiella phage vB_KpM_Centimanus	OZ240615
New taxon	Species	*Efquatrovirus MFDL*	Enterococcus phage vB_EfaS_MF-DL	PQ799575
New taxon	Species	*Kuravirus PE006*	Escherichia phage vB_EcoM_PE006	PQ812250
New taxon	Species	*Gilesvirus ZM2*	Mycobacterium phage ZM2	PQ821648
New taxon	Species	*Karamvirus id4496*	Enterobacter phage vB_Ecl_id4496	PQ824230
New taxon	Species	*Nanditavirus quinnavery*	Arthrobacter phage QuinnAvery	PQ844483
New taxon	Species	*Corndogvirus vagabond*	Mycobacterium phage Vagabond	PQ844484
New taxon	Species	*Birdsnestvirus hashim76*	Mycobacterium phage Hashim76	PQ844485
New taxon	Species	*Przondovirus HJK2*	Klebsiella phage HJK2	PQ858442
New taxon	Species	*Rosenblumvirus cap046*	Staphylococcus phage CapO46	PV007823
New taxon	Species	*Tequatrovirus BMB16*	Escherichia phage vB_EcoM_BMB16	PV102577

2025.009B.Ac.v3.Ceeteevirinae_1nsf_1ng_15ns

Title: Create one new genus, *Margaretvirus,* with seven species in a new subfamily, *Ceeteevirinae* (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

Summary:

Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy: These are unclassified lytic siphoviruses which are related to *Aziravirus, Ponsvirus and Emalynvirus*

Proposed taxonomic change(s): Create a new genus *(Margaretvirus)* and cluster it with *Aziravirus,* Ponsvirus *and Emalynvirus* in a new *subfamily, Ceeteevirinae.*

Justification: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in accord with the criteria for the establishment of new species, genera and subfamilies this group of viruses belong to a new subfamily which we have chosen to call *Ceeteevirinae* after Cluster CT in the Actinobacteriophage Database[8].

Submitted: —; *Revised:* 19/08/2025

TABLE 14 - *Ceeteevirinae*, 17 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Ceeteevirinae*		
New taxon	Species	*Aziravirus fribs8*	Gordonia phage Fribs8	OR553910
New taxon	Species	*Aziravirus nibbles*	Gordonia phage Nibbles	OR253918
New taxon	Species	*Ponsvirus manor*	Gordonia phage MAnor	PQ184784
New taxon	Species	*Ponsvirus summitacademy*	Gordonia phage SummitAcademy	OP297531
New taxon	Species	*Ponsvirus elinal*	Gordonia phage Elinal	OR553897
New taxon	Species	*Emalynvirus swatntears*	Gordonia phage SweatNTears	MK967383
New taxon	Species	*Emalynvirus billdoor*	Gordonia phage BillDoor	PP208920
New taxon	Species	*Emalynvirus tolls*	Gordonia phage Tolls	MW862988
New taxon	Genus	*Margaretvirus*		
New taxon	Species	*Margaretvirus orla*	Gordonia phage Orla	MT889367
New taxon	Species	*Margaretvirus yakult*	Gordonia phage Yakult	MK875791
New taxon	Species	*Margaretvirus margaret*	Gordonia phage Margaret	MH271302
New taxon	Species	*Margaretvirus ranchparmcat*	Gordonia phage RanchParmCat	PQ868985
New taxon	Species	*Margaretvirus GiKK*	Gordonia phage GiKK	OL455888
New taxon	Species	*Margaretvirus button*	Gordonia phage Button	ON970621
New taxon	Species	*Margaretvirus jamzy*	Gordonia phage Jamzy	OR159649

TABLE 15 - *Ceeteevirinae*, 3 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Aziravirus*	*Ceeteevirinae*
Move taxon	Genus	*Ponsvirus*	*Ceeteevirinae*

Move taxon	Genus	*Emalynvirus*	*Ceeteevirinae*

2025.011B.Ac.v3.Chaseviridae_1ng_12ns

Title: Add species to existing genera in the family *Chaseviridae* and create one new genus, *Qiaoyingvirus* (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Hany Anany

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The family *Chaseviridae* was created through Taxonomy Proposal 2019.047B. The family currently consists of two subfamilies *(Cleopatravirinae* and *Nefertitivirinae)* and 13 genera.

Proposed taxonomic change(s):
Add new species to the genera *Fifivirus,* Loessnervirus, Carltongylesvirus *Longwangvirus* and *Shantouvirus;* and create a new genus *"Qiaoyingvirus"*

Justification:
Species included in the family *Chaseviridae* are myoviruses which infect members of the genera *Escherichia,* Erwinia, Pectobacterium, *Shewanella* and *Aeromonas.* Common proteins include a RNA polymerase, DNA polymerase, primase and exonuclease. This proposal adds new species to several existing genera and creates one new genus. These genomes satisfy the existing demarcation criteria for the creation of new species and genera.

Submitted: 15/05/2025; *Revised:* 25/08/2025

TABLE 16 - *Chaseviridae*, 13 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Fifivirus EaPF7*	Erwinia phage EaPF7	PQ431420
New taxon	Species	*Fifivirus aioli*	Erwinia phage Aioli	OQ818694
New taxon	Species	*Fifivirus SNUABM27*	Erwinia phage pEa_SNUABM_27	MW349138
New taxon	Species	*Loessnervirus papaline*	Erwinia phage Papaline	OQ818704
New taxon	Species	*Loessnervirus fougasse*	Erwinia phage Fougasse	OQ818698
New taxon	Species	*Carltongylesvirus YSF*	Escherichia phage Ecp_YSF	OR327751
New taxon	Species	*Carltongylesvirus FXie2024a*	Escherichia phage FXie-2024a	PP107930
New taxon	Species	*Carltongylesvirus JL1*	Escherichia phage vB_EcoM_JL1	OR791690
New taxon	Species	*Carltongylesvirus EcoM1*	Escherichia phage EcoM1	PQ818760
New taxon	Genus	*Qiaoyingvirus*		
New taxon	Species	*Qiaoyingvirus A050*	Aeromonas phage phiA050	PP763568
New taxon	Species	*Longwangvirus h1*	Aeromonas phage vB_AhydM-H1	OR795024
New taxon	Species	*Shantouvirus LA93P1*	Aeromonas phage LA93P1	PV258714

2025.012B.Ac.v3.Comeauvirus_1ng_2ns

Title: Create one new genus *Comeauvirus* with two new species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
Create a new genus *"Comeauvirus"* and two new species

Justification:
The majority of the *Vibrio cholerae* phages that we have classified are siphoviruses, while the ones belonging to the proposed genus, "Comeauvirus" are small lytic myoviruses. VIRIDIC and ViPTree analyses reveal that this forms a genus in a cluster of phages including *Yokohamavirus PEi21, Yokohamavirus MSW3* and *Iodovirus PLPE*

Submitted: —; *Revised:* —

TABLE 17 - *Comeauvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Comeauvirus*		
New taxon	Species	*Comeauvirus cv138*	Vibrio phage vB_VchM-138	JQ177064
New taxon	Species	*Comeauvirus CPT1*	Vibrio phage CP-T1	JQ177061

2025.013B.Uc.v4.Crassvirales_reorganisation

Title: Reclassifying the order *Crassvirales* to establish two sister orders and one sister family, with the creation of six new families, 38 new genera, and 99 new species

Authors: Fabian TS Bastiaanssen, Rémi Denise, George S Bouras, Steven R Stockdale, Robert A Edwards, Colin Hil, Andrey N Shkoporov,

Summary:
Taxonomic rank(s) affected:
Realm: Duplodnaviria; Kingdom: Heunggongvirae; Phylum: Uroviricota; Class: *Caudoviricetes;* Order: *Crassvirales*

Description of current taxonomy:
Crassvirales was established under taxonomic proposal 2021.022B

Proposed taxonomic change(s):
We propose:
The establishment of demarcation criteria for the order *Crassvirales*
The establishment of the order *Paracrassvirales* containing one novel family
The establishment of the order *Metacrassvirales* containing one novel family
The adjustment of demarcation criteria for families within *Crassvirales*
The creation of one new family within *Crassvirales*
The moving and renaming of one genus within *Crassvirales*
The adjustment of demarcation criteria for subfamilies within *Crassvirales*

The adjustment of demarcation criteria for genera within *Crassvirales* to reflect ICTV guidelines
The creation of 38 new genera
The adjustment of demarcation criteria for species within *Crassvirales* to reflect ICTV guidelines
The creation of 99 new species

Justification:
Currently, *Crassvirales* lacks demarcation criteria. The existing criteria within *Crassvirales* are ambiguous, unintuitive and based on outdated methods and results. Phylogenetic trees utilizing structural and maximum likelihood approaches based on marker genes reveal the formation of unique clades that align with the proposed orders and support the proposed changes to family, genus and species demarcation criteria.

Submitted: 22/06/2025; *Revised:* 29/10/2025

TABLE 18 - *Crassvirales*, 108 new taxa*. Table too large, see supplementary information sheet supp_info_tab_18

TABLE 19 - *Crassvirales*, 26 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old parent taxon**	**Old taxon name**
Move; rename taxon	Species	*Smehivirus intestinihominis*	*Darmviridae*	*Suoliviridae*	*Burzaovirus intestinihominis*
Move; rename taxon	Species	*Scendivirus animalis*	*Darmviridae*	*Suoliviridae*	*Buhlduvirus animalis*
Move; rename taxon	Species	*Arseivirus communis*		*Coarsevirinae*	*Junduvirus communis*
Move; rename taxon	Species	*Flerehovirus oralis*		*Asinivirinae*	*Kahnovirus oralis*
Move; rename taxon	Species	*Sdahravirus coli*	*Darmviridae*	*Suoliviridae*	*Burzaovirus coli*
Move; rename taxon	Species	*Cervivirus coli*		*Bearivirinae*	*Afonbuvirus coli*
Move; rename taxon	Species	*Ponsivirus faecalis*		*Loutivirinae*	*Buchavirus faecalis*
Move; rename taxon	Species	*Ildiruevirus splanchnicus*		*Loutivirinae*	*Buchavirus splanchnicus*
Move; rename taxon	Species	*Ildiruevirus oralis*		*Loutivirinae*	*Buchavirus oralis*
Move; rename taxon	Species	*Ildiruevirus coli*		*Loutivirinae*	*Buchavirus coli*
Move; rename taxon	Species	*Snepbuvirus splanchnicus*		*Asinivirinae*	*Kehishuvirus splanchnicus*

Move; rename taxon	Species	*Burzaovirus faecalis*	*Darmviridae*	*Suoliviridae*	*Burzaovirus faecalis*
Move; rename taxon	Species	*Ibumevirus hominis*		*Uncouvirinae*	*Birpovirus hominis*
Move; rename taxon	Species	*Buhlduvirus porcinus*	*Darmviridae*	*Suoliviridae*	*Buhlduvirus porcinus*
Move; rename taxon	Species	*Cacepaovirus simiae*	*Darmviridae*	*Suoliviridae*	*Cacepaovirus simiae*
Move; rename taxon	Species	*Snuvovirus hominis*		*Uncouvirinae*	*Aurodevirus hominis*
Move; rename taxon	Species	*Wiibonovirus intestinalis*		*Churivirinae*	*Jahgtovirus intestinalis*
Move; rename taxon	Species	*Sulruvirus americanus*		*Loutivirinae*	*Blohavirus americanus*
Move; rename taxon	Species	*Trofluuvirus faecalis*		*Boorivirinae*	*Canhaevirus faecalis*
Move; rename taxon	Species	*Chuhaivirus simiae*	*Darmviridae*	*Suoliviridae*	*Chuhaivirus simiae*
Move; rename taxon	Species	*Taduhovirus hiberniae*		*Uncouvirinae*	*Aurodevirus hiberniae*
Move; rename taxon	Species	*Shuolduvirus copri*		*Loutivirinae*	*Buchavirus copri*
Move; rename taxon	Species	*Horekuvirus hominis*		*Loutivirinae*	*Buchavirus hominis*
Move; rename taxon	Species	*Horekuvirus hiberniae*		*Loutivirinae*	*Buchavirus hiberniae*
Move; rename taxon	Species	*Shelovirus americanus*		*Boorivirinae*	*Culoivirus americanus*
Move; rename taxon	Species	*Shelovirus intestinalis*		*Boorivirinae*	*Culoivirus intestinalis*

TABLE 20 - *Crassvirales*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Subfamily	*Oafivirinae*	*Darmviridae*	*Suoliviridae*

2025.014B.Ac.v3.Dravavirinae_1nsf_3ng_5ns

Title: Create a new subfamily *Dravavirinae* with three new genera *(Hualiencityvirus, Rodicavirus* and *Tongtianvirus)* and five species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Maja Rupnik, Tomaž Accetto

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The lytic siphophages isolated against *Bacteroides,* Parabacteroides, *Elizabethkingia* and *Alistipes (Order Bacteroidales)* described in this proposal are currently unclassified.

Proposed taxonomic change(s):
Create three new genera, *"Hualiencityvirus", "Tongtianvirus"* and *"Rodicavirus"* consisting of five new species and assign them to a new *subfamily, "Dravavirinae"*

Justification:
These five viruses are lytic, possess a siphophage morphology and have ca. 44.5 kb genomes. On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in keeping with our definitions for what constitute a subfamily, we propose to create *"Dravavirinae"* with three genera *"Hualiencityvirus", "Tongtianvirus"* and *"Rodicavirus"*

Submitted: 15/06/2025; *Revised:* —

TABLE 21 - *Dravavirinae*, 9 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Dravavirinae*		
New taxon	Genus	*Hualiencityvirus*		
New taxon	Species	*Hualiencityvirus TCUEAP2*	Elizabethkingia phage TCUEAP2	OK632025
New taxon	Genus	*Tongtianvirus*		
New taxon	Species	*Tongtianvirus AS73P1*	Alistipes phage AS73P1	OP172640
New taxon	Genus	*Rodicavirus*		
New taxon	Species	*Rodicavirus PD491P1*	Parabacteroides phage PD491P1	OP172815
New taxon	Species	*Rodicavirus PDS1*	Parabacteroides phage PDS1	MN929097
New taxon	Species	*Rodicavirus C185S2P*	Bacteroides phage C1_85S2P	OR296437

2025.015B.Ac.v3.Drulisvirus_1ns

Title: Create one new species in the genus *Drulisvirus*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The genus *Drulisvirus* currently includes 19 species and is included in the subfamily Slopekvirinae,

family *Autoscriptoviridae, order Autographivirales*

Proposed taxonomic change(s):
Create one new species, *Drulisvirus workingina*

Justification:
Escherichia phage vB_VIPECOTPH05B was isolated from Tarlac Provincial Hospital, Tarlac, Philippines. Based on VIRIDIC analysis with other species in the genus *Drulisvirus,* we propose the creation of a new phage species, *Drulisvirus workingina* in honor of the working mothers and diverse individuals of the Virology and Vaccine Institute of the Philippines Program.

Submitted: 04/12/2025; *Revised:* —

TABLE 22 - *Drulisvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Drulisvirus workingina*	Escherichia phage vB_VIPECOTPH05B	PQ429080

2025.016B.Ac.v3.Durvirinae_1nsf_5ng_9ns

Title: Create a new subfamily, *Durvirinae,* with six genera (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified. These lytic siphoviruses are peripherally related to the genus *Sourvirus* (Taxonomy Protocol 2018.122B.A.v1.Sourvirus)

Proposed taxonomic change(s):
Create a new subfamily *("Durvirinae")* with *Sourvirus* and five new proposed genera, *"Mossrosevirus", "Ligmavirus"* , *"Nhagosvirus", "Anclarvirus"* and *Duluthvirus"* based upon The Actinobacteriophage Database Cluster DR phages.

Justification: On the basis of VIRIDIC, ViPTree and phylogenetic analyses we recognize that the lytic siphoviruses belonging to The Actinobacteriophages Database Cluster DR represent five new genera *("Mossrosevirus", "Ligmavirus", "Nhagosvirus", "Anclarvirus"* and *"Duluthvirus")* and propose to cluster these in a new subfamily *"Durvirinae"* with members of the *Sourvirus.*

Submitted: —; *Revised:* 20/08/2025

TABLE 23 - *Durvirinae*, 15 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Durvirinae*		
New taxon	Genus	*Ligmavirus*		
New taxon	Species	*Ligmavirus ligma*	Gordonia phage Ligma	OM105886
New taxon	Species	*Ligmavirus mariokart*	Gordonia phage Mariokart	MT657335
New taxon	Genus	*Mossrosevirus*		

New taxon	Species	*Mossrosevirus mossrose*	Gordonia phage MossRose	OR253912
New taxon	Species	*Mossrosevirus caib*	Gordonia phage CaiB	ON108644
New taxon	Species	*Mossrosevirus makomanhole*	Gordonia phage MakoManhole	PQ184807
New taxon	Genus	*Nhagosvirus*		
New taxon	Species	*Nhagosvirus nhagos*	Gordonia phage Nhagos	MN369758
New taxon	Genus	*Anclarvirus*		
New taxon	Species	*Anclarvirus anclar*	Gordonia phage AnClar	MN908693
New taxon	Species	*Anclarvirus biggitybass*	Gordonia phage BiggityBass	ON260813
New taxon	Genus	*Duluthvirus*		
New taxon	Species	*Duluthvirus littlemuchkin*	Gordonia phage LittleMunchkin	OP751153

TABLE 24 - *Durvirinae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Sourvirus*	*Durvirinae*

2025.017B.Ac.v3.Evaavirus_1ng_1ns

Title: Create one new genus, *Evaavirus,* with a single species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create one new genus, *"Evaavirus"* including one new species.

Justification: While the Actinobacteriophage Database groups lytic Gordonia phage Evaa in Cluster DR our BLASTN analysis reveals that it is sufficiently different from *Sourvirus* to deserve recognition as a separate genus. This is supported by VIRIDIC analysis which reveals that it only shares 44% overall DNA sequence identity with *Sourvirus sour.*
Submitted: —; *Revised:* 18/08/2025

TABLE 25 - *Evaavirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Evaavirus*		
New taxon	Species	*Evaavirus evaa*	Gordonia phage Evaa	OP434461

2025.018B.Ac.v3.Felixounavirus_3ns

Title: Create three new species in the genus *Felixounavirus* (class *Caudoviricetes,* family *Andersonviridae,* subfamily *Ounavirinae)*

Authors: Emilia Andrea V. Sabban, Stephen Kyle C. Arcan, Adonis N. Eclipse, Dexter Bryan L. Esliza, Paul Jeremy C. Lanete, Lindley C. Susi, Gelito Joseph M. Sikat

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Felixounavirus* currently includes 97 species.

Proposed taxonomic change(s):
Add three new species, *Felixounavirus vipecomarii, Felixounavirus vipecomesa* and *Felixounavirus vipecohospii* to the *genus Felixounavirus.*

Justification:
Three new species within the genus *Felixounavirus* are proposed based on the species demarcation criteria of <95% intergenomic similarity. Escherichia phages vB_EcoM_D4, vB_EcoM_E9, and vB_EcoM_H12 are closely related to *Felixounavirus TP1* (GenBank NC_041979.1), exhibiting 92.2% intergenomic similarity.

Submitted: 29/08/2024; *Revised:* 26/08/2025

TABLE 26 - *Felixounavirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Felixounavirus vipecomarii*	Escherichia phage vB_EcoM_D4	PP886228
New taxon	Species	*Felixounavirus vipecomesa*	Escherichia phage vB_EcoM_E9	PP886229
New taxon	Species	*Felixounavirus vipecohospii*	Escherichia phage vB_EcoM_H12	PP952733

2025.019B.Ac.v3.Fenglinvirus_1ng_1ns

Title: Create one new genus *(Fenglinvirus)* with one species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
Create one new genus *"Fenglinvirus"* and one new species

Justification:
Bacillus alcalophilus CGMCC 1.3604 possesses two Mu-like transposable prophages now identified in GenBank as Bacillus phage BalMu-1 copy 1 (KP063902; 39873 bp; and NC_030945.1; Exemplar) and Bacillus phage BalMu-1 copy 2 (KP063903; 39861 bp). We have chosen the first mentioned as the exemplar.

Submitted: —; *Revised:* 19/08/2025

TABLE 27 - *Fenglinvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Fenglinvirus*		
New taxon	Species	*Fenglinvirus BalMu1*	Bacillus phage BalMu-1	KP063902

2025.020B.Ac.v3.Frobishervirinae_1nsf_1ng_1ns

Title: Create a new subfamily, *Frobishervirinae* with one existing *genus, Samwavirus,* and one new genus, *Branvirus* (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The genus *Samwavirus* was created via Taxonomy Proposal 2019.027B and contains five species. *Corynebacterium* phage Bran is currently unclassified.

Proposed taxonomic change(s):
Create a new subfamily *"Frobishervirinae"* containing one new genus *"Branvirus"* with a single species. Move the existing genus *Samwavirus* into the *subfamily "Frobishervirinae"*

Justification: VIRIDIC and Clinker analyses reveal that there is sufficient evidence to create a subfamily for Branvirus and *Samwavirus* [8]

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 28 - *Frobishervirinae*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Frobishervirinae*		
New taxon	Genus	*Branvirus*		
New taxon	Species	*Branvirus bran*	Corynebacterium phage Bran	MK977714

TABLE 29 - *Frobishervirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Samwavirus*	*Frobishervirinae*

2025.021B.Uc.v3.Gelderlandvirus_1ns

Title: Create one new species in the genus *Gelderlandvirus* (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Iwona Gientka, Michał J. Wójcicki

Summary:

Taxonomic rank(s) affected:

Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:

Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Gelderlandvirus* genus includes five species: *Gelderlandvirus cgg41,* Gelderlandvirus melville, Gelderlandvirus s16, Gelderlandvirus stml198, *and Gelderlandvirus stp4a.*

Proposed taxonomic change(s):

Follwing a genomic analysis of phages deposited in the NCBI database we propose to create one new species in the *genus Gelderlandvirus.*

Justification:

Based on DNA and protein similarity, the one proposed new species is coherent and together with the five known species *(Gelderlandvirus cgg41,* Gelderlandvirus melville, Gelderlandvirus s16, Gelderlandvirus stml198, *and Gelderlandvirus stp4a)* can be classified in the genus *Gelderlandvirus.*

Submitted: 20/03/2025; *Revised:* 22/08/2025

TABLE 30 - *Gelderlandvirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Gelderlandvirus SEA1*	Salmonella phage SEA1	OQ927978

2025.023B.Ac.v4.Illiduovirus_1ng_3ns

Title: Create a new genus *(Illiduovirus)* with three species in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru, Andrew Millard

Summary:

Taxonomic rank(s) affected:

Genus, species

Description of current taxonomy:

The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):

To create a new genus, Illiduovirus, with three species of *Pseudomonas phages*

Justification:

The bacterial viruses described in this proposal are lytic myoviruses with genomes of approximately 200 kb. Analysis with ViPTree and VIRIDIC indicate that these viruses form a distinct genus that includes three new species based on the current ICTV demarcation criteria for these ranks.

Submitted: 15/06/2025; *Revised:* 29/08/2025

TABLE 31 - *Illiduovirus*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Illiduovirus*		
New taxon	Species	*Illiduovirus peetri*	Pseudomonas phage vB_PpuM-Peetri	PP496444
New taxon	Species	*Illiduovirus voja6*	Pseudomonas phage vB_PpuM-Voja-6	PP496442
New taxon	Species	*Illiduovirus lauda*	Pseudomonas phage vB_PpuM-Lauda	PP496443

2025.024B.Ac.v3.Huairouvirus_1ng_1ns

Title: Create one new genus *(Huairouvirus)* with a single species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus, *Huairouvirus* with one new species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage P3.1 forms a single species in a new genus in accordance with the established demarcation criteria.

Submitted: —; *Revised:* 29/08/2025

TABLE 32 - *Huairouvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Huairouvirus*		
New taxon	Species	*Huairouvirus P31*	Nocardia phage P3.1	MW582532

2025.025B.Ac.v2.Caudoviricetes_10ns_1rms

Title: Create 10 new species and abolish one species (Class: *Caudoviricetes)*

Authors: Ivan M. Pchelin, , , , , , ,

Summary:Taxonomic rank(s) affected:
Species

Proposed taxonomic change(s):
We propose to;
Abolish one species, *Pbunavirus pv141*
Create of 10 new species in existing genera

Justification:

The proposed species share ≤95% genome similarity with the existing ones. By genome similarity and clustering analysis, all these potential new species reside within existing genera. The species *Pbunavirus pv141* is proposed for removal since it shares >95% genome similarity with other existing species in that genus.

Submitted: 06/12/2025; *Revised:* 09/01/2025

TABLE 33 - *Caudoviricetes*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Pakpunavirus mediocris*	Pseudomonas phage vB_PaeM_37F	PQ758387
New taxon	Species	*Pakpunavirus js*	Pseudomonas phage JS	OQ210008
New taxon	Species	*Pakpunavirus hhbs181*	Pseudomonas phage HHBS18_1	PQ287651
New taxon	Species	*Pakpunavirus hhbs91*	Pseudomonas phage HHBS9_1	PQ287655
New taxon	Species	*Pbunavirus hhbs511*	Pseudomonas phage HHBS51_1	PQ287641
New taxon	Species	*Pbunavirus hhbs122*	Pseudomonas phage HHBS12_2	PQ287652
New taxon	Species	*Webervirus gbh029*	Klebsiella phage vB_Kpn_GBH029	OU342755
New taxon	Species	*Drulisvirus gbh038*	Klebsiella phage vB_Kpn_GBH038	OU509533
New taxon	Species	*Drulisvirus gbh001*	Klebsiella phage vB_Kpn_GBH001	OU509534
New taxon	Species	*Przondovirus gbh014*	Klebsiella phage vB_Kpn_GBH014	OU342754

TABLE 34 - *Caudoviricetes*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	Species	*Pbunavirus PA8P1*

2025.027B.Ac.v3.Jianjiangvirinae_1nsf_2ng_22ns

Title: Create a new subfamily *(Jianjiangvirinae)* with two genera and 22 species (Class *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Juntao Shen

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
There is no taxonomy for these lytic phages isolated against *Bacteroides caccae* and *Bacteroides ovatus* from sewage

Proposed taxonomic change(s):
Add two new genera *(Luojiangvirus* and *Caojiangvirus)* and 22 new species to a new subfamily

Justification:
In accord with the established demarcation criteria for delineating a new subfamily, genus and species [3] these *Bacteroides* phages, isolated in China, fall into two new genera *(Luojiangvirus* and *Caojiangvirus)* in a new subfamily which we have chosen to call *Pearlrivervirinae.*

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 35 - *Jianjiangvirinae*, 25 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Jianjiangvirinae*		
New taxon	Genus	*Luojiangvirus*		
New taxon	Species	*Luojiangvirus BC679P5*	Bacteroides phage BC679P5	OP172651
New taxon	Species	*Luojiangvirus BC669P1*	Bacteroides phage BC669P1	OP172644
New taxon	Species	*Luojiangvirus BC669P2*	Bacteroides phage BC669P2	OP172645
New taxon	Species	*Luojiangvirus BC679P1*	Bacteroides phage BC679P1	OP172647
New taxon	Species	*Luojiangvirus BC679P2*	Bacteroides phage BC679P2	OP172648
New taxon	Species	*Luojiangvirus BC669P3*	Bacteroides phage BC669P3	OP172646
New taxon	Species	*Luojiangvirus BC679P3*	Bacteroides phage BC679P3	OP172649
New taxon	Genus	*Caojiangvirus*		
New taxon	Species	*Caojiangvirus BO668P2*	Bacteroides phage BO668P2	OP172699
New taxon	Species	*Caojiangvirus BK687P4*	Bacteroides phage BK687P4	OP172684
New taxon	Species	*Caojiangvirus BK687P2*	Bacteroides phage BK687P2	OP172682
New taxon	Species	*Caojiangvirus BK687P3*	Bacteroides phage BK687P3	OP172683
New taxon	Species	*Caojiangvirus BK745P1*	Bacteroides phage BK745P1	OP172691
New taxon	Species	*Caojiangvirus BK745P4*	Bacteroides phage BK745P4	OP172693
New taxon	Species	*Caojiangvirus BC422P2*	Bacteroides phage BC422P2	OP172643
New taxon	Species	*Caojiangvirus BK687P1*	Bacteroides phage BK687P1	OP172681
New taxon	Species	*Caojiangvirus BK687P5*	Bacteroides phage BK687P5	OP172685
New taxon	Species	*Caojiangvirus BK745P3*	Bacteroides phage BK745P3	OP172692
New taxon	Species	*Caojiangvirus BK735P2*	Bacteroides phage BK735P2	OP172688
New taxon	Species	*Caojiangvirus BK735P3*	Bacteroides phage BK735P3	OP172689
New taxon	Species	*Caojiangvirus BO668P1*	Bacteroides phage BO668P1	OP172698
New taxon	Species	*Caojiangvirus BK735P1*	Bacteroides phage BK735P1	OP172687
New taxon	Species	*Caojiangvirus BK735P4*	Bacteroides phage BK735P4	OP172690

2025.029B.Ac.v3.Justusliebigvirus_1ns

Title: To create one species in the genus *Justusliebigvirus* (class *Caudoviricetes)*

Authors: Aaryan Harshith, Paul Bollyky, Jessica C. Sacher, Carlo Armijo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Justusliebigvirus* was established by the proposal 2021.080B. The genus currently contains six species.

Proposed taxonomic change(s):
This proposal adds one new species, *Escherichia* phage Cardinal, to the *genus Justusliebigvirus.*

Justification:
VIRIDIC analysis indicates that phage Cardinal satisfies the species similarity threshold proposed by the ICTV Bacterial Viruses Subcommittee. Proteomic and phylogenetic evidence further supports the placement of this phage in the genus *Justusliebigvirus.*

Submitted: 22/01/2025; *Revised:* —

TABLE 36 - *Justusliebigvirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Justusliebigvirus cardinal*	Escherichia phage Cardinal	PQ567651

2025.030B.Ac.v3.Kagunavirus_3ns

Title: Create three new species in the genus *Kagunavirus* (Class *Caudoviricetes,* Family *Sarkviridae)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Kagunavirus* currently includes 12 species. The genus was originally established in 2015 and was included within the family *Sarkviridae* in 2024.

Proposed taxonomic change(s):
Create three new species in the genus *Kagunavirus; Kagunavirus ligaya, Kagunavirus* malou *and* Kagunavirus ohbeberoi

Justification:
Based on VIRIDIC analysis, we propose the creation of three new phage species in the genus *Kagunavirus. Kagunavirus ligaya* is named after the Filipino term "Ligaya" which explicitly means joy or happiness. *Kagunavirus malou* is derived from a nickname of one of co-authors parents. *Kagunavirus* ohbeberoi is derived from the Filipino slang term *"bebe" that* refers to friends and family.

Submitted: 04/12/2025; *Revised:* —

TABLE 37 - *Kagunavirus*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Kagunavirus ohbeberoi*	Escherichia phage vB_VIPECOMC04	PQ423993
New taxon	Species	*Kagunavirus ligaya*	Escherichia phage vB_ VIPECOTH07	PQ417132
New taxon	Species	*Kagunavirus malou*	Escherichia phage vB_ VIPECOTPH05A	PQ429079

2025.031B.Ac.v3.Kanagawavirus_4ns

Title: Create four new species in the genus *Kanagawavirus* (class *Caudoviricetes,* order

Pantevenvirales, family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:
Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Kanagawavirus* genus includes five species: *Kanagawavirus cipnine, Kanagawavirus eclm, Kanagawavirus mime, Kanagawavirus pei20,* and *Kanagawavirus threeohfive.*

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create four new species in the *genus Kanagawavirus.*

Justification:
Based on DNA and protein similarity, the four proposed new species are coherent and together with the five known species *(Kanagawavirus cipnine, Kanagawavirus eclm, Kanagawavirus mime, Kanagawavirus pei20,* and *Kanagawavirus threeohfive)* can be classified in the genus *Kanagawavirus.*

Submitted: 17/03/2025; *Revised:* 28/09/2025

TABLE 38 - *Kanagawavirus*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Kanagawavirus KLB31*	Klebsiella phage vB_KM5a1-KLB31	PP582757
New taxon	Species	*Kanagawavirus ENC9*	MAG: Enterobacter phage ENC9	OL355124
New taxon	Species	*Kanagawavirus Entb45*	Enterobacter phage Entb_45	ON630910
New taxon	Species	*Kanagawavirus ZX14*	Enterobacter phage ZX14	PP236086

2025.032B.Ac.v3.Karamvirus_14ns

Title: Create 14 new species in the genus *Karamvirus* (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:
Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Karamvirus* genus includes four species: *Karamvirus cc31,*

Karamvirus mypsh1140, Karamvirus petcm34, and *Karamvirus pg7.*

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create 14 new species in the *genus Karamvirus.*

Justification:
Based on DNA and protein similarity, the 14 proposed new species are coherent and together with the four known species *(Karamvirus cc31, Karamvirus mypsh1140, Karamvirus petcm34,* and *Karamvirus pg7)* can be classified in the genus *Karamvirus.*

Submitted: 16/03/2025; *Revised:* 29/08/2025

TABLE 39 - *Karamvirus*, 14 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Karamvirus KMB20*	Enterobacter phage vB-EclM_KMB20	OL828291
New taxon	Species	*Karamvirus KMB17*	Enterobacter phage vB-EclM_KMB17	OL849997
New taxon	Species	*Karamvirus EnC07*	Enterobacter phage EnC07	PQ096442
New taxon	Species	*Karamvirus PS49*	Aeromonas phage PS49	PP212877
New taxon	Species	*Karamvirus RZH*	Enterobacter phage vB_EluP_RZH	PQ140450
New taxon	Species	*Karamvirus CW742*	Enterobacter phage vB_ECC_CW742	PV019367
New taxon	Species	*Karamvirus EnC15*	Enterobacter phage EnC15	PQ096439
New taxon	Species	*Karamvirus Entb43*	Enterobacter phage Entb_43	ON585039
New taxon	Species	*Karamvirus VPA32*	Klebsiella phage vB_KpnM_VPA32	OP558005
New taxon	Species	*Karamvirus UFV01*	Enterobacter phage vB_EclM-UFV01	ON454249
New taxon	Species	*Karamvirus Ent31*	Enterobacter phage vB_Ent31	OR567511
New taxon	Species	*Karamvirus AS6*	Enterobacter phage vB_EclM_AS6	OR753410
New taxon	Species	*Karamvirus fGhEcl01*	Enterobacter phage fGh-Ecl01	ON212265
New taxon	Species	*Karamvirus EnA02*	Enterobacter phage EnA02	PQ096440

2025.033B.Ac.v3.Irusalimvirus_1ns

Title: Create one new species in the genus *Irusalimvirus* (class *Caudoviricetes)*

Authors: Jack S Canning, Kak-Ming Ling, Daniel R Laucirica, Joshua J Iszatt, Andrew Vaitekenas, Stephen M Stick, Anthony Kicic,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The current taxonomy for dsDNA bacterial viruses for the proposed change is as follows; *Duplodnaviria,* Heunggongvirae, Uroviricota, Caudoviricetes, Irusalimvirus

Proposed taxonomic change(s):
We propose to establish a new species in the *genus Irusalimvirus*

Justification:
Karil-mokiny-1 possesses 70.8% average nucleotide identity (ANI%) to *Irusalimvirus BCSR52,* meeting the requirements for a new species within the genus *Irusalimvirus.* Currently, the genus *Irusalimvirus* fall under the following ICTV taxonomy; *Duplodnaviria,* Heunggongvirae, Uroviricota, Caudoviricetes, *Irusalimvirus*

Submitted: —; *Revised:* 09/01/2025

TABLE 40 - *Irusalimvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Irusalimvirus karilmokiny1*	Burkholderia phage Karil-mokiny-1	PV388296

2025.034B.Ac.v3.Kayfunavirus_1ns

Title: Create one new species *Kayfunavirus rjtwin* (Class *Caudoviricetes,* Order *Autographivirales)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo,

Summary:Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Kayfunavirus* currently has 19 ICTV listed species.

Proposed taxonomic change(s):
Create one new species, *Kayfunavirus rjtwin*

Justification:
Enterobacter phage vB_VIPECLMCO6 was isolated from Masalasa Creek, Tarlac, Philippines.
The genome is complete with DTR based on checkV analysis and is publicly available in NCBI Genbank database. As a result of comparison of the genome of Enterobacter phage vB_VIPECLMO6 to existing members of the genus *Kayfunavirus* using VIRIDIC, we propose the addition of a new species, *Kayfunavirus rjtwin.*

Submitted: 04/12/2025; *Revised:* —

TABLE 41 - *Kayfunavirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Kayfunavirus rjtwin*	Enterobacter phage vB_ VIPECLMCO6	PQ411323

2025.035B.Ac.v3.Koserivirus_1ng_1ns

Title: Create a new genus *(Koserivirus)* with a single species to the *Tevenvirinae* subfamily (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik

Summary:
Taxonomic rank(s) affected:
Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class *Caudoviricetes,* order *Pantevenvirales, family Straboviridae.*

Description of current taxonomy:
Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species.

Proposed taxonomic change(s):
We performed genomic analysis of Citrobacter phage CkP1. Genome and protein analyses suggest that this bacteriophage belongs to the *Tevenvirinae* subfamily. Still, the differences are too great to assign it to one of the 15 genera within this subfamily. Therefore, we propose to create a new genus, *"Koserivirus",* with one species – *"Koserivirus CkP1".*

Justification:
DNA and protein analysis to other species and genera in the family *Straboviridae* supports the establishment of a new genus.

Submitted: 20/03/2025; *Revised:* —

TABLE 42 - *Koserivirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Koserivirus*		
New taxon	Species	*Koserivirus CkP1*	Citrobacter phage CkP1	MW239124

2025.037B.Ac.v3.Lingdingyangvirus_1ng_22ns

Title: Create a new genus *(Lingdingyangvirus)* with 22 species (Caudoviricetes)

Authors: Andrew M. Kropinski, Cristina Moraru, Juntao Shen

Summary:
Taxonomic rank(s) affected:
Genus and species

Description of current taxonomy:
There is no taxonomy for these lytic phages isolated against *Bacteroides thetaiotaomicron* from sewage

Proposed taxonomic change(s): Add new genus and 22 new species

Justification:

In keeping with the demarcation criteria established for creation of a genus, these 22 phages are significantly different from one another to be considered separate species; and, significantly similar to each other to be considered part of the same genus for which the name *Lingdingyangvirus* is proposed

Submitted: 15/05/2025; *Revised:* 09/01/2025

TABLE 43 - *Lingdingyangvirus*, 23 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Lingdingyangvirus*		
New taxon	Species	*Lingdingyangvirus BT61P1*	Bacteroides phage BT61P1	OP172709
New taxon	Species	*Lingdingyangvirus HNL05*	Bacteroides phage HNL05	MT074143
New taxon	Species	*Lingdingyangvirus BT47P1*	Bacteroides phage BT47P1	OP172708
New taxon	Species	*Lingdingyangvirus BT638P5*	Bacteroides phage BT638P5	OP172723
New taxon	Species	*Lingdingyangvirus SJC22*	Bacteroides phage SJC22	MT074158
New taxon	Species	*Lingdingyangvirus SJC13*	Bacteroides phage SJC13	MT074151
New taxon	Species	*Lingdingyangvirus SJC12*	Bacteroides phage SJC12	MT074150
New taxon	Species	*Lingdingyangvirus ARB14*	Bacteroides phage ARB14	MT074134
New taxon	Species	*Lingdingyangvirus SJC10*	Bacteroides phage SJC10	MT074148
New taxon	Species	*Lingdingyangvirus SJC25*	Bacteroides phage SJC25	MT074160
New taxon	Species	*Lingdingyangvirus BT401P3*	Bacteroides phage BT401P3	OP172713
New taxon	Species	*Lingdingyangvirus BT709P1*	Bacteroides phage BT709P1	OP172730
New taxon	Species	*Lingdingyangvirus BT638P7*	Bacteroides phage BT638P7	OP172725
New taxon	Species	*Lingdingyangvirus BT638P1*	Bacteroides phage BT638P1	OP172719
New taxon	Species	*Lingdingyangvirus BT638P2*	Bacteroides phage BT638P2	OP172720
New taxon	Species	*Lingdingyangvirus BT638P8*	Bacteroides phage BT638P8	OP172726
New taxon	Species	*Lingdingyangvirus BT638P6*	Bacteroides phage BT638P6	OP172724
New taxon	Species	*Lingdingyangvirus BT638P3*	Bacteroides phage BT638P3	OP172721
New taxon	Species	*Lingdingyangvirus BT681P2*	Bacteroides phage BT681P2	OP172727
New taxon	Species	*Lingdingyangvirus BT681P4*	Bacteroides phage BT681P4	OP172729
New taxon	Species	*Lingdingyangvirus BT498P1*	Bacteroides phage BT498P1	OP172714
New taxon	Species	*Lingdingyangvirus BT566P2*	Bacteroides phage BT566P2	OP172718

2025.038B.Ac.v3.Lowersilesiavirus_1ng_6ns

Title: Create new genus, *"Lowersilesiavirus"* with six species (class: *Caudoviricetes)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota, class Caudoviricetes.*

Description of current taxonomy:
Acinetobacter-specific temperate phages isolated and sequenced at the Bacteriophage Laboratory of the Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, have not been assigned to any family or genus of bacteriophages within the *class Caudoviricetes.*

Proposed taxonomic change(s):
We performed genomic analysis of our six *Acinetobacter-specific* temperate bacteriophages. We propose to create a new genus, *"Lowersilesiavirus",* with six species.

Justification:
Based on DNA and protein similarity, *"Lowersilesiavirus"* is a cohesive genus.

Submitted: 24/03/2025; *Revised:* —

TABLE 44 - *Lowersilesiavirus*, 7 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Lowersilesiavirus*		
New taxon	Species	*Lowersilesiavirus Acba3*	Acinetobacter phage Acba_3	OQ101248
New taxon	Species	*Lowersilesiavirus Acba4*	Acinetobacter phage Acba_4	OQ101249
New taxon	Species	*Lowersilesiavirus Acba11*	Acinetobacter phage Acba_11	OQ101254
New taxon	Species	*Lowersilesiavirus Acba13*	Acinetobacter phage Acba_13	OQ101255
New taxon	Species	*Lowersilesiavirus Acba14*	Acinetobacter phage Acba_14	OQ101256
New taxon	Species	*Lowersilesiavirus Acba15*	Acinetobacter phage Acba_15	OQ101257

2025.039B.Ac.v3.Luojiashanvirus_1ng_2ns

Title: Create one new genus *Luojiashanvirus,* with two species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
Create a new genus *"Luojiashanvirus"* and two new species

Justification:
Phages phiSHP3 and vB_SmaS_Bhz63 are both temperate siphoviruses of *Stenotrophomonas maltophilia.* These two phages exhibit 83% intergenomic nucleotide sequence similarity, satisfying the criteria for a new genus and two new species to be created.

Submitted: —; *Revised:* 09/01/2025

TABLE 45 - *Luojiashanvirus*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Luojiashanvirus*		
New taxon	Species	*Luojiashanvirus phiSHP3*	Stenotrophomonas phage phiSHP3	MT872956
New taxon	Species	*Luojiashanvirus Bhz63*	Stenotrophomonas phage vB_SmaS_Bhz63	OR797046

2025.040B.Ac.v3.Lutzviridae_1nf_1ng_1ns

Title: Create one (1) new family *(Lutzviridae),* including one (1) new genus *(Lutzvirus)* [Class: *Caudoviricetes]*

Authors: Adriele J C Santos, Bruna A L Ayupe, Roberto S Dias, Mirelly J F Silva, Carlos H M Da Silva, Andrew M Kropinski, Dann Turner, Sérgio O De Paula

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are *currently unclassified.*

Proposed taxonomic change(s):
We propose a new family, *Lutzviridae,* which includes a single genus, *Lutzvirus,* with a single species represented by Oceanotoga phage vB_OteS-UFV02.

Justification:
We propose the establishment of a new viral family, *Lutzviridae,* including one new genus genus, *Lutzvirus,* and a single species. Phylogenetic analysis based on whole-genome comparisons using VIPTree demonstrates that Oceanotoga phage vB_OteS-UFV02 (accession OR420712.1) forms an isolated clade, showing no close evolutionary relationship to any other known viruses within the class *Caudoviricetes.*
Furthermore, vB_OteS-UFV02 can be considered a genomic orphan, as it shares no significant nucleotide similarity with any previously classified viral genomes. BLASTn and VIRIDIC analyses reveal less than 4% nucleotide identity with its closest match, the unclassified *Clostridium* phage phiCTP1 (accession HM159959.1), which is far below the threshold recommended for family-level classification.
These lines of evidence strongly support the designation of *Lutzviridae* as a novel family within *Caudoviricetes,* encompassing bacteriophages that are highly divergent in both genomic content and evolutionary origin.

Submitted: —; *Revised:* 20/08/2025

TABLE 46 - *Lutzviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Lutzviridae*		
New taxon	Genus	*Lutzvirus*		
New taxon	Species	*Lutzvirus UFV02*	Oceanotoga phage vB_OteS-UFV02	OR420712

2025.041B.Ac.v3.Mariborvirus_1ng_1ns

Title: Create a new genus *Mariborvirus* with a single species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Maja Rupnik, Tomaž Accetto

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal, lytic siphoviruses isolates against *Bacteroides,* are currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Mariborvirus* with a single species.

Justification:
Analysis with VIRIDIC and ViPTree indicates that Bacteroides phage Bacuni_F1 forms a new genus and species that conforms to the established demarcation criteria. Bacteroides phage F2 (MT806186.1, MT806187.1) is probably a member of this genus but the sequence is incomplete

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 47 - *Mariborvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Mariborvirus*		
New taxon	Species	*Mariborvirus bacuniF1*	Bacteroides phage Bacuni_F1	MT635598

2025.042B.Ac.v3.Mariniviridae_1nf

Title: Create a new family, *Mariniviridae,* including one new genus and species

Authors: Manuel Martinez-Garcia, Mart Krupovic

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
The virus vSAG-37-F6 is not closely related to other known members of the *class Caudoviricetes.*

Proposed taxonomic change(s):
We propose classifying uncultured marine virus vSAG-37-F6 into a new species, *"Pelagimarinivirus ubique",* within a new genus, *"Pelagimarinivirus",* and a new family, *"Mariniviridae",* within the class *Caudoviricetes.*

Justification:
The virus vSAG-37-F6 encodes signature proteins conserved in tailed viruses of the class *Caudoviricetes,* but is not closely related to any classified member of this class. Thus, it is proposed to classify vSAG-37-F6 into a separate new family, *"Mariniviridae".*

Submitted: 20/06/2025; *Revised:* 25/08/2025

TABLE 48 - *Mariniviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Mariniviridae*		
New taxon	Genus	*Pelagimarinivirus*		
New taxon	Species	*Pelagimarinivirus ubique*	Pelagibacter virus vSAG-37-F6	PQ625738

2025.043B.Ac.v4.Microviricetes_reorg

Title: Revision of the microvirus taxonomy

Authors: Cristina Moraru, Paul Kirchberger, Simon Roux, Arvind Varsani, Mart Krupovic, Eric Olo Ndela, Francois Enault

Summary:
Taxonomic rank(s) affected:
Monodnaviria; Sangervirae; Phixviricota

Description of current taxonomy:
Phylum Phixviricota currently includes a monotypic family *Microviridae* with two subfamilies *(Bullavirinae and Gokushovirinae).*

Proposed taxonomic change(s):
We propose to elevate *family Microviridae* to the level of a class, the *"Microviricetes",* within phylum *Sangervirae* (realm *Monodnaviria).* Inside this new class, we propose seven orders and 21 families.

Justification:
Metagenomic studies from the past decade have revealed many new microvirus genomes across ecosystems. Phylogenetic assessment confirmed that the established taxonomic structure of two existing subfamilies of *Microviridae* cannot adequately represent the diversity of this viral group. Thus, we propose a reorganization of the established taxonomy of microviruses by assessing the relationships between 21 previously classified and 137 new representative complete microvirus genome sequences obtained from either cultivated viruses or from metagenomic datasets. Orders and families were defined by their separation on the major capsid protein phylogeny.

Submitted: 20/06/2025; *Revised:* 29/08/2025

TABLE 49 - *Microviricetes*, 488 new taxa***.** Table too large, see supplementary information sheet supp_info_tab_49

TABLE 50 - *Microviricetes*, 46 move taxa***.** Table too large, see supplementary information sheet supp_info_tab_50

TABLE 51 - *Microviricetes*, 6 promote taxa*

Operation	**New taxon name**	**Old taxon name**	**Old rank**	**New rank**
Promote taxon	*Microviricetes*	*Malgrandaviricetes*	class	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class
Promote taxon	*Microviricetes*	*Malgrandaviricetes*	class	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class

Promote taxon	*Microviricetes*	*Petitvirales*	order	class

TABLE 52 - *Microviricetes*, 6 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Species	*Chlamydiaduovirus Chp2*	*Chlamydiamicrovirus Chp2*
Rename taxon	Species	*Chlamydiaduovirus CPAR39*	*Chlamydiamicrovirus CPAR39*
Rename taxon	Species	*Chlamydiaduovirus CPG1*	*Chlamydiamicrovirus CPG1*
Rename taxon	Species	*Chlamydiaduovirus Chp2*	*Chlamydiamicrovirus Chp2*
Rename taxon	Species	*Chlamydiaduovirus CPAR39*	*Chlamydiamicrovirus CPAR39*
Rename taxon	Species	*Chlamydiaduovirus CPG1*	*Chlamydiamicrovirus CPG1*

TABLE 53 - *Microviricetes*, 6 abolish taxa*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Order	*Petitvirales*
Abolish taxon	Class	*Malgrandaviricetes*
Abolish taxon	Species	*Bdellovibrio virus MAC1*
Abolish taxon	Order	*Petitvirales*
Abolish taxon	Class	*Malgrandaviricetes*
Abolish taxon	Species	*Bdellovibrio virus MAC1*

TABLE 54 - *Microviricetes*, 4 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old parent taxon**	**Old taxon name**
Move; rename taxon	Genus	*Chlamydiaduovirus*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus*
Move; rename taxon	Species	*Chlamydiaunovirus Chp1*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus Chp1*
Move; rename taxon	Genus	*Chlamydiaduovirus*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus*
Move; rename taxon	Species	*Chlamydiaunovirus Chp1*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus Chp1*

2025.044B.Ac.v3.Miyazakivirus_1ng_1ns

Title: Create one new genus *(Miyazakivirus)* with a single species *(Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus, *Miyazakivirus,* with one species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NS-I forms a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 55 - *Miyazakivirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Miyazakivirus*		
New taxon	Species	*Miyazakivirus NSI*	Nocardia phage NS-I	OP429095

2025.045B.Ac.v3.Mosigvirus_1ns

Title: Create one new species *Mosigvirus lindsay* (Class *Caudoviricetes,* Order *Pantevenvirales,* Family *Straboviridae)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:

The genus *Mosigvirus* currently includes 13 ICTV listed species.

Proposed taxonomic change(s):

Create one new species, *Mosigvirus lindsay*

Justification:
Escherichia phage vB_VIPECOMC06 was isolated from Masalasa Creek, Tarlac, Philippines. The genome is complete with direct terminal repeats based on an analysis with checkV [1] and is publicly available in NCBI Genbank database. Comparison to members of the genus *Mosigvirus* using VIRIDIC indicates that vB_VIPECOMC06 represents a new species in the genus.

Submitted: 04/12/2025; *Revised:* 29/08/2025

TABLE 56 - *Mosigvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Mosigvirus lindsay*	Escherichia phage vB_VIPECOMC06	PQ416618

2025.046B.Ac.v3.Motookavirus_1ng_2ns

Title: Create a new genus *(Motookavirus)* with two species in the Class *Caudoviricetes*

Authors: Ayesha Lone, Andrew M. Kropinski, Cristina Moraru, Jakub Barylski, Hany Anany

Summary:
Taxonomic rank(s) affected: Genus and species

Description of current taxonomy: None for these phages

Proposed taxonomic change(s): To create a new genus *(Motookavirus)* containing two species

Justification: In accordance with the demarcation criteria of what constitutes a new genus and species these two *Bacillus cereus* phages are classified into a new genus (Motookavirus) of jumbo phages

Submitted: 15/06/2025; *Revised:* 27/08/2025

TABLE 57 - *Motookavirus*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Motookavirus*		
New taxon	Species	*Motookavirus edson*	Bacillus phage Edson	PV796108
New taxon	Species	*Motookavirus WH1*	Bacillus phage vB_BceM_WH1	LC597490

2025.047B.Ac.v3.Mweyongvirus_1ng_1ns

Title: Create one new genus *(Mweyongvirus)* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, *species*

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
Create one new genus, *Mweyongvirus* and a single species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Microcystis* phage Mwe-Yong1112-1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 58 - *Mweyongvirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Mweyongvirus*		
New taxon	Species	*Mweyongvirus yong1121*	Microcystis phage Mwe-Yong1112-1	MZ436628

2025.048B.Ac.v3.Mycobacterium_phages_1ng_8ns

Title: Create one new genus *(Peetremavirus)* of *Mycobacterium* phages with eight species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: None. Mycobacterium phage P3MA is defined in the Actinobacteriophage Database as a singleton. The prophages have not been included in the database as of writing (18/08/2025)

Proposed taxonomic change(s): Create one new genus *Peetremavirus* with eight species

Justification: Phage P3MA was isolated on *Mycobacterium abscessus* 330 while the other proposed members of this genus were identified in the genomes of a variety of *M. abscessus* isolates. All of these temperate siphoviruses conform to the criteria which we have established for creation of a genera and associated species.

Submitted: —; *Revised:* 18/08/2025

TABLE 59 - *Mycobacterium*, 9 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Peetremavirus*		
New taxon	Species	*Peetremavirus P3MA*	Mycobacterium phage P3MA	PV089522
New taxon	Species	*Peetremavirus prophi621*	Mycobacterium phage prophi62-1	MW584194
New taxon	Species	*Peetremavirus phiGD342*	Mycobacterium phage phiGD34-2	MW314853
New taxon	Species	*Peetremavirus prophiGD211*	Mycobacterium phage prophiGD21-1	MW584205
New taxon	Species	*Peetremavirus prophiDG112*	Mycobacterium phage prophiGD11-2	MW584151
New taxon	Species	*Peetremavirus prophiGD161*	Mycobacterium phage prophiGD16-1	MW584149
New taxon	Species	*Peetremavirus prophiGD43A2*	Mycobacterium phage prophiGD43A-2	MW584198
New taxon	Species	*Peetremavirus phiGD891*	Mycobacterium phage phiGD89-1	MW314851

2025.049B.Ac.v3.Myosmarvirus_1ns

Title: Create one new species in the genus *Myosmarvirus* (class *Caudoviricetes,* family *Lindbergviridae)*

Authors: Michał J. Wójcicki, Dziyana Shymialevich, Iwona Gientka, Paulina Średnicka, Stanisław B. Błażejak, Barbara Sokołowska

Summary:
Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes, family Lindbergviridae.*

Description of current taxonomy:
Currently, in the *Lindbergviridae* family, 10 genera have been distinguished. The *Myosmarvirus* genus includes three species: *Myosmarvirus* MTx, Myosmarvirus myosmar, *and* Myosmarvirus SMP.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create one new species in the *genus Myosmarvirus.*

Justification:
Based on DNA and protein similarity, the one proposed new species is coherent and together with the three known species *(Myosmarvirus* MTx, Myosmarvirus myosmar, *and* Myosmarvirus *SMP)* can be classified in the genus *Myosmarvirus.*

Submitted: 20/03/2025; *Revised:* —

TABLE 60 - *Myosmarvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Myosmarvirus Spe5P4*	Serratia phage Spe5P4	PP858852

2025.050B.A.v2.Nanchangvirus_1ng_1ns

Title: Create one new genus *(Nanchangvirus)* with a single species *(Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *(Nanchangvirus)* with one species. This virus is related to *Rhodococcus* phage Braxoaddie, a putative member of the *genus Pleakleyvirus*

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NC1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 61 - *Nanchangvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nanchangvirus*		
New taxon	Species	*Nanchangvirus NC1*	Nocardia phage NC1	MW452562

2025.051B.Ac.v3.Nanosmitevirus_1ng_1ns

Title: Create one new genus *(Nanosmitevirus)* with a single species (Caudoviricetes).

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:Taxonomic rank(s) affected:
Genus and species

Description of current taxonomy:
While the Actinobacteriophage Database groups temperate Mycobacterium phage Nanosmite in Cluster M/Subcluster M3 our BLASTN and VIRIDIC analysis reveals that it is sufficiently different from M Cluster viruses to deserve recognition as a separate genus. We have classified M Cluster phages to the subfamily *Mclasvirinae, family Vilmaviridae.*

Proposed taxonomic change(s):
Add new genus and one new species to the subfamily *Mclasvirinae,* family Vilmaviridae

Justification:
Mycobacterium phage Nanosmite is a unique, unclassified temperate virus. BLASTN analysis reveals that it shares 57.9% DNA sequence identity with Mycobacterium phage Rey.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 62 - *Nanosmitevirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nanosmitevirus*		
New taxon	Species	*Nanosmitevirus nanosmite*	Mycobacterium phage Nanosmite	MW578836

2025.052B.Ac.v3.Nitrunavirus_1ng_1ns

Title: Create one new genus *(Nitrunavirus)* with a single species (Caudoviricetes).

Authors: Andrew M. Kropinski, Ipek Kurtböke, , , , ,

Summary:Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *Nitrunavirus* with one new species

Justification:
The bacteriophage NTR1 was isolated from activated sludge and infects three species of *Norcardia.* NTR1 exhibits a siphovirus morphology and possesses a 65.3 kb genome with 97 predicted protein-coding genes and a single tRNA. Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NTR1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 63 - *Nitrunavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nitrunavirus*		
New taxon	Species	*Nitrunavirus NTR1*	Nocardia phage NTR1	MF477236

2025.053B.Ac.v3.Nubrunavirus_1ng_2ns

Title: Create one new genus *(Nubrunavirus)* with a single species (class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *Nubrunavirus* with two species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia phages* NBR1 and *Nocardia* phage *KYD2 represents* a new genus and species that conforms to the established demarcation criteria. BLASTN analysis reveals that these phages are peripherally related to *Nymphadoravirus bunnybear.*

Submitted: —; *Revised:* 09/01/2025

TABLE 64 - *Nubrunavirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nubrunavirus*		
New taxon	Species	*Nubrunavirus NBR1*	Nocardia phage NBR1	JN116828
New taxon	Species	*Nubrunavirus KYD2*	Nocardia phage KYD2	MW654182

2025.054B.Uc.v3.Hirszfeldviridae_1nf_21ng_1mg_5mrs_46ns

Title: Create a new family, *Hirszfeldviridae,* with 22 genera, *Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, *Scipiovirus, Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus,* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Martyna A. Cieślik, Edyta Pawlak, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
According to the current taxonomy, the *Obolenskvirus* genus has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Obolenskvirus* genus includes eight species: *Obolenskvirus AB1, Obolenskvirus AB2, Obolenskvirus AbC62, Obolenskvirus AbP2, Obolenskvirus AP22, Obolenskvirus LZ35, Obolenskvirus WCHABP1,* and *Obolenskvirus WCHABP12.*

Proposed taxonomic change(s):
Create a new family, *Hirszfeldviridae,* with 22 genera, *Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, *Scipiovirus, Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus,* for a group of *Acinetobacter-specific* phages.

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus.* Based on our analysis, we propose the creation of a new family for these phages along with 22 distinct genera.

To create a new family, *Hirszfeldviridae,* with 22 genera.
To create a new genus, *Nosocomialisvirus,* with two species.
To create a new single species genus, *Beijingvirus.*
To create a new single species genus, *Guangzhouvirus.*
To create a new single species genus, *Chinavirus.*
To create a new single species genus, *Pittiivirus.*
To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae.*
To create four new species in genus *Obolenskvirus.*
To create a new single species genus, *Ganjingzivirus.*
To create a new single species genus, *Guizhouvirus.*
To create a new single species genus, *Brutusvirus.*
To create a new single species genus, *Walailakvirus.*
To create a new single species genus, *Scipiovirus.*
To move *Obolenskvirus AB1* from *Obolenskvirus* genus and rename to new *Wenzhouvirus* genus with two species.
To move *Obolenskvirus AbP2* from *Obolenskvirus* genus and rename to new *Burnvirus* genus with 11 species.
To create a new single species genus, *Ankaravirus.*
To create a new genus, *Polandvirus,* with two species.
To create a new single species genus, *Kenyavirus.*
To create a new genus, *Cairovirus,* with two species.
To create a new genus, *Helsinkivirus,* with two species.
To move *Obolenskvirus* WCHABP1 *and* Obolenskvirus *WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species.
To create a new single species genus, *Pakistanvirus.*
To create a new single species genus, *Catovirus.*
To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.

Justification:
After examination of 55 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Hirszfeldviridae,* to accommodate 22 genera *(Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus, *Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus).*

Submitted: 20/06/2025; *Revised:* 23/10/2025

TABLE 65 - *Hirszfeldviridae*, 63 new taxa*. Table too large, see supplementary information sheet supp_info_tab_65

TABLE 66 - *Hirszfeldviridae*, 5 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old taxon name
Move; rename taxon	Species	*Wenzhouvirus AB1*	*Hirszfeldviridae*	*Obolenskvirus AB1*
Move; rename taxon	Species	*Burnvirus AbP2*	*Hirszfeldviridae*	*Obolenskvirus AbP2*
Move; rename taxon	Species	*Sichuanvirus WCHABP1*	*Hirszfeldviridae*	*Obolenskvirus WCHABP1*
Move; rename taxon	Species	*Sichuanvirus WCHABP12*	*Hirszfeldviridae*	*Obolenskvirus WCHABP12*
Move; rename taxon	Species	*Theraphagusvirus AP22*	*Hirszfeldviridae*	*Obolenskvirus AP22*

TABLE 67 - *Hirszfeldviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Obolenskvirus*	*Hirszfeldviridae*

2025.059B.Ac.v3.Peggyvirus_1ng_1ns

Title: Create a new genus *(Peggyvirus)* with a single species in the order *Autographivirales*

Authors: Ayesha Lone, Andrew M. Kropinski, Cristina Moraru, Hany Anany

Summary:
Taxonomic rank(s) affected: Subfamily, Genus

Description of current taxonomy: The family *Autographiviridae* (T7-like phages) has recently been replaced by the order *Autographivirales* which consists of four families, 13 subfamilies, 228 genera, and 968 species (ICTV Taxonomy Proposal 2024.045B.Autographivirales). This proposal affects the *subfamily Slopekvirinae*

Proposed taxonomic change(s): Addition of a new genus, *"Peggyvirus"* to this subfamily

Justification: In accordance with our definition of what constitutes a new genus and species [3] this Cronobacter phage is sufficiently different from other viruses to constitute a new genus in the subfamily *Slopekvirinae.*

Submitted: 15/06/2025; *Revised:* 27/08/2025

TABLE 68 - *Peggyvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Peggyvirus*		
New taxon	Species	*Peggyvirus peggy*	Cronobacter phage Peggy	PV796109

2025.060B.A.v2.Pepevirus_1ns

Title: Reinstatement of the species *Pepevirus spumicola*

Authors: Jānis Rūmnieks, , , , , , ,

Summary:Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Genus *Pepevirus* currently holds six genera of bacterial single-stranded RNA viruses *(class Leviviricetes). Pseudomonas* virus LeviOr01 had previously been assigned to species *Pepevirus spumicola,* but this species is now abolished and in accordance with the current taxonomy, LeviOr01 is an unclassified *Pepevirus.*

Proposed taxonomic change(s):
Create species *"Pepevirus spumicola"* with *Pseudomonas* virus LeviOr01 as the exemplar *virus.* This *would* effectively reinstate a previously abolished species.

Justification:
Sequence analysis suggests that the abolishment of species *Pepevirus spumicola* was unjustified: according to the currently adopted demarcation criteria for *Leviviricetes, Pseudomonas* virus LeviOr01 belongs to genus *Pepevirus* but cannot be assigned to any of the currently recognized constituent species.

Submitted: 16/06/2025; *Revised:* —

TABLE 69 - *Pepevirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Pepevirus spumicola*	ssRNA phage LeviOr01	LT821717

2025.061B.Uc.v3.Pituviridae_1nf_7ng_8ns

Title: Create a new family, *Pituviridae,* including seven new genera and eight new species (Class *Caudoviricetes)*

Authors: Michael Angelou L. Nada, Marel Jan G. Joloro, Ruth Antoinette D. Chin, Mark Christian C. Reterta, Janna Ysabelle O. Casidsid, Anton Roi G. Collado, Aubrey Joy P. Tejada, Sharmen C. Berlin, Joseph B. Ancla, Arra B. Asejo, Rommel J. Gestuveo

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
Klebsiella phages are currently classified in the order *Autographivirales* and the families *Ackermannviridae, Casjensviridae, Demerecviridae, Drexlerviridae, Peduoviridae, Schitoviridae,* and *Straboviridae.* Our taxonomic analysis revealed *that Klebsiella* phage vB_VIPKPNMC05 does not belong to the existing phage families, thus, remains unclassified.

Proposed taxonomic change(s):

Create a new family, *Pituviridae*
Create a new single species *genus, Pituvirus*
Create a new single species *genus, Oxavirus*
Create a new single species *genus, Corunyavirus*
Create a new genus *Vimivirus,* with two species
Create a new single species *genus, Xubiasivirus*
Create a new single species *genus, Keypisivirus*
Create a new single species *genus, Samsivirus*

Justification:

As a result of detailed genomic, proteomic, and phylogenetic analyses using VIRIDIC, ViPTree, VirClust, we propose the creation a new phage family, *Pituviridae,* with seven genera *(Pituvirus, Oxavirus, Corunyavirus, Vimivirus, Xubiasivirus, Keypisivirus,* and *Samsivirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 30/05/2025; *Revised:* 09/01/2025

TABLE 70 - *Pituviridae*, 16 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Pituviridae*		
New taxon	Genus	*Pituvirus*		
New taxon	Species	*Pituvirus akira*	Klebsiella phage vB_VIPKPNMC05	PQ351753
New taxon	Genus	*Oxavirus*		
New taxon	Species	*Oxavirus ST13OXA48phi124*	Klebsiella phage ST13-OXA48phi12.4	MK422450
New taxon	Genus	*Corunyavirus*		
New taxon	Species	*Corunyavirus ST13OXA48phi122*	Klebsiella phage ST13-OXA48phi12.2	MK422452
New taxon	Genus	*Vimivirus*		
New taxon	Species	*Vimivirus ST147VIM1phi72*	Klebsiella phage ST147-VIM1phi7.2	MK448232
New taxon	Species	*Vimivirus Kp48873*	Klebsiella phage Kp4887-3	OK490474
New taxon	Genus	*Xubiasivirus*		
New taxon	Species	*Xubiasivirus EcoS733R5*	Escherichia phage vB_EcoS-733R5	ON470608
New taxon	Genus	*Keypisivirus*		
New taxon	Species	*Keypisivirus ST101KPC2phi63*	Klebsiella phage ST101-KPC2phi6.3	MK416017
New taxon	Genus	*Samsivirus*		
New taxon	Species	*Samsivirus Kp48802*	Klebsiella phage Kp4880-2	OK490458

2025.065B.Ac.v3.Rcapmuvirus_1ng_2ns

Title: Create one new genus *Rcapmuvirus* with two species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:

Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
Create a new genus, *"Rcapmuvirus"* with two new species

Justification: The bacterial viruses RcapMu and RcWaterboi are both temperate siphoviruses that infect *Rhodobacter capsulatus.* VIRIDIC analysis shows that these phages exhibit approximately 83% intergenomic similarity warranting their inclusion within a single genus.

Submitted: —; *Revised:* 09/01/2025

TABLE 71 - *Rcapmuvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Rcapmuvirus*		
New taxon	Species	*Rcapmuvirus capmu*	Rhodobacter phage RcapMu	JN190960
New taxon	Species	*Rcapmuvirus waterboi*	Rhodobacter phage RcWaterboi	MW677528

2025.066B.A.v2.Rename_taxa

Title: Rename three genera within the class *Caudoviricetes*

Authors: Andrew M. Kropinski, , , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus

Description of current taxonomy:
The three affected taxons are *Orchidvirus, Apricotvirus* and *Vhmlvirus.* These taxa are floating genera within the *class Caudoviricetes.*

Proposed taxonomic change(s):
Change the names of the genera *Orchidvirus, Apricotvirus and Vhmlvirus*

Justification:
The names *Apricotvirus* and *Orchidvirus* might lead to a misinterpretation that these viruses infect apricot trees and orchids. *Vhmlvirus* is unpronounceable.

Submitted: —; *Revised:* —

TABLE 72 - *Rename*, 8 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Genus	*Kampevirus*	*Apricotvirus*
Rename taxon	Genus	*Cratervirus*	*Orchidvirus*
Rename taxon	Genus	*Oonoonbavirus*	*Vhmlvirus*
Rename taxon	Species	*Kampevirus apricot*	*Apricotvirus apricot*
Rename taxon	Species	*Cratervirus orchid*	*Orchidvirus orchid*

Rename taxon	Species	*Oonoonbavirus VHML*	*Vhmlvirus VHML*
Rename taxon	Species	*Oonoonbavirus VP85*	*Vhmlvirus VP585*
Rename taxon	Species	*Oonoonbavirus mar*	*Vhmlvirus mar*

2025.067B.Ac.v3.Rhodococcus_phages_2ng_2ns

Title: Create two new genera of *Rhodococcus* phages (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: The viruses described in this proposal are currently unclassified. They are defined in the Actinobacteriophage Database as singletons

Proposed taxonomic change(s): Create two new genera, *"Docdeeseptimavirus"* and *"Eetrevirus"* each with a single species

Justification: Rhodococcus phages Reqi DocB7 and E3 show little similarity to other phages in the extant nucleotide sequence databases when examined using BLASTN. Based on this, we propose that each represents a new species and genus.

Submitted: —; *Revised:* 09/01/2025

TABLE 73 - *Rhodococcus*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Docdeeseptimavirus*		
New taxon	Species	*Docdeeseptimavirus Doc7*	Rhodococcus phage ReqiDocB7	GU580940
New taxon	Genus	*Eetrevirus*		
New taxon	Species	*Eetrevirus E3*	Rhodococcus phage E3	HM114277

2025.068B.Ac.v3.Ricunavirus_1ng_1ns

Title: Create one new genus *Ribunavirus* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Ribunavirus* with a single species

Justification: *Rhizobium* phage RR1-B is a temperate myovirus with a 37.4 kb genome. Analysis of the genome sequence with VIRIDIC supports the creation of a new genus based on the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 74 - *Ricunavirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Ribunavirus*		
New taxon	Species	*Ribunavirus RR1B*	Rhizobium phage RR1-B	JF974315

2025.069B.Ac.v3.Ricunavirus_1ng_1ns

Title: Create one new genus *(Ricunavirus)* with one species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Ricunavirus* and a single species

Justification:
Rhodobacter phage RC1 is a temperate siphovirus with a 39.6 kb genome. Analysis of the genome sequence with VIRIDIC shows it exhibits little similarity to other phages infecting this bacterial genus and supports the establishment of a new genus based on the current demarcation criteria.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 75 - *Ricunavirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Ricunavirus*		
New taxon	Species	*Ricunavirus RC1*	Rhodobacter phage RC1	JF974308

2025.070B.Ac.v3.Riverraidervirus_1ng_1ns

Title: Create one new genus *(Riverraidervirus)* with a single species (Class: *Caudoviricetes,* Family: *Stackebrandtviridae).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified.

Proposed taxonomic change(s):
Create one new genus, *"Riverraidervirus"* and one new species within the family *Stackebrandtviridae.*

Justification:
Gordonia phage RiverRaider is a lytic siphovirus with a 59.6 kb genome. VIRIDIC analysis shows that it shares considerable intergenomic similarity with species of the genera *Vividuovirus* and *Kroosvirus* but is sufficiently different to establish a new genus under the current demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 76 - *Riverraidervirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Riverraidervirus*		
New taxon	Species	*Riverraidervirus riverraider*	Gordonia phage RiverRaider	PQ184823

2025.071B.Ac.v3.Santaclaravirinae_1nsf_3ng_6ns

Title: Create a new subfamily, *Santaclaravirinae* with three genera (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected: subfamily, genus and species

Description of current taxonomy: Phage-plasmids are a novel, hybrid class of mobile genetic element which retain aspects of both phages and plasmids. These genetic elements have not been previously classified by ICTV.

Proposed taxonomic change(s): Create a new subfamily, *Santaclaravirinae* with three genera *Cyranovirus, Westmeadvirus and Suquintavirus*

Justification: These phages represent phage-plasmids, those that exhibit characteristics of both phages as plasmids. These mobile genetic elements can exist as circular replicons and often encode homologs of the ParA/ParB plasmid partitioning proteins. They also have the ability to form virions enabling the lysis and infection of bacteria. The phages described in this proposal share a significant number of protein homologs (c. 83 proteins) and exhibit >50% intergenomic nucleotide sequence similarity, supporting the creation of a new subfamily.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 77 - *Santaclaravirinae*, 8 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Santaclaravirinae*		
New taxon	Species	*Westmeadvirus pJN226*	Klebsiella phage pJN2-26	MZ779062
New taxon	Genus	*Suquintavirus*		
New taxon	Species	*Suquintavirus SSU5*	Salmonella phage SSU5	JQ965645

New taxon	Genus	*Cyranovirus*		
New taxon	Species	*Cyranovirus cryano*	Escherichia phage Cyrano	OV696614
New taxon	Species	*Cyranovirus CMS2020a*	Escherichia phage CMS-2020a	CP054387
New taxon	Species	*Cyranovirus CMS2020b*	Escherichia phage CMS-2020b	CP053388

TABLE 78 - *Santaclaravirinae*, 1 move; rename taxon*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old taxon name**
Move; rename taxon	Genus	*Westmeadvirus*	*Santaclaravirinae*	*Sourvirus*

2025.072B.Ac.v4.Schitoviridae_4_nsf_16ng_78_ns

Title: Create four (4) new subfamilies, sixteen (16) new genera and sixty-one (78) new species in the family *Schitoviridae* (Class *Caudoviricetes)*

Authors: Johannes Wittmann, Dann Turner

Summary:
Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The family *Schitoviridae* was created in 2020 (Taxonomy Proposal). The family is comprised of nine subfamilies, 57 genera and 106 species

Proposed taxonomic change(s):
Here, we propose to create four (4) new subfamilies:
Waldeevirinae, containing three (3) new genera, *Mifoctavirus, Sabivirus* and *Ekoctavirus,* alongside the existing genera *Cbunavirus* and *Efbeekayvirus*
Gaffkyvirinae, containing two (2) genera, *Pacinivirus* and *Vicoquintavirus*
Gebvirinae, containing one (1) new genus, *Dowsonvirus,* and the existing genera *Riverridervirus, Pokkenvirus, Philippevirus* and *Cavevirus*
Brisouvirinae, containing two (2) new genera, *Nacbunavirus* and *Atduovirus* and the existing genus *Exceevirus.*
Additionally, we intend to create ten (10) new genera, *Aracevirus, Axvirus, Dongfangvirus, Aquintavirus, Geeundevigintivirus, Pastisvirus, Peegeeundecimvirus, Manannanvirus,* Roskoffvirus *and Viundeviginityvirus.*

Justification:
Using different tools like VIRIDIC [1], VICTOR [2] or ViPTree [3] (Fig 1. and 2) for pairwise nucleotide identity or whole genome analyses of schitoviruses we propose 4 new subfamilies, *Brisouvirinae, Gaffkyvirinae, Gebvirinae,* and *Waldeevirinae* and 16 new genera. We used 95% and 70% nucleotide sequence identity over the entire length of the genome as criteria for delimiting species and genera, respectively. At the subfamily level, members of the subfamily share at least 20 % intergenomic distance as determined by VIRIDIC analysis.

Submitted: 06/02/2025; *Revised:* 09/02/2025

TABLE 79 - *Schitoviridae*, 98 new taxa*. Table too large, see supplementary information sheet supp_info_tab_79

TABLE 80 - *Schitoviridae*, 10 move taxa*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Genus	*Vicoquintavirus*	*Gaffkyvirinae*	*Schitoviridae*
Move taxon	Genus	*Pacinivirus*	*Gaffkyvirinae*	*Schitoviridae*
Move taxon	Genus	*Cavevirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Philippevirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Pokkenvirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Riverridervirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Exceevirus*	*Brisouvirinae*	*Schitoviridae*
Move taxon	Genus	*Cbunavirus*	*Waldeevirinae*	*Schitoviridae*
Move taxon	Genus	*Efbeekayvirus*	*Waldeevirinae*	*Schitoviridae*
Move taxon	Genus	*Triduovirus*	*Humphriesvirinae*	*Schitoviridae*

2025.075B.Ac.v3.Tabiovirus_1ng_8ns

Title: Create a new genus *(Tabiovirus)* with eight species in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
To create one new genus *Tabiovirus* with eight species of *Xanthomonas phages*

Justification: Based on analysis with ViPTree and VIRIDIC, we propose the creation of one new genus, *Tabiovirus* and eight new species of *Xanthomonas* phages.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 81 - *Tabiovirus*, 9 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Tabiovirus*		
New taxon	Species	*Tabiovirus JUN5*	Xanthomonas phage JUN5	OK913679
New taxon	Species	*Tabiovirus tenjo*	Xanthomonas phage Tenjo	LR743531
New taxon	Species	*Tabiovirus tabio*	Xanthomonas phage Tabio	LR743528
New taxon	Species	*Tabiovirus 10KY502B*	Xanthomonas phage 10KY502B	OQ622092
New taxon	Species	*Tabiovirus MET23P3*	Xanthomonas phage MET23-P3	OK913680
New taxon	Species	*Tabiovirus olaya*	Xanthomonas phage Olaya	MW802488
New taxon	Species	*Tabiovirus Cp2*	Xanthomonas citri phage Cp2	AB720064
New taxon	Species	*Tabiovirus SAC*	Xanthomonas phage SAC	PV012638

2025.076B.A.v2.Tequintavirus_1ns

Title: Create one new species in the genus *Tequintavirus*

Authors: Emilia Andrea V. Sabban, Stephen Kyle C. Arcan, Adonis N. Eclipse, Dexter Bryan L. Esliza, Paul Jeremy C. Lanete, Lindley C. Susi, Gelito Joseph M. Sikat,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Tequintavirus* is classified within the subfamily *Markadamsvirinae,* family *Demerecviridae.* The genus is currently comprised of 70 species.

Proposed taxonomic change(s):
Create one new species *Tequintavirus vipecosubii* in the *genus Tequintavirus.*

Justification:
A new species, represented by Escherichia phage vB_EcoS_I14, is proposed based on a 95% intergenomic similarity threshold. This newly identified species is most closely related to *Tequintavirus S131* (GenBank MH370378.1), sharing 80.1% similarity. This taxonomic proposal is grounded in the principles of phylogenetic analysis and genomic comparison, providing a robust classification for this newly isolated bacteriophage.

Submitted: 29/08/2024; *Revised:* —

TABLE 82 - *Tequintavirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Tequintavirus vipecosubii*	Escherichia phage vB_EcoS_I14	PP892525

2025.078B.Ac.v3.Vibrio_phages_2ng_3ns

Title: Create two new genera of *Vibrio* phages (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified.

Proposed taxonomic change(s): Create two new genera *Strymvirus* and Baybaevirus

Justification: The phages described in this proposal are temperate siphoviruses infecting *Vibrio* spp. Analysis with VIRIDIC and ViPTree support the creation of two new genera and three new species in accordance with the established demarcation criteria.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 83 - *Vibrio*, 5 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Strymvirus*		

New taxon	Species	*Strymvirus H2*	Vibrio phage H2 PGK-2017	KY658673
New taxon	Species	*Strymvirus strym*	Vibrio phage Strym	KX581099
New taxon	Genus	*Baybaevirus*		
New taxon	Species	*Baybaevirus baybae*	Vibrio phage Baybae	OQ079154

2025.079B.Ac.v3.Wallmarkvirinae_1nsf_3ng_9ns

Title: Create a new subfamily *Wallmarkvirinae* with three new genera, *Machiasvirus*

Authors: Andrew M. Kropinski, Cristina Moraru, Jumpei Uchiyama, Małgorzata Łobocka, Andrew D. Millard

Summary:
Taxonomic rank(s) affected:
Subfamily, genus

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):
To create a new subfamily *“Wallmarkvirinae”* with three new genera, *“Machiasvirus”, “Lentusvirus”* and *“Madawaskavirus”* of jumbo *Staphylococcus myophages*

Justification: This proposal covers a clade of bacterial viruses with genomes of greater than 250 kb that infect *Staphylococcus* spp. Comparative analysis at the nucleotide level indicates that this clade of phages exhibit a minimum of 54% inter-genomic similarity. At the protein level, these bacteriophages 163 proteins. This indicates that approximately 60.8% of the phage-encoded proteins are conserved. In accordance with the demarcation criteria, we propose one new subfamily that includes three new genera and nine new species.

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 84 - *Wallmarkvirinae*, 13 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Wallmarkvirinae*		
New taxon	Genus	*Machiasvirus*		
New taxon	Species	*Machiasvirus AH12*	Staphylococcus phage AH12	OR455461
New taxon	Species	*Machiasvirus machias*	Staphylococcus phage Machias	MW349128
New taxon	Species	*Machiasvirus PB50*	Staphylococcus phage vB_StaM_PB50	OR770614
New taxon	Genus	*Lentusvirus*		
New taxon	Species	*Lentusvirus SA1*	Staphylococcus phage vB_StaM_SA1	MW218148
New taxon	Genus	*Madawaskavirus*		
New taxon	Species	*Madawaskavirus LY01*	Staphylococcus phage LY01	OR836606
New taxon	Species	*Madawaskavirus PALS2*	Staphylococcus phage PALS2	MN091626
New taxon	Species	*Madawaskavirus DC4*	Staphylococcus phage vB_SauM-UFV_DC4	MZ779063
New taxon	Species	*Madawaskavirus marshill*	Staphylococcus phage MarsHill	MW248466
New taxon	Species	*Madawaskavirus madawaska*	Staphylococcus phage Madawaska	MW349129

2025.080B.A.v2.Justusliebigvirus_4ns

Title: Create four new species in the genus *Justusliebigvirus* (class *Caudoviricetes,* subfamily *Stephanstirmvirinae)*

Authors: Michał J. Wójcicki, Iwona Gientka, Barbara Sokołowska

Summary:
Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes*

Description of current taxonomy:
The subfamily *Stephanstirmvirinae* comprises two genera, *Justusliebigvirus* and *Phapecoctavirus,* and 19 species. Currently, the *Justusliebigvirus* genus includes six species: *Justusliebigvirus* VEcB, *Justusliebigvirus* PHB05, Justusliebigvirus PD06, Justusliebigvirus alia, Justusliebigvirus phi92, *and* Justusliebigvirus muut.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create four new species in the genus *Justusliebigvirus* (class *Caudoviricetes, subfamily Stephanstirmvirinae).*

Justification:
Based on DNA and protein similarity, the proposed four new species are coherent and together with the six known species *(Justusliebigvirus* VEcB, *Justusliebigvirus* PHB05, Justusliebigvirus PD06, Justusliebigvirus alia, Justusliebigvirus phi92, *and* Justusliebigvirus *muut)* can be classified in the genus *Justusliebigvirus.*

Submitted: 27/03/2025; *Revised:* —

TABLE 85 - *Justusliebigvirus*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Justusliebigvirus UAB1*	Salmonella phage UAB_1	OL656106
New taxon	Species	*Justusliebigvirus SD2*	Escherichia phage SD2	PQ821640
New taxon	Species	*Justusliebigvirus KKP3264*	Serratia phage KKP_3264	OK210077
New taxon	Species	*Justusliebigvirus JLBYU50*	Escherichia phage JLBYU50	OK272470

2025.081B.Ac.v3.Yuavirus_12ns

Title: Add 12 new species to the genus *Yuavirus,* Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The genus *Yuavirus* currently consists of five species. Previous proposals related to this genus are 2012.008a-dB.A.v3.Yualikevirus and 2015.006aB.A.v2.Phage_Genera_ren.

Proposed taxonomic change(s):
To create 12 new species in the *genus Yuavirus*

Justification:
Species classified in the genus *Yuavirus* represent lytic siphoviruses with genomes of approximately 60kb and a characteristic elongated head structure. This proposal adds 12 new species to the genus, based on intergenomic similarity calculated using VIRIDIC.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 86 - *Yuavirus*, 12 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Yuavirus PC1*	Pseudomonas phage PC1	PP596838
New taxon	Species	*Yuavirus bella*	Pseudomonas phage Bella	PP661417
New taxon	Species	*Yuavirus jack*	Pseudomonas phage Jack	PP661418
New taxon	Species	*Yuavirus JM2*	Pseudomonas phage JM2	PP944331
New taxon	Species	*Yuavirus PAC4*	Pseudomonas phage vB_Pa-PAC4	PP408251
New taxon	Species	*Yuavirus PAC6*	Pseudomonas phage vB_Pa-PAC6	PP408253
New taxon	Species	*Yuavirus Epa38*	Pseudomonas phage Epa38	MT118302
New taxon	Species	*Yuavirus PSA20*	Pseudomonas phage PSA20,	MZ089734
New taxon	Species	*Yuavirus PSP2*	Pseudomonas phage PSP2	OR538761
New taxon	Species	*Yuavirus NEU2024*	Pseudomonas phage NEU2024	PQ144889
New taxon	Species	*Yuavirus clover*	Pseudomonas phage Clover	OQ992553
New taxon	Species	*Yuavirus HLL23*	Pseudomonas phage vB_Pae_HLL23	PP760143

2025.082B.A.v2.Yuavirus_2ns

Title: Create two new species in the genus *Yuavirus* (class *Caudoviricetes)*

Authors: Aaryan Harshith, Paul Bollyky, Jessica C. Sacher, Carlo Armijo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Yuavirus* was established under proposal 2012.008a-dB.A.v3.Yualikevirus. The genus currently consists of five species.

Proposed taxonomic change(s):
Create two new species in the *genus Yuavirus.*

Justification:
VIRIDIC analysis indicates that both phages satisfy the species similarity threshold proposed by the ICTV Bacterial Viruses Subcommittee. Proteomic and phylogenetic evidence further supports the placement of phages Vanta and Luminis in the genus *Yuavirus.*

Submitted: 22/01/2025; *Revised:* —

TABLE 87 - *Yuavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Yuavirus vanta*	Pseudomonas phage vanta	PQ628237
New taxon	Species	*Yuavirus luminis*	Pseudomonas phage Luminis	PQ632788

2025.083B.Uc.v3.Zimmerviridae_1nf_3nsf_4ng_9ns

Title: Create a new family *Zimmerviridae* (Class: *Caudoviricetes)*

Authors: Julien Lossouarn , Susan (M) Lehman , Igor Tolstoy, Andrew (M) Kropinski, Evelien Adriaenssens , Marie-Agnès Petit

Summary:
Taxonomic rank(s) affected
Family, subfamily, genus, species

Description of current taxonomy:
Since its discovery in the early 1950's to the mid 1980's, the temperate bacterial virus (phage) lambda was at the heart of the research which played a crucial role in our current understanding of molecular genetics. Over the years, many phages related to lambda, and susceptible to recombine with it, were isolated and named « lambdoids » (or « lambda-like »). Until recently, lambda and most of the lambdoid phages were taxonomically assigned into the family Siphoviridae, according to a classification scheme based on prokaryotic virion morphotype. In the last years, this morphological taxonomy was abandoned in favor of a molecular taxonomy, based upon overall DNA and protein similarity, for which lambda still remains unclassified at the family level.

Proposed taxonomic change(s):
Create a new family, *Zimmerviridae,* with two new subfamilies, six new genera and eight new species Move the genera *Jouyvirus,* Bievrevirus, Glaedevirus, Nesevirus, Alegriavirus, Radostvirus and *Lambdavirus* into the newly created *Jacobvirinae subfamily*

Justification:
We have applied whole proteome and phylogenetic approaches to analyse a set of 98 lambdoid genomes and 2 outliers, *Escherichia* phage T1 *(Tunavirus T1)* and T7 *(Teseptimavirus T7).* Based on these results, 22 of the 98 genomes form a cohesive and monophyletic group; we consequently propose a new family, named *"Zimmerviridae"* to honour microbiologist Esther Zimmer Lederberg. We propose to divide this family into two subfamilies, forming distinct monophyletic clades. We propose to name them *"Jacobvirinae"* and *"Wollmanvirinae"* to celebrate respectively microbiologists François Jacob and Elie Wollman. Seven previously defined genera and 14 previously defined species are clustered in the *"Jacobvirinae",* while intergenomic nucleotide similarities helped us to define three more genera and five species within the *"Wollmanvirinae"* subfamily.

Submitted: —; *Revised:* 11/03/2025

TABLE 88 - *Zimmerviridae*, 17 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Zimmerviridae*		
New taxon	Subfamily	*Jacobvirinae*		
New taxon	Subfamily	*Wollmanvirinae*		

New taxon	Genus	*Limmatquaivirus*		
New taxon	Species	*Limmatquaivirus mEp460*	Enterobacteria phage mEp460	JQ182728
New taxon	Species	*Limmatquaivirus mEp460_4F5*	Escherichia virus mEp460_4F5	LR595868
New taxon	Genus	*Dotonborivirus*		
New taxon	Species	*Dotonborivirus cdtl*	Enterobacteria phage cdtl	AB285204
New taxon	Species	*Dotonborivirus Ayreon*	Escherichia phage Ayreon	MF807953
New taxon	Genus	*Vilvertvirus*		
New taxon	Species	*Vilvertvirus mEp460ev081*	Escherichia phage mEp460_ev081	LR597641
New taxon	Genus	*Yvettevirus*		
New taxon	Species	*Yvettevirus Gifsy1*	Salmonella typhimurium phage Gifsy-1	NC_010392
New taxon	Genus	*Essonnevirus*		
New taxon	Species	*Essonnevirus Gifsy2*	Salmonella typhimurium phage Gifsy-1	NC_010393
New taxon	Genus	*Schuylkillvirus*		
New taxon	Species	*Schuylkillvirus Fels1*	Salmonella phage Fels-1	NC_010391

TABLE 89 - *Zimmerviridae*, 7 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Jouyvirus*	*Zimmerviridae*
Move taxon	Genus	*Bievrevirus*	*Zimmerviridae*
Move taxon	Genus	*Glaedevirus*	*Zimmerviridae*
Move taxon	Genus	*Nesevirus*	*Zimmerviridae*
Move taxon	Genus	*Alegriavirus*	*Zimmerviridae*
Move taxon	Genus	*Radostvirus*	*Zimmerviridae*
Move taxon	Genus	*Lambdavirus*	*Zimmerviridae*

2025.084B.Ac.v3.Zizhuyuanvirus_1ng_1ns

Title: Create one new genus, *Zizhuyuanvirus,* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:

Taxonomic rank(s) affected:

Genus, species

Description of current taxonomy:

The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):

Create one new genus, *Zizhuyuanvirus* and a single species

Justification:

Leptolyngbya phage Lsp-JY19 is a temperate siphovirus with a 37.4 kb genome. Analysis of the genome sequence with VIRIDIC reveals very low intergenomic similarity (<20%) to two phages which infect *Stenotrophomonas* sp. Based on the lack of similarity to other phages, we propose that the creation of a new species and genus, *Zizhuyuanvirus.*

Submitted: —; *Revised:* 09/01/2025

TABLE 90 - *Zizhuyuanvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Zizhuyuanvirus*		
New taxon	Species	*Zizhuyuanvirus JY19*	Leptolyngbya phage Lsp-JY19	PP438411

2025.085B.A.v2.Friunavirus_32ns

Title: Create 32 new species in the genus *Friunavirus* (class *Caudoviricetes, order* Autographivirales, *family* Autoscriptoviridae, *subfamily Beijerinckvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Edyta Pawlak, Iwona Gientka, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes, order* Autographivirales, *family* Autoscriptoviridae, *subfamily Beijerinckvirinae.*

Description of current taxonomy:
The subfamily *Beijerinckvirinae* comprises four genera (i.e., *Aristophanesvirus,* Daemvirus, Friunavirus, *Pettyvirus) and* 68 species. Currently, the *Friunavirus* genus includes 65 species.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create 32 new species in the *genus Friunavirus.*

Justification:
Based on DNA and protein similarity, the 32 proposed new species are coherent and together with the 65 known species can be classified in the genus *Friunavirus.*

Submitted: 20/06/2025; *Revised:* —

TABLE 91 - *Friunavirus*, 32 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Friunavirus AB3*	Acinetobacter phage AB3	KC311669
New taxon	Species	*Friunavirus 1137KEN02*	Acinetobacter phage vB_Ab_1137_KEN_02	PP841130
New taxon	Species	*Friunavirus 1137KEN05*	Acinetobacter phage vB_Ab_1137_KEN_05	PP841136
New taxon	Species	*Friunavirus 1137KEN03*	Acinetobacter phage vB_Ab_1137_KEN_03	PP841131
New taxon	Species	*Friunavirus 5899STDY8049184*	Acinetobacter phage MD-2021b strain 5899STDY8049184	OV298668
New taxon	Species	*Friunavirus NC12*	Acinetobacter phage AB_NC12	PV022100
New taxon	Species	*Friunavirus SWHAb1*	Acinetobacter phage SWH-Ab-1	NC_047896
New taxon	Species	*Friunavirus 5899STDY8049183*	Acinetobacter phage MD-2021b strain 5899STDY8049183	OV298628
New taxon	Species	*Friunavirus TCUAN2*	Acinetobacter phage TCUAN2	ON531987
New taxon	Species	*Friunavirus 5899STDY8049180*	Acinetobacter phage MD-2021b strain 5899STDY8049180	OV298791

New taxon	Species	*Friunavirus 1137KEN06*	Acinetobacter phage vB_Ab_1137_KEN_06	PP841137
New taxon	Species	*Friunavirus Margaret*	Acinetobacter phage vB_AbaP_Margaret	OZ038333
New taxon	Species	*Friunavirus phiAB440*	Acinetobacter phage phiAB440	PP792915
New taxon	Species	*Friunavirus Tama*	Acinetobacter phage vB_AbaP_Tama	OZ038331
New taxon	Species	*Friunavirus Fanak*	Acinetobacter phage vB_AbaP_Fanak	OZ075095
New taxon	Species	*Friunavirus Bhz16*	Acinetobacter phage vB_AbaS-Bhz16	PV067733
New taxon	Species	*Friunavirus A43Y*	Acinetobacter phage A43Y	PV467368
New taxon	Species	*Friunavirus Acba19*	Acinetobacter phage Acba_19	PV067698
New taxon	Species	*Friunavirus APK44*	Acinetobacter phage vB_AbaP_APK44	MN604238
New taxon	Species	*Friunavirus ZC2*	Acinetobacter phage vB_Aba_ZC2	PQ351672
New taxon	Species	*Friunavirus 164KEN02*	Acinetobacter phage vB_Ab_164_KEN_02	PP841133
New taxon	Species	*Friunavirus 5899STDY8049177*	Acinetobacter phage MD-2021b strain 5899STDY8049177	OV298630
New taxon	Species	*Friunavirus 5899STDY8049181*	Acinetobacter phage MD-2021b strain 5899STDY8049181	OV298725
New taxon	Species	*Friunavirus Fishpie*	Acinetobacter phage vB_AbaP_Fishpie	OZ038332
New taxon	Species	*Friunavirus EAB11*	Acinetobacter phage vB_AbaA_EAB11	PV208534
New taxon	Species	*Friunavirus 02KEN01*	Acinetobacter phage vB_Ab_02_KEN_01	PP841128
New taxon	Species	*Friunavirus ABW132*	Acinetobacter phage vB_AbaP_ABW132	OZ038338
New taxon	Species	*Friunavirus A31Y*	Acinetobacter phage A31Y	PV467367
New taxon	Species	*Friunavirus ABW311*	Acinetobacter phage vB_AbaP_ABW311	OZ038334
New taxon	Species	*Friunavirus W8*	Acinetobacter phage vB_AbaP_W8	PP174318
New taxon	Species	*Friunavirus Ab11*	Acinetobacter phage Ab11	PP763255
New taxon	Species	*Friunavirus AbaSI4*	Acinetobacter phage vB_AbaSI_4	PQ382035

2025.086B.Uc.v3.Luriaviridae_1nf_3ng_1mg_12ns

Title: Create a new family, *Luriaviridae,* with four genera, *Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus,* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Iwona Gientka, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:
Taxonomic rank(s) affected:
Family, genus, species

Description of current taxonomy:
Currently, the *Saclayvirus* genus includes three species: *Saclayvirus Aci011, Saclayvirus Aci022,* and *Saclayvirus Aci05.*

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create a new family *(Luriaviridae)* with four genera *(Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus)* for a group of *Acinetobacter-specific* phages (realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Saclayvirus.* Based on our analysis, we propose the creation of a new family for these phages along with four distinct genera.

To create a new family, *Luriaviridae,* with four genera.
To create a new single species genus, *Queenastridvirus.*
To create a new genus, *Wulsvirus,* with three species.
To move the genus, *Saclayvirus,* to a new family, *Luriaviridae.*
To create six new species in genus *Saclayvirus.*
To create a new genus, *Dalianvirus,* with two species.

Justification:
After examination of bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Luriaviridae,* to accommodate four genera *(Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 20/06/2025; *Revised:* 17/10/2025

TABLE 92 - *Luriaviridae*, 16 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Luriaviridae*		
New taxon	Genus	*Queenastridvirus*		
New taxon	Species	*Queenastridvirus Acibel004*	Acinetobacter phage vB_AbaM_Acibel004	KJ473422
New taxon	Genus	*Wulsvirus*		
New taxon	Species	*Wulsvirus Acba22*	Acinetobacter phage Acba_22	PV067693
New taxon	Species	*Wulsvirus KissB*	Acinetobacter phage vB_AbaM_KissB	OZ038335
New taxon	Species	*Wulsvirus Rocket*	Acinetobacter phage vB_AbaM_Rocket	OZ038337
New taxon	Species	*Saclayvirus Ab121*	Acinetobacter phage Ab_121	MT623546
New taxon	Species	*Saclayvirus CP14*	Acinetobacter phage vB_AbaM_CP14	OP585105
New taxon	Species	*Saclayvirus Liucustia*	Acinetobacter phage Liucustia	MW349133
New taxon	Species	*Saclayvirus phi1092033*	Acinetobacter phage phi1_092033	PQ859668
New taxon	Species	*Saclayvirus TAC1*	Acinetobacter phage TAC1	MK170160
New taxon	Species	*Saclayvirus 14CRR8*	Acinetobacter phage vB_AbaM_14/CRR8	PV611675
New taxon	Genus	*Dalianvirus*		
New taxon	Species	*Dalianvirus D22*	Acinetobacter phage vB_AbaM_D22	MT188223
New taxon	Species	*Dalianvirus P1*	Acinetobacter phage vB_AbaM_P1	OL960030

TABLE 93 - *Luriaviridae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Saclayvirus*	*Luriaviridae*

2025.088B.Uc.v3.Caudoviricetes_2ng_2ns

Title: Create two new single-species genera – *Odravirus* and *Solivirus* (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Edyta Pawlak, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The Acinetobacter phage Acjo_20 and Acinetobacter phage phiAC-1 have not yet been classified by the ICTV. Analysis of the NCBI database indicates their closest similarity to phages from the *Obolenskvirus* genus, but the degree of relatedness is too low to link them to the *Obolenskvirus genus.*

Proposed taxonomic change(s):
To create two new single-species genera – *Odravirus* and *Solivirus* (class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus.* Based on our analysis, we propose the creation of a two distinct genera, not classified to the family level.

To create a new single species genus, *Odravirus.*
To create a new single species *genus, Solivirus.*

Justification:
Analysis performed using VIRIDIC and ViPTree indicates that the Acinetobacter phage Acjo_20 and Acinetobacter phage phiAC-1 each form a single species in two new genera. The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 20/06/2025; *Revised:* 23/10/2025

TABLE 94 - *Caudoviricetes*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Odravirus*		
New taxon	Species	*Odravirus Acjo20*	Acinetobacter phage Acjo_20	PV067699
New taxon	Genus	*Solivirus*		
New taxon	Species	*Solivirus phiAC1*	Acinetobacter phage phiAC-1	JX560521

2025.089B.Ac.v3.Acarajevirus_1ng_1ns

Title: Proposal of a new genus, *Acarajevirus,* harboring a new species belonging to the *Peduoviridae* family

Authors: Poliane Alfenas-Zerbini, Rafael R. Rezende , ,

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy: *Peduoviridae* is orphan family associated with *Caudoviricetes* order harboring a total of 58 genera and 126 species.

Proposed taxonomic change(s): We proposed the Ralstonia phage AB1 be classified as new species "Acarajevirus bahia" belonging to a new genus named "Acarajevirus" associated with the family *Peduoviridae (Caudoviricetes class)*

Justification:
According to recommendation of ICTV to bacterial viruses taxonomy, the Ralstonia phage AB1 is related to other viruses from *Peduoviridae* family, but no sharing intergenomic similarity enough to be classified to establish species or genus.

Submitted: —; *Revised:* —

TABLE 95 - *Acarajevirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Acarajevirus*		
New taxon	Species	*Acarajevirus bahia*	Ralstonia phage AB1	PP316168

2025.090B.Ac.v3.Anamaviridae_1nf

Title: The description of new *Ralstonia* phage and its related phage fill some gaps on *Caudoviricetes* taxonomy

Authors: Poliane Alfenas-Zerbini, Rafael R. Rezende

Summary:
Taxonomic rank(s) affected:
Genus, species, subfamily, family.

Description of current taxonomy: The *Bakolyvirus* and *Naesvirus* comprise genera unrelated to any family. As for *Tsukubavirus, Beograduvirus* and *Xanthovirus* are associated with the subfamily *Kantovirinae,* which is not associated with any family.

Proposed taxonomic change(s): Recently, we described a new temperate phage named Ralstonia phage CA1 that infects bacteria *Ralstonia solanacearum* and *Ralstonia pseudosolanacearum.* The taxonomy classification of this virus results in the proposal of a new family, *"Anamaviridae",* harboring the subfamilies *"Mascarenevirinae"* a new family, and *Kantovirinae,* previously not associated with the established family. Also, we proposed the creation of "Cocadavirus alagoinhas" species *(Cocadavirus* genus) related to the "Mascarenevirinae" subfamily. At last, we proposed moving the "Cocadavirus", *Bakolyvirus,* and *Naesvirus* to the new subfamily "Mascarenevirinae".

Justification: Based on whole-sequence intergenomic similarity analysis, it was possible to reclassify 28 isolates into species associated with a new genus and other established genera and further, based on the sharing of protein orthogroups, a new subfamily was created, which was associated with a new family and established as a subfamily. This proposal eliminated some taxonomic gaps in families and genera from the *Caudoviricetes* class.

Submitted: —; Revised: —

TABLE 96 - *Anamaviridae*, 21 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Anamaviridae*		
New taxon	Subfamily	*Mascarenevirinae*		
New taxon	Genus	*Cocadavirus*		
New taxon	Species	*Cocadavirus alagoinhas*	Ralstonia phage CA1	PP316168
New taxon	Species	*Bakolyvirus elie*	Ralstonia phage Elie	MT740735
New taxon	Species	*Bakolyvirus adzire*	Ralstonia phage Adzire	MT740725
New taxon	Species	*Bakolyvirus sarlave*	Ralstonia phage Sarlave	MT740746
New taxon	Species	*Bakolyvirus jenny*	Ralstonia phage Jenny	MT740744
New taxon	Species	*Tsukubavirus xpp6*	Xanthomonas phage XPP6	MG944231
New taxon	Species	*Tsukubavirus xpp2*	Xanthomonas phage XPP2	MG944228
New taxon	Species	*Tsukubavirus xpp3*	Xanthomonas phage XPP3	MG944229
New taxon	Species	*Tsukubavirus xpp8*	Xanthomonas phage XPP8	MG944232
New taxon	Species	*Tsukubavirus xpp9*	Xanthomonas phage XPP9	MG944233
New taxon	Species	*Tsukubavirus pxoo2107*	Xanthomonas phage pXoo2107	OP067662
New taxon	Species	*Tsukubavirus x2*	Xanthomonas phage X2	MW435566
New taxon	Species	*Tsukubavirus xpv3*	Xanthomonas phage XPV3	MG944236
New taxon	Species	*Tsukubavirus xpv2*	Xanthomonas phage XPV2	MG944235
New taxon	Species	*Beograduvirus BsXeu*	Xanthomonas phage BsXeu269p/3	ON996340
New taxon	Species	*Beograduvirus myk3*	Xanthomonas phage MYK3	OK275494
New taxon	Genus	*Xanthovirus*		
New taxon	Species	*Xanthovirus neb7*	Xanthomonas phage NEB7	OQ676962

TABLE 97 - *Anamaviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Bakolyvirus*	*Anamaviridae*
Move taxon	Genus	*Naesvirus*	*Anamaviridae*
Move taxon	Subfamily	*Kantovirinae*	*Anamaviridae*

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Fungal and Protist Viruses Subcommittee

Contents

2025.001F.A.v3.Dinodnavirus_1spren_Rhizidiovirus_abolish

Title: Rename one species in the genus *Dinodnavirus* and abolish one species in the genus *Rhizidiovirus*

Authors: Sead Sabanadzovic, Arvind Varsani, Mart Krupovic, Keizo Nagasaki, Jens H Kuhn

Summary:
Taxonomic rank(s) affected:
Species, genus

Description of current taxonomy:
Dinodnavirus; Heterocapsa circularisquama DNA virus *01*
Rhizidiovirus; Rhizidiomyces virus

Proposed taxonomic change(s):
Rename one species in the genus *Dinodnavirus* and abolish one species in the genus *Rhizidiovirus.*

Justification:
Currently, there are two species of DNA viruses under the remit of the ICTV Fungal and Protist Viruses Subcommittee with nomenclature not conforming to the ICTV's binomial standards. We propose renaming the species *Heterocapsa* circularisquama DNA virus *01* in the genus *Dinodnavirus* to *"Dinodnavirus heterocapsae".* Furthermore, we propose abolishing the sole species *Rhizidiomyces virus* in the unassigned genus *Rhizidiovirus* due to the lack of any available genome sequence information for its representative member, Rhizidiomyces virus, which renders its classification impossible based on current ICTV standards. Accordingly, being a monospecific taxon, the genus *Rhizidiovirus* is also proposed to be abolished.

Submitted: 25/06/2025; *Revised:* —

TABLE 1 - *Dinodnavirus*, 2 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	Species	*Rhizidiomyces virus*
Abolish taxon	Genus	*Rhizidiovirus*

TABLE 2 - *Dinodnavirus*, 1 rename taxon*

Operation	Rank	Previous taxon name	New taxon name
Rename taxon	Species	*Heterocapsa circularisquama DNA virus 01*	*Dinodnavirus heterocapsae*

2025.002F.A.v3.Sobelivirales_2spren

Title: Rename two species in the order *Sobelivirales*

Authors: Sead Sabanadzovic, Arvind Varsani, Mart Krupovic, Jens H Kuhn

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy:
Sobelivirales; Alvernaviridae; Dinornavirus; Heterocapsa circularisquama RNA virus *01*
Sobelivirales; Barnaviridae; Barnavirus; Mushroom bacilliform virus

Proposed taxonomic change(s):
Rename two species of RNA viruses in the order *Sobelivirales* to conform with the mandated binomial nomenclature.:
Sobelivirales; Alvernaviridae; Dinornavirus; "Dinornavirus heterocapsae"
Sobelivirales; Barnaviridae; Barnavirus; "Barnavirus agarici"

Justification:
At present, there are two species of RNA viruses, *Heterocapsa* circularisquama RNA virus *01 (Sobelivirales; Alvernaviridae; Dinornavirus)* and *Mushroom* bacilliform *virus (Sobelivirales; Barnaviridae; Barnavirus),* under the remit of the Fungal and Protist Viruses Subcommittee. These names are not in line with the ICTV's mandated binomial format. Therefore, we propose renaming them using Latinized binomials, as *"Dinornavirus heterocapsae* "and *"Barnavirus agarici",* respectively.

Submitted: 25/06/2025; *Revised:* —

TABLE 3 - *Sobelivirales*, 2 rename taxa*

Operation	Rank	Previous taxon name	New taxon name
Rename taxon	Species	*Heterocapsa circularisquama RNA virus 01*	*Dinornavirus heterocapsae*
Rename taxon	Species	*Mushroom bacilliform virus*	*Barnavirus agarici*

2025.003F.A.v2.Alphapithovirus_spren

Title: Rename one species in the genus *Alphapithovirus*

Authors: Jean Michel Claverie, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Pimascovirales; Ocovirineae; Pithoviridae; Orthopithovirinae; Alphapithovirus; Alphapithovirus sibericum

Proposed taxonomic change(s):
Rename current species *Alphapithovirus* sibericum *to* Alphapithovirus *siberiense,* as it was listed in the original proposal.

Justification:
During the multiple rounds of the review process of a complex taxonomic proposal concerning reorganization of the order *Pimascovirales* submitted in 2024 (), the name of one species was accidentally reported erroneously in the accompanying Excel file (). With this action we seek correction of that clerical error to reflect original idea of TP authors.

Submitted: 18/06/2025; *Revised:* —

TABLE 4 - *Alphapithovirus*, 1 rename taxon*

Operation	**Rank**	**Previous taxon name**	**New taxon name**
Rename taxon	Species	*Alphapithovirus sibericum*	*Alphapithovirus siberiense*

2025.004F.A.v2.Deltanormycoviridae_rename

Title: Rename *family Deltanormycoviridae*

Authors: Marco Forgia, Massimo Turina, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected: Family

Description of current taxonomy:
Orpoviricetes; Bormycovirales; Deltanormycoviridae

Proposed taxonomic change(s):
Orpoviricetes; Bormycovirales; Deltaormycoviridae

Justification:
During the preparation of taxonomic proposal submitted in 2024 proposing the creation of a new class of RNA mycoviruses *Orpoviricetes* with two orders, five families, seven genera and 26 species, inadvertently a typo was introduced in the Excel file ( ) resulting in an unintended name of one of the new families *(Deltanormycoviridae).* This error went unnoticed during the review process and was transferred into a current version of the Master Species List, making *Deltanormycoviridae* the official

name for this family. With this proposal we seek correction of that unfortunate error to reflect the original idea of the TP authors to name the taxon *Deltaormycoviridae,* as originally reported in the Word file of the proposal *().*

Submitted: 23/06/2025; *Revised:* —

TABLE 5 - *Deltanormycoviridae*, 1 rename taxon*

Operation	Rank	Previous taxon name	New taxon name
Rename taxon	Family	*Deltanormycoviridae*	*Deltaormycoviridae*

2025.005F.Ac.v3.Ambiguiviridae_newfam

Title: Create new family in order *Tolivirales* with 3 new genera and 42 new species

Authors: Michael J Adams , Xiaohan Mo, Hongying Zheng

Summary:
Taxonomic rank(s) affected:
Order Tolivirales

Description of current taxonomy:
Two families: *Tombusviridae and Carmotetraviridae*

Proposed taxonomic change(s):
Creation of a new family *"Ambiguiviridae"* in the order *Tolivirales* to accommodate three new genera and a total of 42 new species.

Justification:
Over the past two decades, a substantial number of evolutionary related viruses with bicistronic RNA(+) genome, ranging from 2.6 kb to ~5.5 kb in length, have been discovered mostly from fungi and from metagenomic studies. Their ORF1 encodes a protein of unknown function but with conserved domains, while ORF2 codes for a putative RNA-dependent RNA polymerase (RdRP) with similarity to those of plant-infecting viruses in the family *Tombusviridae.* As this group of viruses is not part of the official virus taxonomy yet, we formally propose their classification in a new family *"Ambiguiviridae"* in the order *Tolivirales.*

Submitted: 26/05/2025; *Revised:* 30/08/2025

TABLE 6 - *Ambiguiviridae*, 46 new taxa*. Table too large, see supplementary information sheet supp_info_tab_6

2025.006F.Ac.v3.Polymycoviridae_3ngen_18nsp

Title: Polymycoviridae_reorganization

Authors: Poliane Alfenas-Zerbini, Cauê N. Oliveira, Ioly Kotta-Loizou, Robert H. A. Coutts, Sead Sabanadzovic

Summary:Taxonomic rank(s) affected:
This proposal affects the family *Polymycoviridae* and its sole *genus Polymycovirus.*

Description of current taxonomy:
Polymycoviridae comprises a single genus, *Polymycovirus,* with 10 species recognized by the ICTV.

Proposed taxonomic change(s):
We propose to split genus *Polymycovirus* into three genera namely, *Polymycovirus, "Multimycovirus",* and *"Plurimycovirus"* in the family *Polymycoviridae.* Consequently, we propose to move and rename the 5 established species in the family *Polymycoviridae* based on the novel genus they are assigned in. Additionally, we propose to establish 18 novel species in the family *Polymycoviridae,* 4 in the genus *Polymycovirus,* 13 in the genus *"Multimycovirus",* and 1 in the genus *"Plurimycovirus".*

Justification:
We propose reorganization of the family by splitting the genus *Polymycovirus* into three novel genera to better reflect the evolutionary relationships among classified and novel polymycovirus-related isolates. Additionally, we propose establishing 18 new species in *the Polymycoviridae* family, representing almost threefold fold increase in species number in this taxon. We believe that this new organization will facilitate further work on classifying the increasing number of polymycovirids.

Submitted: 13/06/2025; *Revised:* 22/09/2025

TABLE 7 - *Polymycoviridae*, 20 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Polymycovirus aspeflavi*	Aspergillus flavus polymycovirus 1	RNA1: LC763247; RNA2: LC763248; RNA3: LC763249; RNA4: LC763250; RNA5: LC763251
New taxon	Species	*Polymycovirus metarhizae*	Metarhizium robertsii polymycovirus 1	RNA1: PV166302; RNA2: PV166303; RNA3: PV166304; RNA4: PV166305
New taxon	Species	*Polymycovirus turcicalternatae*	Setosphaeria turcica polymycovirus 2	RNA1: OQ433940; RNA2: OQ433941; RNA3: OQ433942; RNA4: OQ433943; RNA5: OQ433944
New taxon	Species	*Polymycovirus erynecati*	Erysiphe necator associated polymycovirus 2	RNA1: MN617800; RNA2: MN617801; RNA3: MN617802; RNA4: MN617803
New taxon	Genus	*Multimycovirus*		
New taxon	Species	*Multimycovirus secuphyllostictae*	Phyllosticta capitalensis polymycovirus 2	RNA1: PP359416; RNA2: PP359417; RNA3: PP359418; RNA4: PP359419; RNA5:PP359420
New taxon	Species	*Multimycovirus priphyllostictae*	Phyllosticta capitalensis polymycovirus 1	RNA1: PP359411; RNA2: PP359412; RNA3: PP359413; RNA4: PP359414; RNA5: PP359415
New taxon	Species	*Multimycovirus metabrunnei*	Metarhizium brunneum polymycovirus 1	RNA1: OP524132; RNA2: OP524133; RNA3: OP524134; RNA4: OP524135

New taxon	Species	*Multimycovirus talaromyci*	Talaromyces amestolkiae polymycovirus 1	RNA1: OP096450; RNA2: OP096451; RNA3: OP096452; RNA4: OP096453; RNA5: OP096454; RNA6: OP096455
New taxon	Species	*Multimycovirus miniphaeocremonii*	Phaeoacremonium minimum tetramycovirus 1	RNA1: MK584824; RNA2: MK584825; RNA3: MK584826; RNA4: MK584827
New taxon	Species	*Multimycovirus magnaporyzae*	Magnaporthe oryzae polymycovirus 2	MW752168; MW752169; MW752170; MW752171
New taxon	Species	*Multimycovirus cladosplasmoniae*	Cladosporium ramotenellum polymycovirus 1	RNA1: OQ053977; RNA2: OQ053978; RNA3: OQ053979; RNA4: OQ053980; RNA5: OQ053981; RNA6: OQ053982
New taxon	Species	*Multimycovirus erynecati*	Erysiphe necator associated polymycovirus 6	RNA1: MN617815; RNA2: MN617816; RNA3: MN617817
New taxon	Species	*Multimycovirus beauvessiana*	Beauveria bassiana polymycovirus 4	RNA1: MW385785; RNA2: MW385786; RNA3: MW385787; RNA4: MW385788; RNA5: MW385789; RNA6: MW385790
New taxon	Species	*Multimycovirus trichodermae*	Trichoderma barbatum polymycovirus 1	RNA1: OM307406; RNA2: OM307407; RNA3: OM307408; RNA4: OM307409
New taxon	Species	*Multimycovirus turcicae*	Setosphaeria turcica polymycovirus 1	RNA1: MW429374; RNA2: MW429375; RNA3: MW429376; RNA4: MW429377; RNA5: MW429378
New taxon	Species	*Multimycovirus alternatae*	Alternaria alternata polymycovirus 1	RNA1: MT345016; RNA2: MT345017; RNA3: MT345018; RNA4: MT345019; RNA5: MT345020; RNA6: MT345021; RNA7: MT345022; RNA8: MT345023
New taxon	Species	*Multimycovirus camesinensis*	Pseudopestalotiopsis camelliae-sinensis polymycovirus 1	RNA1: PP359405; RNA2: PP359406; RNA3: PP359407; RNA4: PP359408; RNA5: PP359409; RNA6: PP359410
New taxon	Genus	*Plurimycovirus*		
New taxon	Species	*Plurimycovirus cladosporidae*	Cladosporium cladosporioides polymycovirus 2	RNA1: OQ054008; RNA2: OQ054009; RNA3: OQ054010; RNA4: OQ054011;

				RNA5: OQ054012; RNA6: OQ054013

TABLE 8 - *Polymycoviridae*, 5 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old parent taxon	Old taxon name
Move; rename taxon	Species	*Multimycovirus aspelaei*	*Multimycovirus*	*Polymycovirus*	*Polymycovirus aspelaei*
Move; rename taxon	Species	*Multimycovirus aspergilli*	*Multimycovirus*	*Polymycovirus*	*Polymycovirus aspergilli*
Move; rename taxon	Species	*Multimycovirus botryosphaeriae*	*Multimycovirus*	*Polymycovirus*	*Polymycovirus botryosphaeriae*
Move; rename taxon	Species	*Multimycovirus magnaporthis*	*Multimycovirus*	*Polymycovirus*	*Polymycovirus magnaporthis*
Move; rename taxon	Species	*Plurimycovirus penidigitati*	*Plurimycovirus*	*Polymycovirus*	*Polymycovirus penidigitati*

2025.007F.Ac.v3.Mycopleornaviricetes_nclass_Xenadelphovirales_nord

Title: Create new class and new order to accommodate two orphan mycoviral families

Authors: Poliane Alfenas-Zerbini, Cauê N. Oliveira, Ioly Kotta-Loizou, Robert H. A. Coutts, Yuri I. Wolf, Nobuhiro Suzuki, Sead Sabanadzovic

Summary:Taxonomic rank(s) affected:
This proposal affects primarily the phylum *Pisuviricota,* by establishing a novel class and a novel order to accommodate two established families yet unassigned to higher taxa.

Description of current taxonomy:
Polymycoviridae is an orphan family within the realm *Riboviria,* not yet assigned to taxa of the order-kingdom ranks. *Polymycoviridae* is phylogenetically related to *Hadakaviridae,* a family assigned to the phylum *Pisuviricota,* kingdom *Orthornavirae,* realm *Riboviria* but not yet assigned to an order or class.

Proposed taxonomic change(s):
We propose to move *Polymycoviridae* to the phylum *Pisuviricota* and create a novel class, *"Mycopleornaviricetes"* and a novel order, *"Xenadelphovirales",* to accommodate the *Polymycoviridae* and *Hadakaviridae families.*

Justification:
Polymycoviridae and *Hadakaviridae* are two families of mycoviruses, belonging to a monophyletic clade within the phylum *Pisuviricota* and more closely related to each other than to other viral families within the same phylum. Currently, *Polymycoviridae* is not assigned to order-kingdom taxa, while *Hadakaviridae* is assigned to phylum *Pisuviricota* but not to an order or class. Therefore, we propose establishing a novel class and order to accommodate this monophyletic clade of mycoviruses.

Submitted: 30/04/2025; *Revised:* 30/08/2025

TABLE 9 - *Mycopleornaviricetes*, 2 new taxa*

Operation	**Rank**	**New taxon name**
New taxon	Class	*Mycopleornaviricetes*
New taxon	Order	*Xenadelphovirales*

TABLE 10 - *Mycopleornaviricetes*, 2 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Family	*Polymycoviridae*	*Orthornavirae*
Move taxon	Family	*Hadakaviridae*	*Mycopleornaviricetes*

2025.008F.A.v2.Tobaliviridae_newfam

Title: Create one new family, one genus and 9 species in the order *Martellivirales*

Authors: Sead Sabanadzovic, Nina Aboughanem-Sabanadzovic, Massimo Turina, Nobuhiro Suzuki, Mart Krupovic

Summary:
Taxonomic rank(s) affected:
Order, family, genus, species

Description of current taxonomy:
The order *Martellivirales* currently contains seven families *(Bromoviridae,* Closteroviridae, Endornaviridae, Kitaviridae, Mayoviridae, *Togaviridae* and *Virgaviridae)* of (+)RNA viruses encoding alphavirus-like replicases.

Proposed taxonomic change(s):
We propose establishing a new family *"Tobaliviridae"* in the order *Martellivirales* to classify a growing group of "tobamo-like" viruses characterized from fungi. The proposed family will contain a single genus *"Tobalivirus"* with nine species.

Justification:
Despite obvious similarities in genome organization and possible expression strategy between tobamoviruses (family *Virgaviridae)* and "tobamo-like" mycoviruses, differences in:
primary hosts (plant versus fungi)
genome size (6.3-6.6 versus 10-13 kb),
size and nature of proteins encoded by ORF3,
CP size (17 kDa versus 36 kDa),
virion morphology (rigid versus flexuous rods) and
phylogenetically distinct RdRP lineage
justify the proposal for creation of a new family *"Tobaliviridae"* with a single genus, *"Tobalivirus",* containing nine species to classify a set of well-characterized viruses.

Submitted: 20/06/2025; *Revised:* —

TABLE 11 - *Tobaliviridae*, 11 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Tobaliviridae*		

New taxon	Genus	*Tobalivirus*		
New taxon	Species	*Tobalivirus acidomyci*	Acidomyces richmondensis tobamo-like virus 1	MK279511
New taxon	Species	*Tobalivirus armillariae*	Armillaria borealis mycovirgavirus 1	MW423800
New taxon	Species	*Tobalivirus auricolariae*	Auricularia heimuer mycovirgavirus 1	MN928963
New taxon	Species	*Tobalivirus macrophominae*	Macrophomina phaseolina tobamo-like virus	KF537660
New taxon	Species	*Tobalivirus lentinulae*	Lentinula edodes tobamo-like virus 1	MN744727
New taxon	Species	*Tobalivirus nigrosporae*	Nigrospora aurantiaca tobamo-like virus 1	OR228589
New taxon	Species	*Tobalivirus podosphaerae*	Podosphaera prunicola tobamo-like virus	KY420046
New taxon	Species	*Tobalivirus ibericum*	Plasmopara viticola lesion associated tobamo-like virus 1	MN565665
New taxon	Species	*Tobalivirus uromyci*	Uromyces fabae virus	OQ995224

2025.009F.Ac.v3.Potyliviridae_newfam

Title: Create new family *“Potyliviridae”* in the order *Patatavirales*

Authors: Nina Aboughanem-Sabanadzovic, Massimo Turina, Mart Krupovic, Jens H Kuhn, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected: Order

Description of current taxonomy:
Order *Patatavirales* currently includes a single family, *Potyviridae* (13 genera; 259 species).

Proposed taxonomic change(s):
To create a second family in the order *Patatavirales,* with proposed name *“Potyliviridae”* comprising one new genus *(“Potylivirus”)* to classify two new species.

Justification:
Creation of a new family *“Potyliviridae”* comprising a new genus *“Potylivirus”* with two species is proposed to classify recently discovered group of viruses with monocistronic (+)RNA genomes of ≈7.5-8.0 kb in length. Members of the *“Potyliviridae”* are distantly related to members of the family *Potyviridae,* in particular to viruses belonging to the genus *Potyvirus.* The creation of a new family is strongly supported by phylogenetic analyses.

Submitted: 25/06/2025; *Revised:* 30/08/2025

TABLE 12 - *Potyliviridae*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Potyliviridae*		
New taxon	Genus	*Potylivirus*		
New taxon	Species	*Potylivirus italicum*	Plasmopara viticola lesion associated poty-like virus 1	MN551108
New taxon	Species	*Potylivirus uromyci*	Uromyces potyvirus A	MK231047

2025.010F.Uc.v3.Chlorovirus_3ngen_16nsp_2mergesp

Title: Creation of 3 new subgenera and 16 new species within the genus *Chlorovirus (Phycodnaviridae)* to position and name chloroviruses isolates

Authors: Rodrigo A L Rodrigues, João Victor RP Carvalho, Letícia R Henriques, David D Dunigan, James L Van Etten

Summary:
Taxonomic rank(s) affected: The genus *Chlorovirus* includes large DNA viruses capable of replicating in chlorella-like green algae. The chloroviruses have been isolated since the 1980s, found in inland waters worldwide. Genomic and biological data indicate the existence of three groups of chloroviruses.

Description of current taxonomy: Included in the family *Phycodnaviridae,* there are currently six species of chloroviruses. Dozens of isolates have been described over the last years, but a formal proposal to adequately classify these viruses has not yet been made.

Proposed taxonomic change(s): Here, we propose the creation of three subgenera, named *"Alphachlorovirus", "Betachlorovirus",* and *"Gammachlorovirus",* to classify the different groups of chloroviruses. This classification is demarcated by phylogenetic analysis based on the several genes, usually used for phylogenetic reconstructions of giant viruses. Furthermore, based on the nucleotide identity of the whole viral genome (≥94%), we propose the creation of 16 new chlorovirus species and the abolition of two others, which should be merged with other existing species.

Justification: The genus *Chlorovirus* was formally created in 1998. Since then, many chloroviruses have been obtained and characterized. However, limited progress has been made regarding the taxonomy. With dozens of isolates with available genomes, it is clear that there are three large groups of chloroviruses that must be properly classified. Furthermore, with many isolates, we can now advance the taxonomy of these viruses and establish new species. This will guide the group's taxonomy, hoping that new viruses can emerge and be properly classified.

Submitted: 20/06/2025; *Revised:* 01/11/2025

TABLE 13 - *Chlorovirus*, 19 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subgenus	*Alphachlorovirus*		
New taxon	Species	*Chlorovirus primosyngense*	only-Syngen Nebraska virus	KX857749
New taxon	Species	*Chlorovirus alphanebraskense*	chlorovirus N-NE-4	PP681873
New taxon	Species	*Chlorovirus syngense*	chlorovirus O-NE-18	PP681894
New taxon	Species	*Chlorovirus alphaalkalinus*	chlorovirus O-NE-11	PP681887
New taxon	Species	*Chlorovirus alphagardense*	chlorovirus O-NE-13	PP681889
New taxon	Subgenus	*Betachlorovirus*		
New taxon	Species	*Chlorovirus longinquus*	Paramecium bursaria Chlorella virus NE-JV-1	JX997176

New taxon	Species	*Chlorovirus betanebraskense*	Paramecium bursaria Chlorella virus CZ-2	JX997166
New taxon	Subgenus	*Gammachlorovirus*		
New taxon	Species	*Chlorovirus novaeterrae*	Acanthocystis turfacea Chlorella virus Br0604L	JX997155
New taxon	Species	*Chlorovirus guatemalense*	Acanthocystis turfacea Chlorella virus GM0701.1	JX997168
New taxon	Species	*Chlorovirus gammanebraskense*	Acanthocystis turfacea Chlorella virus NTS-1	JX997180
New taxon	Species	*Chlorovirus arcticum*	chlorovirus GNLD-22	PQ067566
New taxon	Species	*Chlorovirus solusgardense*	chlorovirus S-NE-20	PQ067562
New taxon	Species	*Chlorovirus gammagardense*	chlorovirus S-NE-18	PQ067560
New taxon	Species	*Chlorovirus multilacus*	Acanthocystis turfacea Chlorella virus Canal-1	JX997158
New taxon	Species	*Chlorovirus insulalacus*	chlorovirus S-NE-11	PQ067554
New taxon	Species	*Chlorovirus minnesotense*	Acanthocystis turfacea Chlorella virus MN0810.1	JX997174

TABLE 14 - *Chlorovirus*, 4 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old parent taxon	Old taxon name
Move; rename taxon	Species	*Chlorovirus vanettense*	*Alphachlorovirus*	*Chlorovirus*	*Chlorovirus vanettense*
Move; rename taxon	Species	*Chlorovirus americanus*	*Alphachlorovirus*	*Chlorovirus*	*Chlorovirus americanus*
Move; rename taxon	Species	*Chlorovirus conductrix*	*Betachlorovirus*	*Chlorovirus*	*Chlorovirus conductrix*
Move; rename taxon	Species	*Chlorovirus heliozoae*	*Gammachlorovirus*	*Chlorovirus*	*Chlorovirus heliozoae*

TABLE 15 - *Chlorovirus*, 1 merge taxa*

Operation	Rank	Old taxon 1	Old taxon 2	Merged taxon
Merge taxa	Species	Chlorovirus illinoense	Chlorovirus newyorkense	Chlorovirus vanettense

2025.011F.A.v2.Imitervirales_newtaxa

Title: Create 2 suborders, 4 genera and 9 species within the order *Imitervirales*

Authors: Victoria F Queiroz, Frank O Aylward, Jônatas S Abrahão, Corina Brussaard, Matthias Fischer, Rohit Ghai, Mohammad Moniruzzaman, Hiroyuki Ogata, Frederik Schulz, Curtis Suttle

Summary:
Taxonomic rank(s) affected:
Order, Suborder, genus and species.

Description of current taxonomy:
The *Imitervirales* order currently comprises 4 families, 3 subfamilies, 14 genera and 22 species (proposal #2022.004F).

Proposed taxonomic change(s):
Here, we propose to create 4 new genera and 9 new species following the currently valid demarcation criteria, and create 2 suborders to accommodate the existing viral families of the *order Imitervirales.*

Justification:
A new knowledge generated in the past few years require updates in the taxonomy of the order *Imitervirales* by adding new isolates and representatives that had not been previously classified. In order to accurately depict the novel knowledge, we propose to reorganize the order by creating 2 suborders, 4 genera and 9 new species to classify new viruses in this order.

Submitted: —; *Revised: —*

TABLE 16 - *Imitervirales*, 43 move taxa*. Table too large, see supplementary information sheet supp_info_tab_16

TABLE 17 - *Imitervirales*, 15 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Suborder	*Orthomivirineae*		
New taxon	Genus	*Catovirus*		
New taxon	Species	*Catovirus klosterense*	Catovirus naegleriensis	OZ003748
New taxon	Species	*Moumouvirus maliense*	Moumouvirus maliensis; Borely moumouvirus	MK978772; MN175499
New taxon	Species	*Moumouvirus lavasanguinense*	Moumouvirus lavasanguinem	LC813553
New taxon	Species	*Megavirus caiporense*	Megavirus caiporense	OP925046
New taxon	Suborder	*Paramivirineae*		
New taxon	Genus	*Budvirus*		
New taxon	Species	*Budvirus rimovense*	Budvirus	OY749542
New taxon	Genus	*Punuivirus*		
New taxon	Species	*Punuivirus latens*	Punuivirus	PV354230
New taxon	Species	*Tethysvirus bergenense*	Prymnesium kappa virus	PV100844
New taxon	Species	*Tethysvirus norvegense*	Haptolina ericina virus	PV100843
New taxon	Genus	*Criusvirus*		
New taxon	Species	*Criusvirus kaneoense*	Florenciella sp. virus	PP542043

2025.012F.Uc.v3.Hypofuvirales_neworder

Title: Reclassifying families *Hypo*- and *Fusariviridae* into a new order *"Hypofuvirales" (Stelpaviricetes: Pisuviricota)* and their reorganization

Authors: Massimo Turina, Sotaro Chiba, Leonardo Velasco, Maria A. Ayllón, Nobuhiro Suzuki, Shin-Yi Lee-Marzano, Liying Sun, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected:
Species, Genus, Family, Order, Class

Description of current taxonomy:
Currently, families *Hypoviridae* and *Fusariviridae* are members of the *order Durnavirales* in the *class Duplopiviricetes* in the phylum *Pisuviricota.* Such assignment was based on a previous "megataxonomy" analysis that associated viruses in the family Hypoviridae with members of the

order *Durnavirales, yet* with rather poor statistical support.

Proposed taxonomic change(s):
We propose to move the families *Hypoviridae* and *Fusariviridae* to a newly created order *"Hypofuvirales"* in the *Stelpaviricetes* class. Additionally, we propose to create a new family *"Parahypoviridae"* to move current genus *Betahypovirus.* We also propose to create a new genus *"Iotahypovirus"* in the family *Hypoviridae* and a new genus *"Deltafusarivirus"* in the *Fusariviridae.* Finally, we propose creation of 51 new species to be classified in these three families, of which 27 in the family *Hypoviridae,* 5 in the newly *proposed "Parahypoviridae"* and 19 in *the Fusariviridae.*

Justification:
The original classification of the two families, *Hypoviridae* and *Fusariviridae, (Duplopiviricetes; Durnavirales)* was not well supported. A newly performed phylogenetic analysis performed on RdRPs of members of the currently recognized classes in the phylum *Pisuviricota* shows strong support for the reclassification of the two families in the class *Stelpaviricetes* and justifying creation of a new order to accommodate both families (and another newly created *"Parahypoviridae",* proposed here) to recognize their distinction from members of orders *Stellavirales* and *Patatavirales.* Also, importantly, there is a basic difference between members of the *Hypoviridae* (which are infectious as ssRNA) and members of the *Durnavirales* (which are mostly confirmed dsRNA viruses and are not infectious as ssRNA).

Submitted: 20/06/2025; *Revised:* 29/10/2025

TABLE 18 - *Hypofuvirales*, 55 new taxa***.** Table too large, see supplementary information sheet supp_info_tab_18

TABLE 19 - *Hypofuvirales*, 3 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**	**Old parent taxon**
Move taxon	Family	*Fusariviridae*	*Stelpaviricetes*	*Duplopiviricetes*
Move taxon	Family	*Hypoviridae*	*Stelpaviricetes*	*Duplopiviricetes*
Move taxon	Genus	*Betahypovirus*	*Stelpaviricetes*	*Duplopiviricetes*

2025.013F.Uc.v3.Botourmiaviridae_reorgan

Title: Botourmiaviridae reorganization

Authors: María A. Ayllón, Livia Donaire, Massimo Turina, Luca Nerva, Shin-Yi Marzano, Jiatao Xie, Daohong Jiang, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected:
Genus, Family, Order

Description of current taxonomy:
The family *Botourmiaviridae* is currently the only family in the order *Ourlivirales.* It includes twelve genera with 159 species: *Ourmiavirus, Botoulivirus, Betabotoulivirus, Magoulivirus, Scleroulivirus, Betascleroulivirus, Betascleroulivirus, Gammascleroulivirus, Epsilonscleroulivirus, Rhizoulivirus, Betarhizoulivirus, and Penoulivirus.*

Proposed taxonomic change(s):
We propose to reorganize current family *Botourmiaviridae by* creating additional two new families *"Ourmiaviridae" and "Rhizouliviridae"* in the order *Ourlivirales* by to better reflect phylogenetic

relationships among members of this order of (+)RNA viruses.

Justification: Results of updated phylogenetic analyses of the RNA dependent RNA polymerases (RdRPs) of viruses belonging to the family *Botourmiaviridae* and newly characterized, related and yet unclassified, viruses showed three main clades supported by high bootstrap values. One group includes ten genera currently classified in the family *Botourmiaviridae,* second clade is composed of the two genera *(Rhizoulivirus* and *Betarhizoulivirus)* of viruses exclusively reported from the basidiomycetous *hosts,* while the third comprises members of the three plant-infecting members of a current *genus Ourmiavirus* along *with* several recently sequenced closely related *viruses.* The three well-supported clades are proposed to represent three families in the order *Ourlivirales.*

Submitted: 06/10/2025; *Revised:* 31/10/2025

TABLE 20 - *Botourmiaviridae*, 36 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Rhizouliviridae*		
New taxon	Family	*Ourmiaviridae*		
New taxon	Genus	*Alphaourmiavirus*		
New taxon	Species	*Alphaourmiavirus crustaceae*	Wenling narna-like virus 1	KX883607
New taxon	Species	*Alphaourmiavirus fluminis*	ripasyc virus	PP173676
New taxon	Species	*Alphaourmiavirus octopi*	Beihai narna-like virus 4	KX883508
New taxon	Species	*Alphaourmiavirus penaeus*	Wenzhou narna-like virus 2	KX883549
New taxon	Genus	*Betaourmiavirus*		
New taxon	Species	*Betaourmiavirus fluminis*	ripablyj virus	PP172563
New taxon	Species	*Betaourmiavirus mollusci*	Hubei narna-like virus 2	KX883578
New taxon	Species	*Betaourmiavirus conchyli*	Beihai narna-like virus 1	KX883515
New taxon	Genus	*Gammaourmiavirus*		
New taxon	Species	*Gammaourmiavirus conchyli*	Beihai narna-like virus 2	KX883512
New taxon	Genus	*Deltaourmiavirus*		
New taxon	Species	*Deltaourmiavirus fluminis*	ripazant virus	PP172404
New taxon	Genus	*Epsilonourmiavirus*		
New taxon	Species	*Epsilonourmiavirus striata*	Kummerowia striata ourmiavirus 1	MN831445
New taxon	Species	*Epsilonourmiavirus lespedezae*	Kummerowia striata ourmiavirus 2	MN831446
New taxon	Species	*Epsilonourmiavirus croci*	saffron associated botourmia-like virus	BK067260
New taxon	Genus	*Zetaourmiavirus*		
New taxon	Species	*Zetaourmiavirus culex*	Serbia narna-like virus 3	MT822185
New taxon	Species	*Zetaourmiavirus insecti*	Laodelphax striatellus narna-like virus 1	LC851054
New taxon	Genus	*Etaourmiavirus*		
New taxon	Species	*Etaourmiavirus humi*	chrocasust virus	PP172054
New taxon	Species	*Etaourmiavirus agri*	chrocaniss virus	PP171944
New taxon	Genus	*Thetaourmiavirus*		
New taxon	Species	*Thetaourmiavirus pasti*	Sopadaq virus	PP174063
New taxon	Species	*Thetaourmiavirus fluminis*	ripabruz virus	PP172646
New taxon	Species	*Thetaourmiavirus terrae*	sonajac virus	PP173876
New taxon	Species	*Thetaourmiavirus agri*	chrocapent virus	PP171969
New taxon	Genus	*Iotaourmiavirus*		
New taxon	Species	*Iotaourmiavirus agri*	chrocafask virus	PP171834

New taxon	Species	*Iotaourmiavirus mollusci*	chrocabim virus	PP171760
New taxon	Species	*Iotaourmiavirus fluminis*	flumine botourmiavirus 3	OM953858
New taxon	Genus	*Kappaourmiavirus*		
New taxon	Species	*Kappaourmiavirus terrae*	sonatrut virus	PP173830

TABLE 21 - *Botourmiaviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Genus	*Rhizoulivirus*	*Rhizouliviridae*	*Botourmiaviridae*
Move taxon	Genus	*Betarhizoulivirus*	*Rhizouliviridae*	*Botourmiaviridae*
Move taxon	Genus	*Ourmiavirus*	*Ourmiaviridae*	*Botourmiaviridae*

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 Plant viruses Subcommittee

Contents

2025.001P.Ac.v3.Aspiviridae_splitgen_1ng_14nsp

Title: Split one genus, and create one genus and 14 species in the family *Aspiviridae*

Authors: Nicolas Bejerman, Humberto Debat, Selma Gago-Zachert, John Hammond, Laura Miozzi, Tomohide Natsuaki, Yutaro Neriya , Vicente Pallás, Carina A Reyes, Mark PS Rivarez, Takahide Sasaya , Ioannis Tzanetakis, Anna Maria Vaira, Martin Verbeek

Summary:

Taxonomic rank(s) affected:

Genus *Ophiovirus, family Aspiviridae*

Description of current taxonomy:

The family *Aspiviridae* comprises the single genus *Ophiovirus.* Eight virus species are currently classified in the genus *Ophiovirus,* six of which infect dicotyledonous plants of widely different taxonomy, and the other two have monocot species as their plant host. The assignment of viruses to this genus is based on the placement of viruses in a Maximum Likelihood tree inferred from complete RdRp or CP protein sequences.

Proposed taxonomic change(s):
Split the genus *Ophiovirus,* creating one new genus *("Miraophiovirus")* and assigning the current *Ophiovirus* species to the appropriate genus; create 14 new species in the family *Aspiviridae.*

Justification:
Recently, 14 new putative ophioviruses were discovered, which we propose to classify into 14 new species. The phylogenetic relationships of the now significantly expanded number of known ophiovirus species provide support for splitting the genus *Ophiovirus* to establish two genera *(Ophiovirus* and *"Miraophiovirus")* that represent distinct evolutionary lineages.

Submitted: 16/05/2025; *Revised:* 08/12/2025

TABLE 1 - *Aspiviridae*, 15 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Ophiovirus allii*	Allium ophiovirus	BK062657; BK062658; BK062659
New taxon	Species	*Ophiovirus arctotis*	Arctotis ophiovirus	BK062660; BK062661; BK062662
New taxon	Species	*Ophiovirus chrysanthemi*	Chrysanthemum ophiovirus	BK062669; BK062670; BK062671
New taxon	Species	*Ophiovirus citrulli*	Citrullus ophiovirus	BK062675; BK062676; BK062677
New taxon	Species	*Ophiovirus daturae*	Datura ophiovirus	BK062682; BK062683; BK062684
New taxon	Species	*Ophiovirus gentianae*	Gentiana ophiovirus	BK062690; BK062691; BK062692
New taxon	Species	*Ophiovirus osteospermi*	Osteospermum ophiovirus	BK062711; BK062712; BK062713
New taxon	Genus	*Miraophiovirus*		
New taxon	Species	*Miraophiovirus caladeniae*	Caladenia ophiovirus	BK062666; BK062667; BK062668
New taxon	Species	*Miraophiovirus carotae*	carrot ophiovirus 1	OM419178; OM419179; OM419180; OM419181
New taxon	Species	*Miraophiovirus cyrtomii*	Cyrtomium ophiovirus	BK062679; BK062680; BK062681
New taxon	Species	*Miraophiovirus erythranthis*	Erythranthe ophiovirus	BK062687; BK062688; BK062689
New taxon	Species	*Miraophiovirus lepidoziae*	Lepidozia ophiovirus	BK062699; BK062700; BK062701
New taxon	Species	*Miraophiovirus violae*	Viola ophiovirus	BK062735; BK062736; BK062737

New taxon	Species	*Miraophiovirus xerochrysi*	Xerochrysum ophiovirus	BK062740; BK062741; BK062742

TABLE 2 - *Aspiviridae*, 6 move; rename taxa*

Operation	**Rank**	**New taxon name**	**Old taxon name**	**New parent taxon**	**Old parent taxon**
Move; rename taxon	Species	*Miraophiovirus capsici*	*Ophiovirus capsici*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus freesiae*	*Ophiovirus freesiae*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus lactucae*	*Ophiovirus lactucae*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus mirafioriense*	*Ophiovirus mirafioriense*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus ranunculi*	*Ophiovirus ranunculi*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus tulipae*	*Ophiovirus tulipae*	*Riboviria*	*Riboviria*

2025.002P.Ac.v3.Alphaflexiviridae_Allexivirus_1nsp

Title: Create one (1) new species in the family *Alphaflexiviridae*

Authors: Peter Abrahamian, Miguel A. Aranda, Thierry Candresse, Livia Donaire, John Hammond, Beata Hasiów-Jaroszewska, Luisa Rubino, Anna Maria Vaira

Summary:
Taxonomic rank(s) affected:
Genus *Allexivirus* in the family *Alphaflexiviridae*

Description of current taxonomy:
The *family Alphaflexiviridae* currently includes 72 virus species in genera *Allexivirus* (14), *Botrexvirus* (3), *Lolavirus* (1), *Platypuvirus* (1), *Potexvirus* (52) and *Sclerodarnavirus* (1).

Proposed taxonomic change(s):
This taxonomic proposal considers the creation of one (1) new species belonging to genus *Allexivirus* within the family *Alphaflexiviridae.*

Justification:
Throughout the family, isolates of different species should have less than 72% nucleotide identity (or 80% amino acid identity) between their respective coat protein or polymerase genes (or proteins). Viruses from different genera usually have less than about 45% nucleotide identity in these genes. The nucleotide and amino acid sequences of the virus belonging to the newly proposed species fit well within these demarcation criteria.

Submitted: 06/06/2025; *Revised:* 28/08/2025

TABLE 3 - *Alphaflexiviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Allexivirus sauroandrogyni*	Sauropus androgynus virus	PQ177843

2025.003P.A.v3.Caulimoviridae_Badnavirus_1nsp

Title: Create one (1) new species in the genus *Badnavirus*

Authors: Marie Umber , Indranil Dasgupta , Andrew D.W. Geering , Anders Hafrén , Roger Hull , Jan Kreuze , Scott M. Leisner , Emmanuelle Muller , Hanu Pappu , Mikhail Pooggin , Katja Richert-Poeggeler , Susan Seal , Livia Stavolone , Pierre Yves Teycheney

Summary:

Taxonomic rank(s) affected:
Genus *Badnavirus* in the *family Caulimoviridae*

Description of current taxonomy:
The family *Caulimoviridae* [1] currently comprises 11 genera whose members share similar genome organization. The molecular species demarcation criterion is < 80% identity of nucleotide sequences in the reverse transcriptase (RT) / ribonuclease H (RNase H) region of the polymerase. Genus *Badnavirus* [2] currently includes 74 species and is the largest genus within the *family Caulimoviridae.*

Proposed taxonomic change(s):
We propose the creation of one new species in the genus *Badnavirus: "Badnavirus urticae"*

Justification:
The complete genomes of nettle badnavirus 1 (NBV1), was sequenced and published recently. Its organization is similar to that of other members of genus *Badnavirus.* Phylogenetic analyses place NBV1 in this genus as distinct representative of a novel species.

Submitted: 13/06/2025; *Revised:* 28/08/2025

TABLE 4 - *Caulimoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Badnavirus urticae*	nettle badnavirus 1	PP792697

2025.004P.Ac.v3.Kitaviridae_13nsp

Title: Create one (1) new species in the genus *Cilevirus,* and 12 novel species in the genus *Blunervirus,* family *Kitaviridae,* order *Martellivirales.*

Authors: Caixia Yang, Avijit Roy, Juliana Freitas-Astúa, Antonio Tiberini, Li Jun-Min, Kavi Sidharthan, Mónica Madariaga-Villarroel, Sergey Y. Morozov, Pedro L. Ramos-González

Summary:

Taxonomic rank(s) affected:
Genera *Cilevirus* and *Blunervirus* in the *family Kitaviridae*

Description of current taxonomy:
Kitaviruses comprise a group of plant-infecting viruses with single-stranded (ss), positive-sense (+), segmented RNA genomes. The family *Kitaviridae,* order *Martellivirales,* consists of three genera, currently including eight species in the genus *Cilevirus,* and three in each of the *genera Higrevirus* and

Blunervirus. Most members of the genera *Cilevirus* and *Higrevirus* are transmitted by tenuipalpid mites of the genus *Brevipalpus,* whereas at least two blunerviruses are shown to be transmitted by eriophyid mites.

Proposed taxonomic change(s):
Create one and 12 new species in the genera *Cilevirus and Blunervirus,* respectively, in the family *Kitaviridae,* order *Martellivirales.*

Justification:
Novel identified viruses possess relatively high nucleotide sequence identity, a compatible genomic organization, and/or a phylogenetic relationship with members of the known species within the family *Kitaviridae.* Biological and molecular characterization of a virus identified in large periwinkle *(Vinca major)* plants demonstrated that it should be classified into a novel species within the genus *Cilevirus.* Genomic analyses of other 12 novel viruses, obtained from either original high-throughput sequencing (HTS) data or publicly accessible sequence repositories, indicate they belong to new species in the genus *Blunervirus.* Deduced amino acid sequences of these novel viruses share less than 70% amino acid sequence identity with those of known and novel tentative blunerviruses. Phylogenetic analyses using the replication proteins place these novel viruses in the clade containing viruses of the known species of blunerviruses.

Submitted: 06/03/2025; *Revised:* 20/08/2025

TABLE 5 - *Kitaviridae*, 13 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Cilevirus chilense*	Vinca ringspot virus	RNA1: OQ116675; RNA2: OQ116676
New taxon	Species	*Blunervirus cinnamomi*	camphor tree blunervirus 1	RNA1: BK068192; RNA2: BK068193; RNA3: BK068194; RNA4: BK068195
New taxon	Species	*Blunervirus torreyae*	Chinese nutmeg tree blunervirus 1	RNA1: BK068220; RNA2: BK068221; RNA3: BK068222; RNA4: BK068223
New taxon	Species	*Blunervirus chrysanthemi*	Chrysanthemum blunervirus 1	RNA1: BK068200; RNA2: BK068201; RNA3: BK068202; RNA4: BK068203
New taxon	Species	*Blunervirus cupressus*	cypress blunervirus 1	RNA1: BK068188; RNA2: BK068189; RNA3: BK068190; RNA4: BK068191
New taxon	Species	*Blunervirus festucae*	Festuca sinensis blunervirus 1	RNA1: BK068204; RNA2: BK068205; RNA3: BK068206; RNA4: BK068207
New taxon	Species	*Blunervirus quercus*	oak blunervirus 1	RNA1: BK068208; RNA2: BK068209; RNA3: BK068210; RNA4: BK068211
New taxon	Species	*Blunervirus portulacae*	purslane blunervirus 1	RNA1: BK068216; RNA2: BK068217; RNA3: BK068218; RNA4: BK068219

New taxon	Species	*Blunervirus liquidambarum*	sweetgum blunervirus 1	RNA1: BK068212; RNA2: BK068213; RNA3: BK068214; RNA4: BK068215
New taxon	Species	*Blunervirus tritici*	wheat blunervirus 1	RNA1: BK068196; RNA2: BK068197; RNA3: BK068198; RNA4: BK068199
New taxon	Species	*Blunervirus paulowniae*	Paulownia tomentosa blunervirus	RNA1: GEFV01158142; RNA2: GEFV01018191; RNA3: GEFV01018861; RNA4: GEFV01018726
New taxon	Species	*Blunervirus ulmi*	elm blunervirus 1	RNA1: OL865294; RNA2: OL865295; RNA3: OL865296; RNA4: OL865297
New taxon	Species	*Blunervirus mali*	apple blunervirus 1	RNA1: OL344039; RNA2: OL344040; RNA3: OL344041; RNA4: OL344042; RNA5: OL344043

2025.005P.Benyviridae_Benyvirus_1nsp

Title: Create one new species in the *genus* Benyvirus *(Hepelivirales: Benyviridae)*

Authors: Juliana B. Valente, Fernando P. Sartori, Lucas A. Stempkowski, Monica Farias, Paulo R. Kuhnem, Douglas Lau, Thor V.M. Fajardo, Antonio Nhani Junior, Ricardo T. Casa, Amauri Bogo, Fábio N. Silva

Summary:

Taxonomic rank(s) affected:
Genus *Benyvirus* in the *family Benyviridae*

Description of current taxonomy:
Riboviria › Orthornavirae › Kitrinoviricota › Alsuviricetes › Hepelivirales › Benyviridae › *Benyvirus*
The genus *Benyvirus* consists of four species.

Proposed taxonomic change(s):
Create one species in *the genus Benyvirus: "Benyvirus tritici"*

Justification:
Based on the genomic organization of *P. graminis-associated* WhSMV-infected plant samples, as well as the nucleotide and amino acid sequences of the viral isolates characterized in this study, we propose that wheat stripe mosaic virus (WHSMV) is classified into a novel putative species within the family *Benyviridae,* for which the name *"Benyvirus tritici"* is *suggested.*

Submitted: 06/03/2025; *Revised:* 15/10/2025

TABLE 6 - *Benyviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**

New taxon	Species	*Benyvirus tritici*	wheat stripe mosaic virus	RNA1: MH151795; RNA 2: MH151801

2025.006P.Ac.v3.Konkoviridae_5nsp

Title: Create five (5) new species in the genus *Olpivirus (Hareavirales: Konkoviridae]*

Authors: Yutaro Neriya, Timo M Breit, Laura Miozzi, Anna Maria Vaira, Yasuhiro Tomitaka, Takahide Sasaya

Summary:Taxonomic rank(s) affected:
Genus *Olpivirus* in the *family Konkoviridae*

Description of current taxonomy:
The family *Konkoviridae* consists of the single genus *Olpivirus.* Two virus species are currently classified in the genus *Olpivirus,* Olpivirus *lactucae* and *Olpivirus tulipae.* The assignment of virus species to this genus is based on the placement of the corresponding viruses on a Neighbor-joining tree inferred from the complete RdRP protein sequences.

Proposed taxonomic change(s):
Create five new species in the genus *Olpivirus* to classify five newly *discovered konkoviruses.*

Justification:
Recently, five new putative konkoviruses were discovered. We propose the creation of five new species within the genus *Olpivirus* based on the species demarcation criterion of <90% identity in the amino acid sequence of the *RdRP.*

Submitted: 06/04/2025; *Revised:* 25/08/2025

TABLE 7 - *Konkoviridae*, 5 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Olpivirus freesiae*	Freesia konkovirus 1	RNA1: PQ490803; RNA2: PQ490804; RNA3: PQ490805; RNA4: PQ490806
New taxon	Species	*Olpivirus lachenaliae*	Lachenalia konkovirus 1	RNA1: PQ067367; RNA2: PQ067368; RNA3: PQ067369; RNA4: PQ067370
New taxon	Species	*Olpivirus soli*	soil associated konkovirus	RNA1: BK070195; RNA2: BK070196; RNA3: BK070197; RNA4: BK070198
New taxon	Species	*Olpivirus tripterocalicis*	Tripterocalyx associated konkovirus 1	RNA1: BK070397; RNA2: BK070398; RNA3: BK070399
New taxon	Species	*Olpivirus waitziae*	Waitzia associated konkovirus 1	RNA1: BK070191; RNA2: BK070192; RNA3: BK070193; RNA4: BK070194

2025.007P.Ac.v3.Tospoviridae_8nsp

Title: Create eight [8] new species in the genus *Orthotospovirus (Elliovirales: Tospoviridae)*

Authors: Scott Adkins, Marleen Botermans, Jiahong Dong, Denis Kutnjak, David Read, Ronel Roberts, Zhongkai Zhang, Amalendu Ghosh, Holly R. Hughes, Naidu Rayapati, Massimo Turina, Anna Whitfield, Paolo Margaria

Summary:

Taxonomic rank(s) affected:

Genus *Orthotospovirus* in the family *Tospoviridae*

Description of current taxonomy:

Negarnaviricota, Polyploviricotina, Bunyaviricetes, Elliovirales, Tospoviridae, *Orthotospovirus.*
The genus *Orthotospovirus* is the only genus in the *family Tospoviridae.* It. currently includes 28 virus species.

Proposed taxonomic change(s):

Create eight (8) new species in the genus *Orthotospovirus* to classifyieight (8) novel orthotospoviruses on the basis of the species demarcation criterion in the % amino acid sequence identity (<90%) of the nucleocapsid protein (N).

Justification:

The identity value of the nucleocapsid (N) protein sequence of the eight novel orthotospoviruses to other established orthotospoviruses and across themselves, is below 90%, satisfying the criterion for novel species demarcation in the genus *Orthotospovirus* based on sequence identity of the amino acid sequence of the N protein.

Submitted: 15/06/2025; *Revised:* 23/08/2025

TABLE 8 - *Tospoviridae*, 8 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Orthotospovirus tomatonecroanuli*	tomato necrotic ringspot virus	L: MW256413; M: MW256414; S: MW256415
New taxon	Species	*Orthotospovirus limonii*	Limonium orthotospovirus 1	L: PQ587430; M: PQ587431; S: PQ587432
New taxon	Species	*Orthotospovirus barlerichlorosis*	Barleria chlorosis-associated virus	L: MW251496; M: MW251497; S: MW251498
New taxon	Species	*Orthotospovirus scadoxiflavianuli*	Scadoxus chlorotic ringspot virus	L: MW080808; M: MW080809; S: MW080810
New taxon	Species	*Orthotospovirus macadamianuli*	Macadamia ringspot-associated virus	L: OP604037; M: OP604038; S: OP604039
New taxon	Species	*Orthotospovirus mercurialis*	Mercurialis orthotospovirus 1	L: OL471964; M: OL471965; S: OL471966

New taxon	Species	*Orthotospovirus capsiciflavianuli*	chilli yellow ringspot virus isolate	L: MH779497; M: MH779496; S: MH779495
New taxon	Species	*Orthotospovirus tomatonecromaculae*	tomato necrotic spot-associated virus	L: KT984754; M: KT984753; S: KM355773

2025.008P.Ac.v3.Betaflexiviridae_9nsp_2abolishsp

Title: Create nine (9) new species and abolish two (2) species in the family *Betaflexiviridae*

Authors: Tatsuya Nagata, Arnaud G Blouin, Thierry Candresse, Mengji Cao, Won K Cho, Fiona Constable, Massimiliano Morelli, Sead Sabanadzovic, Ioannis E Tzanetakis, Dan EV Villamor

Summary:Taxonomic rank(s) affected:
Genera *Banmivirus, Carlavirus, Robigovirus, Capillovirus, Chordovirus, Citrivirus, Vitivirus* in the *family Betaflexiviridae*

Description of current taxonomy:
The family *Betaflexiviridae* is divided into two subfamilies, *Quinvirinae* (5 genera) and *Trivirinae* (10 genera). Species in the family *Betaflexiviridae* are classified into the following genera:
Banmivirus (2 species), *Carlavirus* (73), *Foveavirus* (12), *Robigovirus (5),* Sustrivirus *(1),* Capillovirus *(8), Chordovirus* (4), *Citrivirus* (2), *Divavirus (3), Prunevirus* (4), *Ravavirus* (1), *Tepovirus* (5), *Trichovirus* (10), *Vitivirus* (19), *Wamavirus* (1). The currently approved species demarcation criteria based on sequence identity are <72% nucleotide identity in the replication-associated protein (Rep) or <80% amino acid identity in the capsid protein (CP).

Proposed taxonomic change(s):
We propose that the primary species demarcation criterion for the family *Betaflexiviridae* should be <80% aa identity of the Rep. If the aa identity is in the borderline range (78–82%), the CP aa identity (<85%) can be used as a secondary criterion [1].
Based on these new demarcation criteria, we propose to create nine (9) new species in seven genera of the family *Betaflexiviridae: Banmivirus* (1 new species), *Carlavirus* (1), *Robigovirus* (1), *Capillovirus* (1), *Chordovirus* (1), *Citrivirus* (1) and *Vitivirus* (3). Species *Carlavirus cacti* and *Carlavirus cornutum* will be abolished. The exemplar accessions of seven carlaviruses, one foveavirus and one vitivirus will be changed to other ones which have complete or coding-complete genomes.

Justification:
Recent analyses using all complete genomes available in GenBank and published as the study case by the *Beta-, Delta-* and *Gammaflexiviridae* study group established a more adequate threshold of Rep amino acid sequence identity for species demarcation.
The addition of nine new species is proposed in the family *Betaflexiviridae* since their Rep amino acid sequences identities are below 80%, according to the new species demarcation criteria described above.
Carlavirus cacti and *Carlavirus cornutum* will be abolished due to the lack of sufficient sequence information.

Submitted: 30/05/2025; *Revised:* 14/08/2025

TABLE 9 - *Betaflexiviridae*, 9 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Banmivirus miscanthi*	Miscanthus virus M	ON986335

New taxon	Species	*Carlavirus menthae*	mint virus C	PQ562895
New taxon	Species	*Robigovirus menthae*	Mentha arvensis robigovirus 1	OR397129
New taxon	Species	*Capillovirus paris*	Paris polyphylla severe chlorotic mottle virus	MW822017
New taxon	Species	*Chordovirus angelicae*	Angelica chordovirus	OR656535
New taxon	Species	*Citrivirus rudbeckiae*	Rudbeckia citrivirus A	ON216317
New taxon	Species	*Vitivirus muviti*	grapevine virus M	MK492703
New taxon	Species	*Vitivirus rhoviti*	grapevine virus P	LC746753
New taxon	Species	*Vitivirus gammactinidiae*	Actinidia virus C	MN022352

TABLE 10 - *Betaflexiviridae*, 2 abolish taxa*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Carlavirus cacti*
Abolish taxon	Species	*Carlavirus cornutum*

2025.009P.Ac.v3.Potyviridae_5nsp

Title: Create one (1) new species in genus *Arepavirus,* one (1) new species in genus *Macluravirus,* one (1) new species in genus *Poacevirus* and two (2) new species in genus *Potyvirus (Patatavirales: Potyviridae)*

Authors: Alice K Inoue-Nagata, Ramon Jordan, Jan F Kreuze, Fan Li, Juan J López-Moya, Kristiina Mäkinen, Kazusato Ohshima, Stephen J Wylie

Summary:
Taxonomic rank(s) affected:
Genera *Arepavirus, Macluravirus, Poacevirus, Potyvirus* in the family *Potyviridae*

Description of current taxonomy:
The family *Potyviridae* includes 13 genera and 259 species. Genus *Arepavirus* consists of 2 species, *Macluravirus* of 12 species, *Poacevirus* of 3 species and *Potyvirus* of 214 species. For the remaining 9 genera no recommendation for changes is proposed.

Proposed taxonomic change(s):
Creation of 5 new species: 1 species in the genus *Arepavirus ("Arepavirus karnatakense"),* 1 species in the genus *Macluravirus ("Macluravirus amomi"),* 1 species in the genus *Poacevirus ("Poacevirus avenae")* and 2 species in the genus *Potyvirus ("Potyvirus* heraclei", "Potyvirus shilinense").

Justification:
According to the ICTV Report chapter on *Potyviridae,* the 13 genera are distinguished based on biological criteria - primarily transmission by specific vectors - and molecular data, with members of different genera sharing less than 46% nucleotide sequence identity. Viruses from different species typically have complete ORF sequences that share less than 76% nucleotide identity and less than 82% amino acid identity. The genome sequences of the five proposed new viruses analyzed showed nucleotide and amino acid identities below the species demarcation thresholds. Additionally, biological data were available to support their classification as members of new species.

Submitted: 06/05/2025; *Revised:* 19/08/2025

TABLE 11 - *Potyviridae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Arepavirus karnatakense*	areca palm necrotic ringspot virus 2	PQ197196
New taxon	Species	*Macluravirus amomi*	tsaoko stripe mosaic virus	PQ068101
New taxon	Species	*Poacevirus avenae*	wild oat poacevirus 1	PQ561517
New taxon	Species	*Potyvirus heraclei*	hogweed virus Y	OR537212
New taxon	Species	*Potyvirus shilinense*	Paris potyvirus 5	OR608917

2025.010P.Ac.v4.Geminiviridae_Begomovirus_3nsp

Title: Create three (3) new species in the genus *Begomovirus* (family *Geminiviridae)*

Authors: F Murilo Zerbini, José T Ascencio- Ibáñez, Cica Urbino, Jean-Michel Lett, Paola López-Lambertini, Jesús Navas-Castillo, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Arvind Varsani

Summary:
Taxonomic rank affected:
Genus *Begomovirus* in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus*
Begomovirus is one of the largest genera in the virosphere, with 464 species. Within the genus *Begomovirus,* viruses are classified into species based on a 91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity threshold [1].

Proposed taxonomic changes:
Creation of 3 new species to classify new begomoviruses that have been identified and described in the literature over the past two years.

Justification:
Members of all 3 proposed new species share <91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity with sequences of members of currently established begomovirus species.

Submitted: 06/05/2025; *Revised:* 28/08/2025

TABLE 12 - *Geminiviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Begomovirus clitoriae*	butterfly pea yellow mosaic virus	DNA-A: PQ298353; DNA-B: PQ298354
New taxon	Species	*Begomovirus melochiasecundi*	Melochia associated virus	DNA-A: PP897773
New taxon	Species	*Begomovirus citharexyli*	Citharexylum leaf curl virus	DNA-A: OR437368

2025.011P.Ac.v3.Geminiviridae_Capulavirus_1nsp

Title: Create one (1) new species in the *genus* Capulavirus *(Geplafuvirales: Geminiviridae)*

Authors: Philippe Roumagnac, Jose T Ascencio- Ibáñez, Jean-Michel Lett, Paola M. López-Lambertini, Darren P. Martin, Jesús Navas-Castillo, Simone Ribeiro, Cica Urbino, Arvind Varsani, F. Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Genus Capulavirus in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria / Shotokuvirae / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae / Capulavirus*

Proposed taxonomic change(s):
We proposed to create one new species in the *genus Capulavirus: "Capulavirus betae"*

Justification:
Similar to members of the *Capulavirus* genus, members of the proposed new species *"Capulavirus betae"* have the virion-strand origin of replication nonanucleotide motif 'TAATATTAC' and show a typical capulavirus organization, with putative multiple overlapping short ORFs (V3 and V4) upstream of the CP gene that encode putative movement proteins. In addition, genome-wide pairwise analysis of the representative genomes of capulaviruses showed that beet capulavirus 1 sequence genome shared less than 78% identity with all representative genomes of capulaviruses. Since 78% nucleotide identity is the genome-wide species demarcation threshold for capulaviruses, we conclude that beet capulavirus 1 can be classified into the species *"Capulavirus betae",* a new species in the genus *Capulavirus.*

Submitted: 06/10/2025; *Revised:* 22/08/2025

TABLE 13 - *Geminiviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Capulavirus betae*	beet capulavirus 1	PQ682516

2025.012P.Ac.v3.Geminiviridae_Mastrevirus_5nsp

Title: Create five new species in the genus *Mastrevirus* (family *Geminiviridae)*

Authors: Arvind Varsani, Jean-Michel Lett, José T Ascencio- Ibáñez , Cica Urbino, Jesús Navas-Castillo, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, F Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Genus *Mastrevirus* in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria; Shotokuvirae; Cressdnaviricota; Repensiviricetes; Geplafuvirales; Geminiviridae; Mastrevirus

There are currently 50 established species in the genus *Mastrevirus.* New species in the genus *Mastrevirus* are determined based on a 78% pairwise identity threshold coupled with phylogenetic support.

Proposed taxonomic change(s):
Create five new species in the *genus Mastrevirus*

Justification:
In the last year, eight genomes of mastreviruses have been identified that cannot be classified at the species level within the current taxonomy framework. These can be classified into five new species sharing <78% pairwise identity with all classified mastreviruses.

Submitted: 06/06/2025; *Revised:* 22/08/2025

TABLE 14 - *Geminiviridae*, 5 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Mastrevirus cenchri*	Cenchrus echinatus associated virus	PQ434710
New taxon	Species	*Mastrevirus croci*	Mastrevirus sp. croci	PQ392009
New taxon	Species	*Mastrevirus mexicoense*	Mastrevirus sp. UHMV-1.PC-W	MN203180
New taxon	Species	*Mastrevirus purpurei*	Cenchrus purpureus mild streak virus	PQ434729
New taxon	Species	*Mastrevirus tripterygii*	Tripterygium mastrevirus A	MT159331

2025.013P.Ac.v3.Alphasatellitidae_2ng_8nsp

Title: Create two (2) new genera and 8 new species in the family *Alphasatellitidae*

Authors: F Murilo Zerbini, José T Ascencio- Ibáñez, Cica Urbino, Jean-Michel Lett, Jesús Navas-Castillo, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Arvind Varsani

Summary:Taxonomic rank affected:
Family *Alphasatellitidae*

Description of current taxonomy:
The family *Alphasatellitidae* is divided into three subfamilies: *Geminialphasatellitinae, Nanoalphasatellitinae,* and *Petromoalphasatellitinae,* consisting of 7, 6 and 5 genera, respectively.

Proposed taxonomic changes:
We propose the creation of 2 new genera (1 in subfamily *Geminialphasatellitinae* and 1 in subfamily *Nanoalphasatellitinae)* and 8 new species (4 in the 2 new genera, 4 in previously existing genera) to classify new alphasatellites that have been identified and described in the literature over the last two years.

Justification:
The exemplar members of the 3 proposed new species in the proposed new genus *"Banaphisatellite"* (subfamily *Nanoalphasatellitinae)* have <67% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily. The exemplar member of the 1 proposed new species in the proposed new genus *"Whedwasatellite"* (subfamily *Geminialphasatellitinae)* has <70% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily. The exemplar members of the 4 proposed new species in the genera *Clecrusatellite, Colecusatellite* and *Gosmusatellite* (subfamily *Geminialphasatellitinae)* have <88% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily.

Submitted: 13/06/2025; *Revised:* 22/08/2025

TABLE 15 - *Alphasatellitidae*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Banaphisatellite*		
New taxon	Species	*Banaphisatellite alphamusae*	banana bunchy top alphasatellite 4	OK546212
New taxon	Species	*Banaphisatellite betamusae*	banana bunchy top alphasatellite 5	ON960014
New taxon	Species	*Banaphisatellite gammamusae*	banana bunchy top alphasatellite 6	ON960025
New taxon	Genus	*Whedwasatellite*		
New taxon	Species	*Whedwasatellite triticiparvi*	wheat dwarf virus-associated alphasatellite	PP445014
New taxon	Species	*Colecusatellite asystasiae*	Asystasia yellow mosaic alphasatellite 1	LC724062
New taxon	Species	*Gosmusatellite asystasiae*	Asystasia yellow mosaic alphasatellite 2	LC724021
New taxon	Species	*Gosmusatellite lactucae*	pepper leaf curl Yunnan alphasatellite	PQ352199
New taxon	Species	*Clecrusatellite solanumbrasiliense*	tomato golden vein alphasatellite	MT214093

2025.014P.Ac.v3.Betasatellite_1nsp

Title: Create one new species in the genus *Betasatellite* (family *Tolecusatellitidae)*

Authors: Jesús Navas-Castillo, José T Ascencio-Ibáñez, Cica Urbino, Jean-Michel Lett, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Cica Urbino, Arvind Varsani, F Murilo Zerbini

Summary:Taxonomic rank affected:
Genus *Betasatellite* in the family *Tolecusatellitidae*

Description of current taxonomy:
Tolecusatellitidae -> *Betasatellite*
To date, the genus *Betasatellite* consists of 119 species.
Within the genus *Betasatellite,* DNA satellites are classified into species based on a 91% genome-wide pairwise identity threshold [1].

Proposed taxonomic changes:
Creation of one (1) new species to classify a new betasatellite that has been identified and described in the literature over the past four years.

Justification:
The member of the proposed new species shares <91% genome-wide pairwise identity with sequences of members of currently established betasatellite species.

Submitted: 13/06/2025; *Revised:* 22/08/2025

TABLE 16 - *Betasatellite*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Betasatellite trigonellae*	fenugreek leaf curl betasatellite	MZ648030

2025.015P.Ac.v3.Deltasatellite_1nsp

Title: Create one new species in the *genus* Deltasatellite *(Tolecusatellitidae)*

Authors: Jesús Navas-Castillo, Philippe Roumagnac, Jose T Ascencio-Ibáñez, Jean-Michel Lett, Paola M. López-Lambertini, Darren P. Martin, Simone Ribeiro, Cica Urbino, Arvind Varsani, F. Murilo Zerbini

Summary:Taxonomic rank affected:
Genus Deltasatellite in the *family* Tolecusatellitidae

Description of current taxonomy:
Tolecusatellitidae / Deltasatellite
The genus *Deltasatellite* consists of 12 species.

Proposed taxonomic change:
We proposed to create one new species in the *genus Deltasatellite: "Deltasatellite brassicae".*

Justification:
Similar to members of the *genus Deltasatellite,* members of the proposed new species *"Deltasatellite brassicae"* have all conserved features of deltasatellites, including an A-rich region, a stem-loop with the TAATATTAC nonanucleotide motif, and a region with identity to betasatellites. The isolates share 100% nucleotide identity among themselves, and ≤73.9% identity with known deltasatellites, below the 91% species demarcation threshold. Phylogenetic analysis shows the group forms a distinct clade within New World deltasatellites. We conclude that *"Deltasatellite brassicae"* represents a new species in the genus *Deltasatellite.*

Submitted: 06/05/2025; *Revised:* 22/08/2025

TABLE 17 - *Deltasatellite*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Deltasatellite brassicae*	cabbage leaf curl deltasatellite	OK073969

2025.016P.Ac.v3.Geminiviridae_3ng_3nsp

Title: Create three new species and three new genera in the *family Geminiviridae* (order *Geplafuvirales).*

Authors: Philippe Roumagnac, Jose T Ascencio- Ibáñez, Jean-Michel Lett, Paola M López-Lambertini, Darren P Martin, Jesús Navas-Castillo, Simone G Ribeiro, Cica Urbino, Arvind Varsani, F Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Family *Geminiviridae* in the *order Geplafuvirales*

Description of current taxonomy:
Monodnaviria / Shotokuvirae / Cressdnaviricota / Repensiviricetes / Geplafuvirales / Geminiviridae
The family *Geminiviridae* consists of 15 genera

Proposed taxonomic change(s):

We proposed to create three new genera into the *Geminiviridae* family: *"Cobecusvirus", "Oleurovirus"* and *"Pylecuvirus".* We also propose to create one new species *("Cobecusvirus phaseoli")* in the new *"Cobecusvirus"* genus, one new species *("Oleurovirus oleae")* in the new *"Oleurovirus"* genus and one new species *("Pylecuvirus petroselini")* in the new *"Pylecuvirus" genus*

Justification:
We propose to classify new geminiviruses into 3 new species based on species demarcation guidelines already established for the family *Geminiviridae.* Based on the inferred genome organizations of these viruses coupled with phylogenetic analysis, we propose to create 3 new genera in the family *Geminiviridae* to accommodate these 3 new species.

Submitted: 06/10/2025; *Revised:* 22/08/2025

TABLE 18 - *Geminiviridae*, 6 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Cobecusvirus*		
New taxon	Species	*Cobecusvirus phaseoli*	common bean curly stunt virus	MK673513
New taxon	Genus	*Oleurovirus*		
New taxon	Species	*Oleurovirus oleae*	Olea europaea geminivirus	MW316657
New taxon	Genus	*Pylecuvirus*		
New taxon	Species	*Pylecuvirus petroselini*	parsley yellow leaf curl virus	MN243534

2025.017P.Ac.v3.Secoviridae_53nsp_3abolishsp

Title: Create 53 new species and abolish three previously recognized species in the family *Secoviridae (Picornavirales)*

Authors: Marc Fuchs, Jean-Michel Hily, Hélène Sanfaçon, Lucy Stewart, Jeremy Thompson, Rene Van der Vlugt, Thierry Wetzel

Summary:
Taxonomic rank(s) affected:
Genera *Comovirus, Cheravirus, Fabavirus, Nepovirus, Sadwavirus, Stralarivirus, Torradovirus, Sequivirus, Waikavirus* in the *family Secoviridae*

Description of current taxonomy:
The recognition of new virus species is based on demarcation criteria in the family *Secoviridae* of less than 75% amino acid sequence identity in the coat protein (CP)(s) and/or less than 80% amino acid sequence identity in the conserved Protease (Pro)-Polymerase (Pol) region (from the protease CG motif to the polymerase GDD motif), *and/or* distinct plant hosts and biological properties.

Proposed taxonomic change(s):
Create two new species in the genus *Comovirus: "Comovirus caricae", "Comovirus cardaminis"*
Create three new species in the genus *Cheravirus: "Cheravirus lagerstroemiae", "Cheravirus corymbii", "Cheravirus pternopetali"*
Create five new species in the genus *Fabavirus: "Fabavirus phipiperis", "Fabavirus camphorae", "Fabavirus reaumuriae", "Fabavirus multiflorum", "Fabavirus squamellariae"*
Create 25 new species in the genus *Nepovirus: "Nepovirus alphacucumis", "Nepovirus thymi", "Nepovirus paeoniae", "Nepovirus chrysanthemi", "Nepovirus pinnatifolium", "Nepovirus glycyrrhizae", "Nepovirus pholismae", "Nepovirus berberidopsis", "Nepovirus silenis", "Nepovirus galax", "Nepovirus saururi", "Nepovirus musae", "Nepovirus cenchri", "Nepovirus hypolepsis", "Nepovirus pogonati", "Nepovirus begoniae", "Nepovirus caladeniae", "Nepovirus astragali", "Nepovirus gentianae", "Nepovirus leucadendri", "Nepovirus yunnanense", "Nepovirus rhododendri", "Nepovirus hanseniae",*

"Nepovirus beldersayense", "Nepovirus jasmini"
Create two new species in the *genus* Sadwavirus: *"Sadwavirus kappananas", "Sadwavirus morifolii"*
Create two new species in the genus *Stralarivirus: "Stralarivirus beldersayense", "Stralarivirus scaevolae"*
Create four new species in the *genus* Torradovirus: *"Torradovirus rorippae", "Torradovirus ophistopappi", "Torradovirus lophophyti", "Torradovirus sesami"*
Create one new species in the genus *Sequivirus: "Sequivirus primulae"*
Create nine new species in the genus *Waikavirus: "Waikavirus convallariae", "Waikavirus euphorbiae", "Waikavirus swalleniae", "Waikavirus gentianae", "Waikavirus lycopi", "Waikavirus pagodae", "Waikavirus heveae", "Waikavirus artemisiae", "Waikavirus duoplantae"*
Abolish two previously recognized species in the genus *Nepovirus:* Nepovirus americaense, Nepovirus *australiense*
Abolish one previously recognized species in the genus *Waikavirus:* Waikavirus anthrisci

Justification:
The creation of the proposed new 53 species is justified based on less than 75% amino acid sequence identity in the CP(s) and/or less than 80% amino acid sequence identity in the conserved Pro-Pol region (from the protease CG motif to the polymerase GDD motif) compared with classified species of the family *Secoviridae.*
The abolishment of three previous recognized species *(Nepovirus* americaense, Nepovirus australiense, Waikavirus *anthrisci)* is justified based on a lack of sequence information.

Submitted: 06/04/2025; *Revised:* 18/08/2025

TABLE 19 - *Secoviridae*, 53 new taxa***.** Table too large, see supplementary information sheet supp_info_tab_19

TABLE 20 - *Secoviridae*, 3 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	Species	*Nepovirus americaense*
Abolish taxon	Species	*Nepovirus australiaense*
Abolish taxon	Species	*Waikavirus anthrisci*

2025.018P.Ac.v3.Tombusviridae_1ng_9nsp

Title: Create one (1) new genus containing nine (9) new species in the family *Tombusviridae*

Authors: W. Allen Miller, Zachary Lozier, , , , , ,

Summary:
Taxonomic rank(s) affected:
Subfamily *Procedovirinae* in the *family Tombusviridae*

Description of current taxonomy:
Currently there are 19 genera and 93 species in the family *Tombusviridae.* Genera are grouped based on genome organization and sequence similarities of RNA-dependent RNA polymerase (RdRp).

Proposed taxonomic change(s):
Create one new genus in the subfamily *Procedovirinae,* called *"Rimosavirus",* and classify nine new viruses (maize-associated rimosavirus 1 (MaRV1), *Plasmopara viticola* lesion-associated rimosavirus 1 (PVLaRV1), Taian Tombu tick-associated virus 1 (TTTaV1), Nanning Tombu tick-associated virus 1 (NTTaV1), Hubei rimosavirus 2 (HubRV2), *Brassica caulorapa-associated* rimosavirus 1 (BCaRV1), *Zizania latifolia-associated* rimosavirus 1 (ZLaRV1), Hubei rimosavirus 1 (HubRV1), tuatara cloaca-

associated rimosavirus 1 (TCaRV1) into nine new species in the *genus "Rimosavirus".*

Justification:
All members of the proposed genus have RdRp sequences more similar to those of other tombusvirids than to viruses in other families, but they diverge from those of other tombusvirid genera by as much as the RdRps in different established genera diverge from each other. Secondly, the *"Rimosavirus"* genome organizations feature tombusvirid-like characteristics such as probable translation of the RdRp (ORF2) by readthrough of a leaky stop codon (placing rimosaviruses in the *Procedovirinae)* and an intergenic region between ORF2 and the coat protein (CP)-encoding ORF (ORF3). Genomes in the proposed genus differ from other tombusvirids by having (i) a predicted 5' untranslated region (UTR) over 400 nt long and containing AUGs, (ii) a possible ORF (ORF4) overlapping with ORF3 starting upstream of ORF3. This would be the first genus to combine translation of the RdRp by translational readthrough (which defines members of the *Procedovirinae* subfamily), with a luteovirus-like readthrough of the ORF3 stop codon.

Submitted: 06/05/2025; *Revised:* 28/08/2025

TABLE 21 - *Tombusviridae*, 10 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Rimosavirus*		
New taxon	Species	*Rimosavirus zeae*	maize-associated rimosavirus 1	OK018181
New taxon	Species	*Rimosavirus plasmoparae*	Plasmopara viticola lesion-associated rimosavirus 1	MT311687
New taxon	Species	*Rimosavirus haemaphysalis*	Taian Tombu tick-associated virus 1	ON746540
New taxon	Species	*Rimosavirus rhipicephali*	Nanning Tombu tick-associated virus 1	ON746539
New taxon	Species	*Rimosavirus unhubeiense*	Hubei rimosavirus 1	KX883244
New taxon	Species	*Rimosavirus duohubeiense*	Hubei rimosavirus 2	KX883240
New taxon	Species	*Rimosavirus brassicae*	Brassica caulorapa-associated rimosavirus 1	MN728812
New taxon	Species	*Rimosavirus zizaniae*	Zizania latifolia-associated rimosavirus 1	MN728813
New taxon	Species	*Rimosavirus sphenodonis*	tuatara cloaca-associated rimosavirus 1	OP080581

2025.019P.Ac.v3.Closteroviridae_31nsp_abolish_1sp

Title: Create 31 new species in the genera *Ampelovirus,* Closterovirus, *Crinivirus, Olivavirus* and *Velarivirus* and abolish one species in the genus *Closterovirus*

Authors: Nina Aboughanem-Sabanadzovic, Moshe Bar-Joseph, Thierry Candresse, Hano J Maree, Michael Melzer, Wulf Menzel, Angelantonio Minafra, Dimitre Mollov, Ioannis E Tzanetakis, Luisa Rubino, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected:
Genera *Ampelovirus,* Closterovirus, *Crinivirus, Olivavirus* and *Velarivirus* in the *family Closteroviridae*

Description of current taxonomy:
Family *Closteroviridae* is currently composed of seven genera that accommodate 58 species, most of

which are classified in one of the four “traditional” genera: *Closterovirus* (17), *Crinivirus* (14), *Ampelovirus* (13) and *Velarivirus* (9). Two of three recently established genera *(Bluvavirus* and *Menthavirus)* are monospecific, while the genus *Olivavirus* includes 3 species.

Proposed taxonomic change(s):
We propose creation of 31 new species in the family based on recently published data on characterization of viruses with affinities with currently recognized members of the family *Closteroviridae.*

Justification:
During the search of GenBank, 31 viral genomes with required quality and completeness along with availability of a valid publication were selected as exemplar isolates for typifying proposed new species. All these viruses meet the molecular criteria for species demarcation in the genera as they differ in amino acid content of all 3 relevant virus-encoded proteins (HSP70h, RdRP and CP) with counterparts of 58 already recognized members of the family.

Submitted: 25/06/2025; *Revised:* 28/08/2025

TABLE 22 - *Closteroviridae*, 31 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Ampelovirus allamandae*	Allamanda chlorotic virus A	PP212980
New taxon	Species	*Ampelovirus alpiniae*	Alpinia vein clearing virus	OQ550018
New taxon	Species	*Ampelovirus unesculentae*	Manihot esculenta associated ampelovirus 1	MT773586
New taxon	Species	*Ampelovirus duesculentae*	Manihot esculenta associated ampelovirus 2	MT773592
New taxon	Species	*Ampelovirus unocitri*	citrus associated ampelovirus 1	MW365401
New taxon	Species	*Ampelovirus duocitri*	citrus associated ampelovirus 2	MW365402
New taxon	Species	*Ampelovirus odontonemae*	firespike leafroll-associated virus	MW147758
New taxon	Species	*Ampelovirus pentananas*	pineapple mealybug wilt-associated virus 5	OQ850040
New taxon	Species	*Ampelovirus hexananas*	pineapple mealybug wilt-associated virus 6	OP860296
New taxon	Species	*Ampelovirus septananas*	pineapple mealybug wilt-associated virus 7	OQ850042
New taxon	Species	*Ampelovirus sacchari*	sugarcane mild mosaic virus	MN116751
New taxon	Species	*Ampelovirus croton*	croton golden spot associated virus A	OR041673
New taxon	Species	*Ampelovirus alphaolivae*	olive virus A	OQ863254
New taxon	Species	*Ampelovirus kaki*	persimmon ampelovirus	LC488185
New taxon	Species	*Ampelovirus perseae*	lingue ampelovirus 1	OQ805851
New taxon	Species	*Closterovirus alphafici*	fig virus A	MN817232
New taxon	Species	*Closterovirus betafici*	fig virus B	MN817233
New taxon	Species	*Closterovirus cnidi*	Cnidium closterovirus 1	OL804208
New taxon	Species	*Closterovirus duocarotae*	carrot closterovirus 2	OP886455
New taxon	Species	*Closterovirus thesii*	Thesium chinense closterovirus 1	OM801605
New taxon	Species	*Closterovirus stellariae*	Stellaria aquatica virus C	PP280820
New taxon	Species	*Closterovirus tritici*	wheat closterovirus 1	LC735716
New taxon	Species	*Closterovirus dregeae*	Dregea volubilis virus 1	MZ779122

New taxon	Species	*Crinivirus kurdistanfragariae*	strawberry Kurdistan virus	RNA1: OR387513; RNA2: OR387514
New taxon	Species	*Crinivirus dioscoreae*	yam virus 1	RNA1: PP378481; RNA2: PP378483
New taxon	Species	*Crinivirus mori*	mulberry crinivirus	RNA1: ON931610; RNA2: ON931611
New taxon	Species	*Crinivirus papyriferae*	paper mulberry crinivirus 1	RNA1: OL344036; RNA2: OL344037
New taxon	Species	*Crinivirus arracaciae*	arracacha latent virus C	RNA1: KY451034; RNA2: KY451035
New taxon	Species	*Olivavirus oleae*	olive leaf mottling virus	PP869314
New taxon	Species	*Velarivirus agapanthi*	Agapanthus velarivirus	MT533601
New taxon	Species	*Velarivirus oleae*	olive virus V	OQ863266

TABLE 23 - *Closteroviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Closterovirus flavarctii*

2025.020P.Solemoviridae_Enamovirus_10nsp

Title: Create ten species in the *genus* Enamovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:
Taxonomic rank(s) affected:
Genus *Enamovirus* in the *family Solemoviridae*

Description of current taxonomy:
Sobelivirales: Solemoviridae: Enamovirus
Currently, the genus *Enamovirus* consists of 15 species.

Proposed taxonomic change(s):
Create ten new species in the *genus Enamovirus*

Justification:
High-throughput sequencing (HTS) of raspberry samples collected in 2021 from Czechia and Norway has revealed 14 isolates of a novel *Enamovirus* candidate, raspberry enamovirus 1 (RaEV1). Carrot enamovirus 1 (CaEV1) was discovered in wild carrot populations in Southwestern France. In addition, the analyses of publicly available plant transcriptome data have enabled the assembly of 16 additional full or partial genome sequences characteristic of enamoviruses: Brunioides conebush enamovirus, Bunge's buttercup enamovirus, cassava enamovirus, common thyme enamovirus, Coriandrum sativum enamovirus, decurrent goldenrod enamovirus, Fukien tea tree enamovirus, oriental arborvitae enamovirus, rubber tree enamovirus, Rugel's plantain enamovirus, sea-buckthorn enamo-like virus, showy sunflower enamovirus, silver birch enamovirus, spruce enamovirus, Western salsify enamovirus, and Yunnan pine enamovirus. Eight of these 16 candidates have genome sequences covering all coding regions, while they also cluster with accepted members in the phylogenetic RdRP tree. In total, ten out of 18 candidate species are proposed as the new members of genus *Enamovirus,* fulfilling the species demarcation criteria and having complete or coding-complete genomes sequences.

Submitted: 16/06/2025; *Revised:* 28/10/2025

TABLE 24 - *Solemoviridae*, 10 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Enamovirus BUBEV*	Bunge's buttercup enamovirus	BK068694
New taxon	Species	*Enamovirus CAEV*	carrot enamovirus	OP886449
New taxon	Species	*Enamovirus CTEV*	common thyme enamovirus	BK068696
New taxon	Species	*Enamovirus CSEV*	Coriandrum sativum enamovirus	BK063225
New taxon	Species	*Enamovirus DEGEV*	decurrent goldenrod enamovirus	BK068695
New taxon	Species	*Enamovirus FTEV*	Fukien tea tree enamovirus	BK068686
New taxon	Species	*Enamovirus ORAEV*	oriental arborvitae enamovirus	BK068685
New taxon	Species	*Enamovirus RAEV*	raspberry enamovirus	OR683427
New taxon	Species	*Enamovirus WSEV*	western salsify enamovirus	BK068692
New taxon	Species	*Enamovirus YPEV*	Yunnan pine enamovirus	BK068688

2025.021P.Solemoviridae_Sobemovirus_1nsp

Title: Create one species in the *genus* Sobemovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:

Taxonomic rank(s) affected:
Genus *Sobemovirus* in the *family Solemoviridae*

Description of current taxonomy:
Currently, the genus *Sobemovirus* consists of 26 members infecting plants from different taxa.

Proposed taxonomic change(s):
Create one new species in the *genus Sobemovirus*

Justification:
The presence of olive virus S (OlVS), a putative novel member of the family *Solemoviridae,* was determined by HTS in 10 samples of olive leaf petioles collected in the commercial orchards in Stellenbosch, South Africa. The assembled genome of OlVS shared sequence similarity with sobemoviruses, being closest to southern bean mosaic virus (SBMV) with an average identity of 52.5%. The terminal genomic sequences were determined by Sanger sequencing of RACE cDNA clones. The genome length and organization of OlVS was characteristic of sobemoviruses. The phylogenetic analysis confirmed clustering within the genus *Sobemovirus.*

Submitted: 16/06/2025; *Revised:* 28/10/2025

TABLE 25 - *Solemoviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Sobemovirus OLVS*	olive virus S	OR252867

2025.022P.Solemoviridae_Polerovirus_17nsp

Title: Create seventeen [17] new species in the *genus* Polerovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:
Taxonomic rank(s) affected:
Genus *Polerovirus* in the family *Solemoviridae*

Description of current taxonomy:
Currently, the genus *Polerovirus* consists of 77 species.

Proposed taxonomic change(s):
Create 17 new species in the *genus Polerovirus*

Justification: Recent high-throughput sequencing projects have revealed 23 putative novel poleroviruses that have not yet been assigned to species. The assembled genomes share the highest sequence identities with poleroviruses. Phylogenetic analysis of their genome nucleotide sequences and the amino acid sequences of their RdRPs confirmed clustering within the genus *Polerovirus.* The putative novel candidate viruses are: *Actinidia* polerovirus, *Ageratum* virus 3, arachis mottle-associated virus, bitter apple aphid-borne yellows virus, bitter gourd yellowing crumple virus, cacao leafroll virus, carrot polerovirus 1, carrot polerovirus 2, Chrysanthemum virus D, *Cynanchum* yellow mottle-associated virus, Ficus esquiroliana polerovirus, gladiolus polerovirus, Ixeridium yellow mottle virus, Musa polerovirus, noble dendrobium polerovirus, parsley polerovirus, pepper vein yellows virus 10, rice dwarf polerovirus, spruce polerovirus, sweet leaf bush polerovirus, tomato necrotic yellowing virus, Viola philippica polerovirus, and wild carrot red leaf virus. We propose that 17 out of these 23 viruses could be recognized as members of species in the genus *Polerovirus.*

Submitted: 16/06/2025; *Revised:* 29/10/2025

TABLE 26 - *Solemoviridae*, 17 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Polerovirus AGV*	Agratum virus 3	PQ675349
New taxon	Species	*Polerovirus ARMOV*	Arachis mottle-associated virus	LC818997
New taxon	Species	*Polerovirus CALRV*	cacao leafroll virus	OR423049
New taxon	Species	*Polerovirus CAPV*	carrot polerovirus 2	OP886451
New taxon	Species	*Polerovirus CHDV*	Chrysanthemum virus D	OR453957
New taxon	Species	*Polerovirus CYMAV*	Cynanchum yellow mottle-associated virus	LC699794
New taxon	Species	*Polerovirus IXYMAV*	Ixeridium yellow mottle virus 1	KT868949
New taxon	Species	*Polerovirus PEVYV10*	pepper vein yellows virus 10	OR225495
New taxon	Species	*Polerovirus RDPV*	rice polerovirus	PP925870
New taxon	Species	*Polerovirus VPPV*	Viola philippica polerovirus	PP770488
New taxon	Species	*Polerovirus ACTPV*	Actinidia polerovirus	BK069690
New taxon	Species	*Polerovirus FEQPV*	Ficus esquiroliana polerovirus	BK068690
New taxon	Species	*Polerovirus GLPV*	Gladiolus polerovirus	BK068697
New taxon	Species	*Polerovirus MUSPV*	Musa polerovirus	BK068683
New taxon	Species	*Polerovirus NBPV*	noble dendrobium polerovirus	BK068693
New taxon	Species	*Polerovirus SPRPV*	spruce polerovirus	BK068705
New taxon	Species	*Polerovirus SLBPV*	sweet leaf bush polerovirus	BK068689

2025.023P.Ac.v3.Rhabdoviridae_Trirhavirus_1nsp

Title: Create one new species in the genus *Trirhavirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Trirhavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae*

Description of current taxonomy:
Five virus species are currently classified in the recently created genus *Trirhavirus,* whose main feature is the tri-segmented genomic organization of their members. The assignment of viruses to this genus is based on their genome composition, and the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create one new species in the genus *Trirhavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* This species is proposed to be named *"Trirhavirus rubi".*

Justification:
A novel tri-segmented rhabdovirus was identified in Rubus [1]**.** The characterization of the genome sequence showed that it should be assigned to a novel species within the genus *Trirhavirus* [1] based on the nucleotide sequence divergence from previously reported trirhaviruses and phylogenetic placement.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 27 - *Rhabdoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Trirhavirus rubi*	Rubus trirhavirus 1	RNA1: PQ317245; RNA2: PQ317246; RNA3: PQ317247

2025.024P.Ac.v3.Rhabdoviridae_Betanucleorhabdovirus_7nsp

Title: Create seven new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Betanucleorhabdovirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genus *Betanucleorhabdovirus* belongs to the subfamily *Betarhabdovirinae,* family *Rhabdoviridae* and consists of 19 species. Viruses classified into species in the genus *Betanucleorhabdovirus* infect a wide range of plants, and the assignment of viruses to this genus is based on the placement of the viruses

on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create seven new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named as *"Betanucleorhabdovirus* alpiniae", "Betanucleorhabdovirus betae", "Betanucleorhabdovirus alphasambuci", "Betanucleorhabdovirus betasambuc"i, "Betanucleorhabdovirus gammasambuci", "Betanucleorhabdovirus *deltasambuci" and* "Betanucleorhabdovirus *epsilonsambuci".*

Justification:
Seven novel rhabdoviruses were identified in *Alpinia purpurata* [1], beet [Mehrvar and Abkho, unpublished (OR227650)] and elderberry [2]. The characterization of these seven viruses showed that they should be classified into novel species within the genus *Betanucleorhabdovirus.*

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 28 - *Rhabdoviridae*, 7 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Betanucleorhabdovirus alpiniae*	Alpinia vein streaking virus	OQ538192
New taxon	Species	*Betanucleorhabdovirus betae*	beet betanucleorhabdovirus 1	OR227650
New taxon	Species	*Betanucleorhabdovirus alphasambuci*	Sambucus betanucleorhabdovirus 1	PP711309
New taxon	Species	*Betanucleorhabdovirus betasambuci*	Sambucus betanucleorhabdovirus 2	PP711310
New taxon	Species	*Betanucleorhabdovirus gammasambuci*	Sambucus betanucleorhabdovirus 3	PP711317
New taxon	Species	*Betanucleorhabdovirus deltasambuci*	Sambucus betanucleorhabdovirus 4	PP711315
New taxon	Species	*Betanucleorhabdovirus epsilonsambuci*	Sambucus betanucleorhabdovirus 5	PP711313

2025.025P.Ac.v3.Rhabdoviridae_Alpha_and_Betacytorhabdovirus_3nsp

Title: Create three (3) new species, one in the genus *Alphacytorhabdovirus,* and the other two in the genus *Betacytorhabdovirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas-A Astúa, Hideki Kondo, Pedro Luis Ramos- González , Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* belong to the subfamily *Betarhabdovirinae,* family *Rhabdoviridae* and consist of 18 and 19 species, respectively. Viruses classified into species in the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* infect a wide range of plants, and the assignment of viruses to these genera is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences

Proposed taxonomic change(s):
Create one new species in the genus *Alphacytorhabdovirus,* and two new species in the genus

Betacytorhabdovirus, subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named *"Alphacytorhabdovirus* lonicerae", "Betacytorhabdovirus dioscoreae" *and* "Betacytorhabdovirus *pyri".*

Justification:
Three novel rhabdoviruses were identified in honeysuckle [1], *Dioscorea rotundata* [Silva et al., unpublished (ON924784)] and pear [2]. The characterization of these viruses showed that the honeysuckle-associated virus should be classified into a novel species within the genus *Alphacytorhabdovirus* [1]; while the *Dioscorea rotundata-associated* and pear-associated viruses should be assigned to novel species within the genus *Betacytorhabdovirus* [Silva et al., unpublished (ON924784) and 2, respectively].

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 29 - *Rhabdoviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Alphacytorhabdovirus lonicerae*	honeysuckle-associated cytorhabdovirus 1	PQ587056
New taxon	Species	*Betacytorhabdovirus dioscoreae*	Dioscorea rotundata virus 1	ON924784
New taxon	Species	*Betacytorhabdovirus pyri*	pear rhabdovirus 1	PP512586

2025.026P.Ac.v3.Rhabdoviridae_Varicosavirus_3nsp

Title: Create three (3) new species in the genus *Varicosavirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Varicosavirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Viruses classified into species in the genus *Varicosavirus* are bi-segmented and infect a wide range of plants. The assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create three new species in the genus *Varicosavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named *"Varicosavirus* agastachi", "Varicosavirus orychophragmi" *and* "Varicosavirus *rubi".*

Justification:
Three novel rhabdoviruses were identified in *Agastache rugosa* [1], *Orychophragmus violaceus* [2] and *Rubus* spp. [3]. The characterization of these three viruses showed that they should be classified into novel species within the genus *Varicosavirus* based on the nucleotide sequence divergence from previously reported varicosaviruses and phylogenetic placement.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 30 - *Rhabdoviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Varicosavirus agastachi*	Agastache rugosa associated varicosavirus	RNA1: PP987314;RNA2: PP987315
New taxon	Species	*Varicosavirus orychophragmi*	Orychophragmus violaceus varicosavirus	RNA1: PP770489; RNA2: PP777177
New taxon	Species	*Varicosavirus rubi*	Rubus varicosavirus 1	RNA1: PQ317243; RNA2: PQ317244

2025.027P.Ac.v3.Rhabdoviridae_Dichorhavirus_2nsp

Title: Create two (2) new species in the genus *Dichorhavirus (Mononegavirales: Rhabdoviridae)*

Authors: Peter J Walker, Nicolas Bejerman, Kim R Blasdell, Humberto Debat, Ralf G Dietzgen, Anthony R Fooks, Juliana Freitas-Astúa, Kyle Garver, Pedro Luis Ramos-González, Hideki Kondo, Mang Shi, Robert B Tesh, Noël Tordo, Nikos Vasilakis, Anna E Whitfield, Monica Madariaga-Villarroel

Summary:Taxonomic rank(s) affected:
Genus *Dichorhavirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genus *Dichorhavirus,* family *Rhabdoviridae,* encompasses viruses assigned to six species. They are plant-infecting viruses transmitted by mites of the genus *Brevipalpus* . The genome of dichorhaviruses includes bi-segmented, negative-sense, single-stranded RNA molecules, in which genes *N, P, P3(ORF3), M,* and *G* are located in RNA1, whereas the gene *L* is in RNA2. In nature, dichorhaviruses cause non-systemic diseases, mostly producing chlorotic and necrotic spots; however, sometimes orchid fleck virus (OFV) can induce systemic infection in orchids. Dichorhaviruses also replicate in their vectors .

Proposed taxonomic change(s):
Create two new species in the genus *Dichorhavirus, subfamily Betarhabdovirinae, family Rhabdoviridae.* The two new taxa are proposed to be named *"Dichorhavirus* chilense" *and* "Dichorhavirus *piracicabense", respectively.*

Justification: Two novel viruses were identified in bleeding-heart vine *(Clerodendrum thomsoniae)* and large periwinkle *(Vinca major)* plants, respectively (Ramos-González et al., unpublished results). Biological and molecular characterization of these viruses demonstrated that they should be classified as novel species within the genus *Dichorhavirus.* The complete sequences of RNA1 and *L* ORF in the RNA2 of both viruses share less than 80% of nucleotide sequence identity with known dichorhaviruses. Phylogenetic analyses using the L proteins place both viruses in a subclade with viruses of the known species of the genus.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 31 - *Rhabdoviridae*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Dichorhavirus chilense*	Vinca chlorotic spot virus	RNA1: OR372158; RNA2: OR372159
New taxon	Species	*Dichorhavirus piracicabense*	Clerodendrum leaf spot virus	RNA1: PV555428; RNA2: PV555429

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the 2026 General Subcommittee

Contents

2025.002G.Ac.v2.Monodnaviria_reorg_4nr

Title: Reorganization of the realm *Monodnaviria* by moving three of the four kingdoms to new realms and renaming the realm *Monodnaviria* to *“Floreoviria”*

Authors: Mart Krupovic, Arvind Varsani, Simon Roux, F. Murilo Zerbini, Jens H. Kuhn, Eugene V. Koonin

Summary:
Taxonomic rank(s) affected:
Realm

Description of current taxonomy:
Realm *Monodnaviria* includes four kingdoms, *Loebvirae, Sangervirae, Shotokuvirae,* and *Trapavirae,* which comprise bacteria-infecting viruses that form filamentous virions, bacteria-infecting viruses that form small icosahedral capsid, eukaryote-infecting viruses that form icosahedral capsids, and archaea-infecting viruses that produce pleomorphic virions, respectively.

Proposed taxonomic change(s):
We propose moving three of the four monodnavirian kingdoms, namely, *Loebvirae, Sangervirae,* and *Trapavirae,* into three new realms and renaming the realm *Monodnaviria* to *“Floreoviria”.*

Justification:
Realm *Monodnaviria* was created to unify viruses with small single-stranded DNA (ssDNA) or double-stranded DNA (dsDNA) genomes that replicate using, in most cases, homologous rolling circle replication initiation endonucleases (Reps) of the HUH superfamily. However, recent comparative sequence and structural analyses showed that Reps encoded by viruses from these different kingdoms are not orthologous and, in some cases, not homologous (that is, some Reps do not belong to the HUH superfamily). Furthermore, the structural modules of these viruses are also unrelated. Thus, grouping of viruses from the four kingdoms within the same realm is unjustified.

Submitted: 07/02/2025; *Revised:* 25/08/2025

TABLE 1 - *Monodnaviria*, 3 new taxa*

Operation	Rank	New taxon name
New taxon	Realm	*Efunaviria*
New taxon	Realm	*Volvereviria*
New taxon	Realm	*Pleomoviria*

TABLE 2 - *Monodnaviria*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Kingdom	*Loebvirae*	*Efunaviria*	*Monodnaviria*
Move taxon	Kingdom	*Sangervirae*	*Volvereviria*	*Monodnaviria*
Move taxon	Kingdom	*Trapavirae*	*Pleomoviria*	*Monodnaviria*

TABLE 3 - *Monodnaviria*, 1 rename taxon*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Realm	*Floreoviria*	*Monodnaviria*

2025.G003.N.v1.Creation_of_ICTV_Bioinformatics_Study_Group

Title: Creation of ICTV Virus Bioinformatics Study Group and its remit

Authors: Alejandro Reyes, Evelien Adriaenssens, Elliot Lefkowitz, Simon Roux

Summary:
Brief description of current situation:

The Virus Bioinformatics Expert Group was an unofficial group within the ICTV that discussed bioinformatics problems and was working towards streamlining and automating taxonomic processes. There never was an official remit or position within the ICTV.

Proposed changes:
We propose a new name and remit for the Virus Bioinformatics Study Group. This group will be placed as a Study Group with affiliation to all subcommittees and will consist of subcommittee chairs and invited virus bioinformatics experts.

Justification:
Having a Virus Bioinformatics Study Group will facilitate taxonomic endeavors and coordination across Study Groups, in support of the long-term goal of automated and scalable virus taxonomic processes.

Submitted: —; *Revised:* —