Taxonomy Proposal Summaries for Ratification Vote, 2025

This document contains a full list of the taxonomy proposals presented for the ICTV Member ratification vote in February, 2025. 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, a tabulated summary of the proposed changes and under the table, links to the text of the full proposal on the ICTV website (Word and Excel modules).

Please note that these summaries are provided solely for the purposes of evaluating the proposals prior to the ratification votes. Links provided to access the full text will expire after the vote. 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 Animal DNA Viruses and Retroviruses Subcommittee, 2024

Main Text

Contents

2024.001D.A.v1.Alphabaculovirus-1nsp

Title: Create the new species *Alphabaculovirus alterhycuneae* in the genus *Alphabaculovirus (Lefavirales: Baculoviridae)*

Authors: Peng X-W, Lei C-F, Hu J, Sun XL (sunxl@wh.iov.cn)

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
In the genus *Alphabaculovirus* (family *Baculoviridae)* there are 65 species*.*

Proposed taxonomic change(s):
New species

Justification:
The genome of the virus (Hypantria cuneae nulceopolyhedrovirus B, (HycuNPV-B)), was fully sequenced using a high-throughput method. The divergence of the phylogenetic tree and the K2P distances based on the 38 core-gene concatenated alignment revealed that the HycuNPV-B isolate belongs to a novel species of *Alphabaculovirus.* For this new species we suggest the species name "Alphabaculovirus alterhycuneae", following the binomial naming proposal as submitted in 2022 and ratified by the ICTV in April 2023.

Submitted: 05/04/2023; *Revised:* -

TABLE 1 - *Alphabaculovirus-1nsp*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Alphabaculovirus alterhycuneae*	Hypantria cunea nucleopolyhedrovirus B	OL686893

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.001D.A.v1.Alphabaculovirus-1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.001D.A.v1.Alphabaculovirus-1nsp.xlsx

2024.002D.A.v2.Circoviridae_5ns

Title: Create five new species in the genus *Circovirus (Cirlivirales: Circoviridae)*

Authors: Tarján ZL (tarjan.zoltan@vmri.hun-ren.hu), Benkő M, Egyed L, Harrach B

Summary:
Taxonomic rank(s) affected:
species

Description of current taxonomy:
155 species (65 circoviruses /CVs/ and 90 cycloviruses /CyVs/) in 2 genera within the family *Circoviridae.*

Proposed taxonomic change(s):
Adding 5 novel species to genus *Circovirus.*

Justification:
Based on genome organization and phylogenetic analyses, we propose the establishment of 5 new species in genus *Circovirus.* The species demarcation was based on the genome-wide pairwise identity between circovirids (less than 80 percent identity as established species demarcation criterion [2, 9]).

Submitted: 21/06/2024; *Revised:* -

TABLE 2 - *Circoviridae*, 5 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Circovirus dever*	bream circovirus 1	KF358279
New taxon	species	*Circovirus razbora*	Pseudorasbora circovirus 1	MN837844
New taxon	species	*Circovirus baizhenhe*	white-naped crane circovirus 1	MN928908
New taxon	species	*Circovirus patkany*	brown rat circovirus 1	OR553090
New taxon	species	*Circovirus python*	black-headed python circovirus 1	MH368042

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.002D.A.v2.Circoviridae_5ns.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.002D.A.v2.Circoviridae_5ns.xlsx

2024.003D.A.v1.Polyomaviridae_4ns

Title: Create 4 new species in the genera *Alphapolyomavirus* and *Betapolyomavirus (Polyomaviridae)*

Authors: Surján A (surjan.andras@vmri.hun-ren.hu), Vidovszky MZ, Postler TS, Harrach B,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
118 species in 8 genera in the family *Polyomaviridae.*

Proposed taxonomic change(s):
Adding 4 novel species; 3 to genus *Alphapolyomavirus,* 1 to *Betapolyomavirus*

Justification:
Novel polyomaviruses have been detected in bat guano and Eurasian beaver kidney tissue samples. Three from the novel bat polyomaviruses and the beaver polyomavirus meet the criteria of establishing a new species. The phylogenetic distance of their LTAg nucleotide sequences is more than 15 percent to members of accepted polyomavirus species and their host species is known, furthermore, they originate from new hosts.

Submitted: 21/06/2024; *Revised:* -

TABLE 3 - *Polyomaviridae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Alphapolyomavirus castoris*	Castor fiber polyomavirus 1	OR735477
New taxon	species	*Alphapolyomavirus epserotini*	Eptesicus serotinus polyomavirus 1	OK428546
New taxon	species	*Alphapolyomavirus myodaubentonii*	Myotis daubentonii polyomavirus 2	OK300052
New taxon	species	*Betapolyomavirus hipposideri*	Rhinolophus hipposideros polyomavirus 1	MT276890

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.003D.A.v1.Polyomaviridae_4ns.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.003D.A.v1.Polyomaviridae_4ns.xlsx

2024.004D.A.v1.Adenoviridae_16ns

Title: Create 16 new species in the genera *Aviadenovirus, Barthadenovirus* and *Mastadenovirus (Rowavirales: Adenoviridae)*

Authors: Benkő M, Arnberg N, Hess M, Kaján GL, Kajon A, Mittal SK, Podgorski II, Postler TS, San Martín C, Wadell G, Watanabe H, Harrach B (harrach.balazs@vmri.hun-ren.hu)

Summary:
Taxonomic rank(s) affected:
Species

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

Proposed taxonomic change(s):
Adding 16 novel species; 7 to genus *Mastadenovirus,* 5 to *Aviadenovirus,* 4 to *Barthadenovirus.*

Justification:
Novel adenovirus sequences have been submitted to GenBank (many from metagenomic data) reflecting very rich diversity (https: //sites.google.com/site/adenoseq). From these sequences, 16 full or almost full (coding-complete) animal adenovirus genomes originating from 7 mammal, 7 bird and 2 reptilian species merit the establishment of new species for them. The phylogenetic distance of their DNA polymerase amino acid sequences is more than 15 percent to members of accepted adenovirus species (this is the main demarcation criterion). Furthermore, they originate from new hosts or from hosts different from those of existing species, or/and have a characteristic whole-genome GC% difference.

Submitted: 21/06/2024; *Revised:* -

TABLE 4 - *Adenoviridae*, 16 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Mastadenovirus marmotae*	marmot adenovirus 1	PP098964
New taxon	species	*Mastadenovirus capreoli*	roe deer adenovirus 1, adenovirus capreolus32301	BK066828
New taxon	species	*Mastadenovirus vespertilionis*	bat adenovirus 33390	BK066631
New taxon	species	*Mastadenovirus desmodi*	vampire bat adenovirus, adenovirus desmodus35011	BK066905
New taxon	species	*Mastadenovirus cardiodermatis*	heart-nosed bat adenovirus	PP711818
New taxon	species	*Mastadenovirus fructus*	Leschenault's rousette adenovirus	OR998962
New taxon	species	*Mastadenovirus arvicolinae*	vole adenovirus 1, myodes38640	BK066403
New taxon	species	*Aviadenovirus phalacrocoracidae*	great cormorant adenovirus 1	OR529407
New taxon	species	*Aviadenovirus oti*	Eurasian scops owl adenovirus 1, Otus scops adenovirus	ON843719
New taxon	species	*Aviadenovirus orioli*	black-naped oriole adenovirus, Oriolus adenovirus	MZ819701
New taxon	species	*Aviadenovirus roseae*	psittacine adenovirus 12	OR871655
New taxon	species	*Aviadenovirus cerasi*	duck adenovirus 6	MK757473
New taxon	species	*Barthadenovirus gerygones*	grey warbler adenovirus 1	OQ986611
New taxon	species	*Barthadenovirus zootherae*	scaly thrush (Zoothera dauma) adenovirus 1	OR233592
New taxon	species	*Barthadenovirus varani*	varanus adenovirus 37597	BK066675
New taxon	species	*Barthadenovirus zootocae*	viviparous lizard adenovirus 1, adenovirus zootoca35082	BK066448

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.004D.A.v1.Adenoviridae_16ns.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.004D.A.v1.Adenoviridae_16ns.xlsx

2024.005D.A.v1.Baculoviridae_4nsp_1absp

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

Authors: van Oers MM, Abd-Alla AMM, Bateman KS, Bojko J, Harrison RL (robert.l.harrison@usda.gov), Herniou EA, Sun XL, Jehle JA, Krell PJ, Ribeiro BM

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy: There are currently 65 species in genus *Alphabaculovirus* and 28 species in genus *Betabaculovirus* of the family *Baculoviridae.*

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

Justification: Analysis of recently sequenced baculovirus genomes have identified four viruses that represent a previously undescribed baculovirus species, in accordance with the species demarcation criteria defined for the family *Baculoviridae.* An analysis of the genomes of viruses from the species *Alphabaculovirus mabrassicae, Alphabaculovirus maconfiguratae* and *Alphabaculovirus altermaconfiguratae* indicates that *Alphabaculovirus altermaconfiguratae* is redundant and should be abolished. The creation of *A. mabrassicae* precedes that of both *A. maconfiguratae* and *A. altermaconfiguratae,* and the exemplar isolate *of A. mabrassicae* falls in the same clade as the exemplar isolate *of A. altermaconfiguratae,* so we propose to abolish *A. altermaconfiguratae.*

Submitted: 30/04/2024; *Revised:* -

TABLE 5 - *Baculoviridae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Alphabaculovirus pastagnalis*	Parapoynx stagnalis nucleopolyhedrovirus	ON704650
New taxon	species	*Alphabaculovirus pavitrealis*	Palpita vitrealis nucleopolyhedrovirus	OL685370
New taxon	species	*Alphabaculovirus spocosmioidis*	Spodoptera cosmioides nucleopolyhedrovirus	MK419955
New taxon	species	*Betabaculovirus psincretae*	Psilogramma increta granulovirus	ON803509

TABLE 6 - *Baculoviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	species	*Alphabaculovirus altermaconfiguratae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.005D.A.v1.Baculoviridae_4nsp_1absp.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.005D.A.v1.Baculoviridae_4nsp_1absp.xlsx

2024.007D.A.v2.Filamentoviridae_1nf_2ngen_3nsp

Title: Create a new virus family in the *Lefavirales* order named *Filamentoviridae* with two genera *Alphafilamentovirus* and *Betafilamentovirus,* and three species.

Authors: Bézier A (annie.bezier@univ-tours.fr), Leobold M, Guinet B, Drezen J-M, Herniou EA, Varaldi J

Summary:
Taxonomic rank(s) affected:
Establishment of a new highly diverse viral family within the *order Lefavirales* in the class *Naldaviricetes,* the *Filamentoviridae,* comprising two genera: the *Alphafilamentovirus,* with the species *Alphafilamentovirus leboulardi,* and the *Betafilamentovirus,* with the species *Betafilamentovirus cocongregatae* and *Betafilamentovirus altercocongregatae*.

Description of current taxonomy:
The class of *Naldaviricetes* currently includes four families: *Baculoviridae, Nudiviridae, Hytrosaviridae,* and *Nimaviridae,* the first three belonging to the order of *Lefavirales.*

Proposed taxonomic change(s):
Create *Filamentoviridae,* a new family in the order *Lefavirales* within *Naldaviricetes,* with two genera *(Alphafilamentovirus* and *Betafilamentovirus),* and three species.

Justification:
New large arthropod-specific dsDNA viruses, which have been described as filamentous particles

since the 1970s, have recently been characterized at the genomic level [7]. These viruses share signatures of the *Naldaviricetes* and the *Lefavirales,* while encoding specific core genes that distinguish them from the established families of this order. Phylogenetic tree reconstruction indicates that these filamentous viruses (FVs) form a monophyletic clade distinct from that of their closest relatives, the *Hytrosaviridae,* and supports the creation of a new family, that we propose to name *Filamentoviridae.* These viruses appear to be preferentially associated with hymenopteran insects with a parasitoid lifestyle [7]. The effects of FVs on their hosts are still poorly assessed, with respect to other members of the *Naldaviricetes.* So far, only the Leptopilina boulardi filamentous virus *(LbFV)* has been studied for its effect and described as inducing a behavioral manipulation of wasp oviposition decisions and benefiting from vertical and horizontal transmission.

Submitted: 04/06/2024; *Revised:* 23/10/2024

TABLE 7 - *Filamentoviridae*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Filamentoviridae*		
New taxon	genus	*Alphafilamentovirus*		
New taxon	species	*Alphafilamentovirus leboulardi*	Leptopilina boulardi filamentous virus	KY009685
New taxon	genus	*Betafilamentovirus*		
New taxon	species	*Betafilamentovirus cocongregatae*	Cotesia congregata filamentous virus 1	OY734801
New taxon	species	*Betafilamentovirus altercocongregatae*	Cotesia congregata filamentous virus 2	OR120048

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.007D.A.v2.Filamentoviridae_1nf_2ngen_3nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.007D.A.v2.Filamentoviridae_1nf_2ngen_3nsp.xlsx

2024.008D.A.v2.Parvoviridae_55nsp

Title: Creating 55 new species in family *Parvoviridae*

Authors: Pénzes J (Judycash08@gmail.com), Canuti M, François S, Söderlund-Venermo M

Summary:
Taxonomic rank(s) affected:
Subfamily *Densovirinae,* genera *Blattambidensovirus, Scindoambidensovirus, Protoambidensovirus*, *Aquambidensovirus.*
Subfamily Parvovirinae, genera *Aveparvovirus, Bocaparvovirus, Dependoparvovirus, Protoparvovirus*

Description of current taxonomy:
The family currently includes:
Subfamily *Densovirinae* with 11 genera and 38 species
Subfamily *Parvovirinae* with 11 genera and 107 species
Subfamily *Hamaparvovirinae* with 5 genera and 42 species
Unassigned genus *Metalloincertoparvovirus* with 1 species

Proposed taxonomic change(s):
This TP describes the creation of 26 new species in the subfamily *Densovirinae* and of 29 new species in the subfamily *Parvovirinae.* Additionally, we modified the virus definition to allow for the classification of sequences derived from cDNA-based metatranscriptomes if specific circumstances are met.

Justification:

Several novel viruses have been described in the literature that fulfill the criteria to be classified as separate species. Additionally, various complete coding genomes derived from metatranscriptomic experiments have been published and we changed the virus definition to allow the classification of these viruses if there are reasons to believe that the sequences originate from viral DNA, i.e the sample preparation did not involve a DNase treatment step.

Submitted: 08/06/2024; *Revised:* -

TABLE 8 - *Parvoviridae*, 55 new taxa*. Table too large, see supplementary information sheet supp_info_tab_8*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.008D.A.v2.Parvoviridae_55nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.008D.A.v2.Parvoviridae_55nsp.xlsx

2024.009D.A.v2.Anelloviridae_4ngen_70nsp

Title: Establish 4 new genera, 70 new species and abolish one genus in the family *Anelloviridae*

Authors: Kraberger S (simona.kraberger@asu.edu), Opriessnig T, Maggi F, Celer V, Okamoto H, Biagini P, Krupovic M, Varsani A

Summary:
Taxonomic rank(s) affected:
New genera (n=4) and species (n=70).

Description of current taxonomy:
The family *Anelloviridae* currently comprises of 34 genera and 173 species [1]. Over the last few years, a large number diverse of anelloviruses have been identified in various animals. Here we update the current anellovirus taxonomy by undertaking an analysis of anelloviruses whose full genome sequences have been determined. Classification is based on the species demarcation criteria of 69% ORF1 nucleotide pairwise identity and phylogenetic analyses [1].

Proposed taxonomic change(s):
Based on our analyses we propose to establish 70 new species to accommodate the unclassified anelloviruses. Further we propose the establishment of 4 new genera.

Justification:
These changes are based on the species demarcation criteria of 69% ORF1 nucleotide pairwise identity and updated phylogenetic analyses of the ORF1 protein sequences.

Submitted: 14/06/2024; *Revised:* 04/10/2024

TABLE 9 - *Anelloviridae*, 74 new taxa*. Table too large, see supplementary information sheet supp_info_tab_9

TABLE 10 - *Anelloviridae*, 6 move; rename taxa*

Operation	Rank	New taxon name	Old parent taxon	New parent taxon	Old taxon name
Move; rename taxon	species	*Upsilontorquevirus ursid6*	*Dalettorquevirus*	*Upsilontorquevirus*	*Dalettorquevirus ursid6*
Move; rename taxon	species	*Sadetorquevirus hominid8*	*Hetorquevirus*	*Sadetorquevirus*	*Hetorquevirus hominid8*
Move; rename taxon	species	*Sadetorquevirus hominid7*	*Hetorquevirus*	*Sadetorquevirus*	*Hetorquevirus hominid7*

Move; rename taxon	species	*Petorquevirus ixodi1*	*Thetatorquevirus*	*Petorquevirus*	*Thetatorquevirus ixodi1*
Move; rename taxon	species	*Petorquevirus canid1*	*Thetatorquevirus*	*Petorquevirus*	*Thetatorquevirus canid1*
Move; rename taxon	species	*Petorquevirus viver4*	*Thetatorquevirus*	*Petorquevirus*	*Thetatorquevirus viver4*

TABLE 11 - *Anelloviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	genus	*Dalettorquevirus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.009D.A.v2.Anelloviridae_4ngen_70nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.009D.A.v2.Anelloviridae_4ngen_70nsp.xlsx

2024.010D.A.v2.Varidnaviria_reorg

Title: Reorganization of the realm *Varidnaviria*

Authors: Koonin EV (koonin@ncbi.nlm.nih.gov), Fischer MG, Yutin N, Kuhn JH, Krupovic M (mart.krupovic@pasteur.fr)

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

Description of current taxonomy: Realm currently including two kingdoms: *Bamfordvirae* (two phyla with a total of six classes and one unassigned family) and *Helvetiavirae* (one phylum including one class)

Proposed taxonomic change(s): Create a new realm to accommodate *Helvetiavirae;* create a new varidnavirian kingdom to accommodate five previously bamfordviraen orders; create two subphyla in bamfordviraen phylum *Preplasmiviricota;* assign *Tectiliviricetes* to one and the remaining taxa to the other, which is also expanded by three new classes to accommodate polinton-like viruses and *Adenoviridae.*

Justification: A thorough genomic and proteomic analysis revealed previously unrecognized evolutionary relationships among the various varidnaviraen taxa.

Submitted: 21/06/2024; *Revised:* 04/10/2024

TABLE 12 - *Varidnaviria*, 13 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	realm	*Singelaviria*		
New taxon	kingdom	*Abadenavirae*		
New taxon	phylum	*Produgelaviricota*		
New taxon	class	*Belvinaviricetes*		
New taxon	subphylum	*Prepoliviricotina*		
New taxon	subphylum	*Polisuviricotina*		
New taxon	class	*Pharingeaviricetes*		
New taxon	class	*Aquintoviricetes*		
New taxon	order	*Archintovirales*		
New taxon	family	*Phypoliviridae*		
New taxon	genus	*Tetrivirus*		

New taxon	species	*Tetrivirus crimaeaense*	Tetraselmis viridis virus S1	HQ332143
New taxon	class	*Mriyaviricetes*		

TABLE 13 - *Varidnaviria*, 11 move taxa*

Operation	**Rank**	**Taxon name**	**Old parent taxon**	**New parent taxon**
Move taxon	kingdom	*Helvetiavirae*	*Varidnaviria*	*Singelaviria*
Move taxon	class	*Ainoaviricetes*	*Bamfordvirae*	*Abadenavirae*
Move taxon	order	*Atroposvirales*	*Bamfordvirae*	*Abadenavirae*
Move taxon	order	*Belfryvirales*	*Bamfordvirae*	*Abadenavirae*
Move taxon	order	*Coyopavirales*	*Bamfordvirae*	*Abadenavirae*
Move taxon	order	*Vinavirales*	*Bamfordvirae*	*Abadenavirae*
Move taxon	family	*Autolykiviridae*	*Bamfordvirae*	*Abadenavirae*
Move taxon	class	*Tectiliviricetes*	*Preplasmiviricota*	*Prepoliviricotina*
Move taxon	order	*Rowavirales*	*Preplasmiviricota*	*Polisuviricotina*
Move taxon	class	*Polintoviricetes*	*Preplasmiviricota*	*Polisuviricotina*
Move taxon	family	*Yaraviridae*		*Nucleocytoviricota*

TABLE 14 - *Varidnaviria*, 3 move; rename taxa*

Operation	**Rank**	**New taxon name**	**Old parent taxon**	**New parent taxon**	**Old taxon name**
Move; rename taxon	class	*Virophaviricetes*	*Preplasmiviricota*	*Polisuviricotina*	*Maveriviricetes*
Move; rename taxon	family	*Eupolintoviridae*	*Preplasmiviricota*	*Polisuviricotina*	*Adintoviridae*
Move; rename taxon	order	*Amphintovirales*	*Preplasmiviricota*	*Polisuviricotina*	*Orthopolintovirales*

TABLE 15 - *Varidnaviria*, 1 rename taxon*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	species	*Asfivirus haemorrhagiae*	*African swine fever virus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.010D.A.v2.Varidnaviria_reorg.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.010D.A.v2.Varidnaviria_reorg.xlsx

2024.012D.A.v2.Shotokuvirae_newphylum

Title: Create a new phylum ‘Commensaviricota’ for the kingdom *Shotokuvirae* and family *Anelloviridae*

Authors: Varsani A, Butkovic A, Kraberger S, Koonin EV, Krupovic M (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected:
Monodnaviria, Shotokuvirae

Description of current taxonomy:
Currently, kingdom *Shotokuvirae* includes 2 phyla, with eukaryotic ssDNA and related dsDNA viruses classified into phyla *Cressdnaviricota* and *Cossaviricota,* respectively. *Anelloviridae* is the only family of eukaryotic ssDNA viruses not assigned to the realm *Monodnaviria.*

Proposed taxonomic change(s):
Move family *Anelloviridae* into a new order, within a new class and a new phylum *‘Commensaviricota’*

within the kingdom *Shotokuvirae.* The intermediate taxa between the phylum and family, will be order *'Sanitavirales'* and a class *'Cardeaviricetes'.*

Justification:
Sequence and structural comparisons suggest that anelloviruses have evolved from a circovirus-like ancestor through gradual augmentation of the capsid protein and loss of the Rep protein genes.

Submitted: 24/06/2024; *Revised:* -

TABLE 16 - *Shotokuvirae*, 3 new taxa*

Operation	Rank	New taxon name
New taxon	phylum	*Commensaviricota*
New taxon	class	*Cardeaviricetes*
New taxon	order	*Sanitavirales*

TABLE 17 - *Shotokuvirae*, 1 move taxon*

Operation	Rank	Taxon name	Old parent taxon	New parent taxon
Move taxon	family	*Anelloviridae*		*Monodnaviria*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.012D.A.v2.Shotokuvirae_newphylum.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.012D.A.v2.Shotokuvirae_newphylum.xlsx

2024.013D.A.v1.Belpaoviridae_spren_v1

Title: Rename all species to conform with the ICTV-mandated binomial format *(Ortervirales: Belpaoviridae)*

Authors: Krupovic M (mart.krupovic@pasteur.fr), Kuhn JH

Summary:
Taxonomic rank(s) affected: species

Description of current taxonomy:
Belpaoviridae: Semotivirus (11 species).

Proposed taxonomic change(s):
Rename all belpaovirid/semotivirus species to conform with the ICTV-mandated binomial format.

Justification:
Species in the family *Belpaoviridae* do not conform with the ICTV-mandated binomial format.

Submitted: 21/06/2024; *Revised:* -

TABLE 18 - *Belpaoviridae*, 11 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Semotivirus mooseanophelae*	*Anopheles gambiae Moose virus*
Rename taxon	species	*Semotivirus tamyantheraeae*	*Antheraea semotivirus Tamy*
Rename taxon	species	*Semotivirus tasascaridis*	*Ascaris lumbricoides Tas virus*
Rename taxon	species	*Semotivirus paobombycis*	*Bombyx mori Pao virus*
Rename taxon	species	*Semotivirus certredecimum*	*Caenorhabditis elegans Cer13 virus*
Rename taxon	species	*Semotivirus beldrosophilae*	*Drosophila melanogaster Bel virus*
Rename taxon	species	*Semotivirus roodrosophilae*	*Drosophila melanogaster Roo virus*

Rename taxon	species	*Semotivirus maxdrosophilae*	*Drosophila semotivirus Max*
Rename taxon	species	*Semotivirus ninjadrosophilae*	*Drosophila simulans Ninja virus*
Rename taxon	species	*Semotivirus sinbadschistosomae*	*Schistosoma semotivirus Sinbad*
Rename taxon	species	*Semotivirus suzutakifugu*	*Takifugu rubripes Suzu virus*

*Source / full text:

https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.013D.A.v1.Belpaoviridae_spren_v1.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.013D.A.v1.Belpaoviridae_spren_v1.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Animal dsRNA and ssRNA- viruses Subcommittee, 2024

Main Text

Contents

2024.001M.A.v1.Alpharhabdovirinae_1ng_11nsp

Title: In the subfamily *Alpharhabdovirinae,* create 9 new species in 6 existing genera *(Alphapaprhavirus, Sigmavirus, Merhavirus, Tupavirus, Alphanemrhavirus, Alpharicinrhavirus),* rename the existing genus *Thriprhavirus* (as *Alphathriprhavirus),* and create the new genus *Betathriprhavirus* including two new species *(Mononegavirales: Rhabdoviridae)*

Authors: Walker PJ (peter.walker@uq.edu.au), Bejerman N, Blasdell KR, Debat H, Dietzgen RG, Fooks AR, Freitas-Astúa J, Ramos-Gonzáles PL , Kondo H, Kurath G, Shi M, Tesh RB, Tordo N, Vasilakis N , Whitfield AE

Summary:Taxonomic rank(s) affected:
Genus and species *(Mononegavirales: Rhabdoviridae: Alpharhabdovirinae)*

Description of current taxonomy:
The subfamily *Alpharhabdovirinae* currently comprises 33 genera and 235 species.

Proposed taxonomic change(s):
Create 9 new species in 6 existing genera *(Alphapaprhavirus, Sigmavirus, Merhavirus, Tupavirus, Alphanemrhavirus* and *Alpharicinrhavirus)* for viruses recently detected in bats, shrew or various invertebrates by metagenomic sequencing. Rename the existing genus *Thriprhavirus* (as *Alphathriprhavirus)* and create a new genus *Betathriprhavirus* including 2 new species for viruses detected in thrips by metagenomic sequencing.

Justification:
The viruses cluster phylogenetically with others in the existing or proposed genera in ML trees inferred using L protein sequences. All new species in existing genera meet established demarcation criteria. The proposed renamed and new genera for viruses detected in thrips are well-separated phylogenetically.

Submitted: 09/06/2024; *Revised:* -

TABLE 1 - *Alpharhabdovirinae*, 12 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Betathriprhavirus*		
New taxon	species	*Betathriprhavirus variabilis*	soybean thrips rhabdo-like virus 1	MT224147
New taxon	species	*Betathriprhavirus midwest*	soybean thrips rhabdo-like virus 2	MT224148
New taxon	species	*Alphapaprhavirus gata*	Gata virus	KX852388
New taxon	species	*Alphapaprhavirus orgi*	Orgi virus	KX852386
New taxon	species	*Sigmavirus hangzhou*	Hangzhou rhabdovirus 4	MZ209737
New taxon	species	*Sigmavirus dorsalis*	Bactrocera dorsalis sigmavirus	MN745080
New taxon	species	*Tupavirus wufeng*	Wufeng bat tupavirus 2	OQ715690
New taxon	species	*Alpharicinrhavirus heilongjiang*	Tahe rhabdovirus 2	ON408171
New taxon	species	*Merhavirus subalbatus*	Armigeres subalbatus rhabdovirus	LC775065
New taxon	species	*Merhavirus cambodia*	Cambodia Anophales rhabdovirus	OR479699
New taxon	species	*Alphanemrhavirus wufeng*	Wufeng shrew rhabdovirus 1	OQ715689

TABLE 2 - *Alpharhabdovirinae*, 1 rename taxon*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	genus	*Alphathriprhavirus*	*Thriprhavirus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.001M.A.v1.Alpharhabdovirinae_1ng_11nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.001M.A.v1.Alpharhabdovirinae_1ng_11nsp.xlsx

2024.002M.A.v1.Antennavirus_1nsp

Title: Create one new species in genus *Antennavirus (Hareavirales; Arenaviridae)*

Authors: Grimwood RG (rebecca.grimwood@postgrad.otago.ac.nz), Geoghegan JL, Kuhn JH

Summary:
Taxonomic rank(s) affected: *Hareavirales: Arenaviridae: Antennavirus*

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

Proposed taxonomic change(s): Establishment of one new species in genus *Antennavirus* for Ross Sea rockcod virus, identified in a scaly rockcod *(Trematomus loennbergii* Regan, 1913) and a slender scalyhead *(Trematomus lepidorhinus* (Paul Pappenheim, 1911)) from the Ross Sea, Antarctica.

Justification: Divergence of the coding-complete genome sequence of Ross Sea rockcod virus meets the established species demarcation criteria for genus *Antennavirus.*

Submitted: 06/06/2024; *Revised:* -

TABLE 3 - *Antennavirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Antennavirus trematomi*	Ross Sea rockcod virus	L: PP590693; S: PP590768; NP: PP590769

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.002M.A.v1.Antennavirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.002M.A.v1.Antennavirus_1nsp.xlsx

2024.003M.A.v1.Artoviridae_4nsp

Title: Create two new species in genus *Peropuvirus* and two new species in genus *Hexartovirus (Mononegavirales: Artoviridae)*

Authors: Økland, AL (arnfinn.lodden.okland@zoetis.com), Kuhn, J, Ye, G, Vasilakis, N

Summary: Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The family *Artoviridae* currently includes two genera, *Hexartovirus* (2 species) and *Peropuvirus* (7 species).

Proposed taxonomic change(s):
Create two new species in genus *Hexartovirus* and two new species in genus *Peropuvirus.*

Justification:
The viruses proposed to be assigned to novel species have a minimum amino acid divergence of 44 % in their L proteins compared to classified family members and occupy different ecological niches.

Submitted: 21/06/2024; *Revised:* -

TABLE 4 - *Artoviridae* , 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Peropuvirus pteropi*	bat faecal associated arto-like virus 2	ON872573
New taxon	species	*Peropuvirus wufengense*	Wùfēng shrew peropuvirus 1	OQ715590
New taxon	species	*Hexartovirus caligi*	Caligus clemensi hexartovirus 1	MZ484467
New taxon	species	*Hexartovirus artemiae*	brine shrimp artovirus 1	OL472418

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.003M.A.v1.Artoviridae_4nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.003M.A.v1.Artoviridae_4nsp.xlsx

2024.004M.A.v2.Bornaviridae_3nsp

Title: Create three new species in family *Bornaviridae (Mononegavirales)*

Authors: Briese T, Dürrwald R, Horie M, Hyndman TH, Jiménez-Clavero MA, Kuhn JH, Nowotny N, Pfaff F (florian.pfaff@fli.de), Rubbenstroth D, Tomonaga K

Summary:
Taxonomic rank(s) affected:
Genus *(Cultervirus, Orthobornavirus)*

Description of current taxonomy:
Riboviria: Orthornavirae: Negarnaviricota: Haploviricotina: Monjiviricetes: Mononegavirales: Bornaviridae: Cultervirus (three species) and *Orthobornavirus* (nine species).

Proposed taxonomic change(s):
Add two (2) new species to genus *Cultervirus (Cultervirus harpadoni, Cultervirus poeciliae)* and add one (1) new species to genus *Orthobornavirus (Orthobornavirus iridiscincum*).

Justification:
The proposed new species are based on newly released genome sequences in GenBank that meet the current bornavirid species demarcation criteria.

Submitted: 21/06/2024; *Revised:* 20/09/2024

TABLE 5 - *Bornaviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Cultervirus poeciliae*	Pará molly bornavirus	BK063657
New taxon	species	*Cultervirus harpadoni*	Bombay duck fish bornavirus	BK063658
New taxon	species	*Orthobornavirus iridiscincum*	Carlia munda bornavirus	PP711183

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.004M.A.v2.Bornaviridae_3nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.004M.A.v2.Bornaviridae_3nsp.xlsx

2024.005M.A.v2.Cardoreovirus_1nsp

Title: Create one new species in the genus *Cardoreovirus (Reovirales: Sedoreoviridae)*

Authors: Zhao M (mzhao@rvc.ac.uk), Schott E (schott@umces.edu), Tavares

Summary:
Taxonomic rank(s) affected:
Cardoreovirus genus

Description of current taxonomy:
The genus *Cardoreovirus* currently has only one species of *Cardoreovirus eriocheiris* whose exemplar member is Eirocheir sinensis reovirus (EsRV).

Proposed taxonomic change(s):
A new species *(Cardoreovirus callinectes)* belonging to the *Cardoreovirus* genus should be established.

Justification:
The exemplar virus (Callinectes sapidus reovirus 2, CsRV2) of the proposed new species – *Cardoreovirus callinectes* – exhibits amino acid sequence similarities ranging from 46% to 79% for segments 1-12 compared to EsRV in the established species - *Cardoreovirus eriocheiris.* The maximum likelihood phylogenetic tree indicates that CsRV2 falls on a different branch but within the same clade as EsRV, suggesting that a new species should be classified within the *Cardoreovirus* genus.

Submitted: 14/06/2024; *Revised:* -

TABLE 6 - *Cardoreovirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**

New taxon	species	*Cardoreovirus callinectes*	Callinectes sapidus reovirus 2	MW208677 - MW208688

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.005M.A.v2.Cardoreovirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.005M.A.v2.Cardoreovirus_1nsp.xlsx

2024.006M.A.v1.Deltarhabdovirinae_4nsp

Title: In the subfamily *Deltarhabdovirinae,* create 1 new species in the genus *Stangrhavirus,* 1 new species in the genus *Primrhavirus,* and 2 new species in the genus *Alphahymrhavirus*

Authors: Walker PJ (peter.walker@uq.edu.au), Bejerman N, Blasdell KR, Debat H, Dietzgen RG, Fooks AR, Freitas-Astúa J, Ramos-Gonzáles PL , Kondo H, Kurath G, Shi M, Tesh RB, Tordo N, Vasilakis N , Whitfield AE

Summary:Taxonomic rank(s) affected:
Species *(Mononegavirales: Rhabdoviridae: Deltarhabdovirinae*)

Description of current taxonomy:
The subfamily *Deltarhabdovirinae* currently comprises 11 genera including
34 species for viruses detected in various invertebrates (arthropods, nematodes and crustaceans).

Proposed taxonomic change(s):
Create 4 new species in the subfamily *Deltarhabdovirinae,* 1 in the genus *Stangrhavirus* for a virus detected in mosquitoes, 1 in the genus *Primrhavirus* for a virus detected in mosquitoes, and 2 in the genus *Alphahymrhavirus* for aviruses detected in ants and wasps.

Justification:
The viruses cluster phylogenetically with others in the existing genera in ML trees inferred using L protein sequences. All new species meet established demarcation criteria for the genera.

Submitted: 09/06/2024; *Revised:* -

TABLE 7 - *Deltarhabdovirinae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Stangrhavirus yunnan*	Xiangyun mono-chu-like virus 11	OL700136
New taxon	species	*Primrhavirus yunnan*	Xiangyun mono-chu-like virus 4	OL700129
New taxon	species	*Alphahymrhavirus electrico*	electric ant rhabdovirus	OP518027
New taxon	species	*Alphahymrhavirus ectemnius*	Ectemnius rhabdovirus	BK063699

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.006M.A.v1.Deltarhabdovirinae_4nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.006M.A.v1.Deltarhabdovirinae_4nsp.xlsx

2024.007M.A.v2.Filoviridae_1nsp

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

Authors: Kuhn, JH (kuhnjens@mail.nih.gov), Liu, Y, Bao, Y

Summary:
Taxonomic rank(s) affected: Genus *(Dianlovirus)*

Description of current taxonomy: *Riboviria: Orthornavirae: Negarnaviricota: Haploviricotina: Monjiviricetes: Mononegavirales: Filoviridae: Dianlovirus: Dianlovirus menglaense*

Proposed taxonomic change(s): Add one species *(Dianlovirus dehongense)*

Justification: The complete genome sequence of Déhóng virus (DEHV) fulfills the pairwise-sequence-based demarcation criterion for the establishment of a novel species.

Submitted: 21/06/2024; *Revised:* 17/09/2024

TABLE 8 - *Filoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Dianlovirus dehongense*	Déhóng virus	OP924273

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.007M.A.v2.Filoviridae_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.007M.A.v2.Filoviridae_1nsp.xlsx

2024.008M.A.v2.Lispiviridae_5ngen_11nsp

Title: Create five new genera and eleven new species in the family *Lispiviridae (Mononegavirales)*

Authors: Li JM (lijunmin@nbu.edu.cn), Ye GY, Wang F, Ye ZX

Summary:
Taxonomic rank(s) affected:
Mononegaviral family *Lispiviridae.*

Description of current taxonomy:
Currently, the family *Lispiviridae* includes 25 genera and 34 species according to ICTV Master Species List (MSL39.v3).

Proposed taxonomic change(s):
We propose the creation of 5 new genera and 11 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: 05/06/2024; *Revised:* 04/07/2024

TABLE 9 - *Lispiviridae*, 16 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Artemvirus*		
New taxon	species	*Artemvirus bsafialis*	brine shrimp arlivirus 1	OL472403
New taxon	species	*Artemvirus bsasecalis*	brine shrimp arlivirus 2	OL472404
New taxon	species	*Artemvirus bsathalis*	brine shrimp arlivirus 3	OL472405
New taxon	species	*Artemvirus bsafalis*	brine shrimp arlivirus 4	OL472406
New taxon	species	*Artemvirus bsafivalis*	brine shrimp arlivirus 5	OL472407
New taxon	species	*Artemvirus bsasialis*	brine shrimp arlivirus 6	OL472411

New taxon	species	*Artemvirus bsaeighalis*	brine shrimp arlivirus 8	OL472416
New taxon	genus	*Canmovirus*		
New taxon	species	*Canmovirus mahaense*	Pedras lispivirus	OQ779241
New taxon	genus	*Coroavirus*		
New taxon	species	*Coroavirus germense*	Blattodean arli-related virus OKIAV101	MT153397
New taxon	genus	*Robevirus*		
New taxon	species	*Robevirus hanzense*	Hángzhōu lispivirus 1	MZ209712
New taxon	genus	*Weflthvirus*		
New taxon	species	*Weflthvirus itaense*	Frankliniella occidentalis associated mononegavirales virus 1	MN714688

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.008M.A.v2.Lispiviridae_5ngen_11nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.008M.A.v2.Lispiviridae_5ngen_11nsp.xlsx

2024.009M.A.v1.Mammarenavirus_1nsp

Title: Create one new species in the genus *Mammarenavirus (Hareavirales: Arenaviridae]*

Authors: Shedroff ES, Martin ML, Whitmer SLM (Evk3@cdc.gov), Brignone J, Garcia JB, Sen C, Nazar Y, Fabbri C, Morales-Betoulle M, Mendez JA, Montgomery JM, Morales MA, Klena JD

Summary:
Taxonomic rank(s) affected: *Hareavirales: Arenaviridae*: *Mammarenavirus*

Description of current taxonomy: Eleven genomes representing four species of American *Mammarenavirus* clade C were present in public records. An additional 13 clade C Mammarenavirus genomes were added to public records following the sequencing of mammarenavirus-positive rodent samples collected in Argentina from 1990-2020.

Proposed taxonomic change(s): Establishment of one new species in genus *Mammarenavirus* for a new virus named vello virus, identified following the sequencing of mammarenavirus-positive rodent samples collected in Argentina from 1990-2020.

Justification: Two of the L segment sequences of 13 clade C mammarenavirus genomes identified following the sequencing of mammareanvirus-positive rodent samples collected in Argentina from 1990-2020, meet current demarcation species criteria for genus *Mammarenavirus.* We propose the two isolates described by Shedroff and Martin et al. to represent one new virus named *"vello virus"* and to assign vello virus to a new species, *Mammarenavirus vello*.

Submitted: 24/05/2024; *Revised:* -

TABLE 10 - *Mammarenavirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Mammarenavirus vello*	Vello virus	L: OR844405; S: OR844394

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.009M.A.v1.Mammarenavirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.009M.A.v1.Mammarenavirus_1nsp.xlsx

2024.010M.A.v2.Orthobunyavirus_4nsp

Title: Create four new species in the genus *Orthobunyavirus,* family *Peribunyaviridae*

Authors: de Souza WM (wmdesouza@uky.edu), Calisher C, Carrera JP , Hughes HR, Nunes MRT, Russell B, Tilston-Lunel NL, Venter M , Xia H

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy: The *Peribunyaviridae* family comprises 148 viral species, classified into eight genera: *Gryffinivirus* (2 viral species), *Herbevirus* (3 viral species), *Khurdivirus* (1 viral species), *Lakivirus* (1 viral species), *Lambavirus* (1 viral species), *Orthobunyavirus* (134 viral species), *Pacuvirus* (5 viral species), and *Shangavirus* (1 viral species).

Proposed taxonomic change(s): We propose the demarcation of four new species in the genus *Orthobunyavirus*.

Justification: Based on the current demarcation criteria of 96% identity of L protein amino acids marking a new species [1], we have confirmed the previous speciation of 134 species and propose the demarcation of two new species in the genus *Orthobunyavirus (Peribunyaviridae).*

Submitted: 11/06/2024; *Revised:* 12/08/2024

TABLE 11 - *Orthobunyavirus*, 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Orthobunyavirus taniyamense*	Taniyama virus	S: LC698002; M: LC698003; L: LC698004
New taxon	species	*Orthobunyavirus lichuanense*	Lichuan virus	S: MT198371; M: MT198372; L: MT198373
New taxon	species	*Orthobunyavirus indianense*	I612045 virus	S: HM627180; M: HM627181; L: HM627182
New taxon	species	*Orthobunyavirus taiense*	Tai orthobunyavirus	S: OQ031275; M: OQ031274; L: OQ031273

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.010M.A.v2.orthobunyavirus_4nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.010M.A.v2.orthobunyavirus_4nsp.xlsx

2024.011M.A.v1.Orthohantavirus_1nsp

Title: Create one new species in the genus *Orthohantavirus (Elliovirales: Hantaviridae): Orthohantavirus ozarkense*

Authors: Mull N (nmull@shawnee.edu), Erdin M, Smura T, Sironen T, Forbes KM

Summary:Taxonomic rank(s) affected:
Hantaviridae: Orthohantavirus

Description of current taxonomy:
35 established species

Proposed taxonomic change(s):

Addition of 1 new species

Justification:
Using a coding-complete genome sequence comprising all three genomic segments, we demonstrate that a virus discovered in hispid cotton rats *(Sigmodon hispidus* Say and Ord, 1825) sampled in the Ozark Plateau, Arkansas, USA, Ozark virus (OZAV) is a genetically unique orthohantavirus. We propose a novel orthohantavirus species, *Orthohantavirus ozarkense,* to include OZAV.

Submitted: 12/05/2024; *Revised:* -

TABLE 12 - *orthohantavirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Orthohantavirus ozarkense*	Ozark virus	S: PP434897; M: PP434896; L: PP4348921

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.011M.A.v1.orthohantavirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.011M.A.v1.orthohantavirus_1nsp.xlsx

2024.012M.A.v1.Orthohantavirus_1nsp

Title: Create one new species in the genus *Orthohantavirus (Elliovirales: Hantaviridae): Orthohantavirus sagercreekense*

Authors: Mull N (nmull@shawnee.edu), Erdin M, Letko M, Seifert S, Sironen T, Smura T, Forbes KM

Summary:
Taxonomic rank(s) affected: *Hantaviridae: Orthohantavirus*

Description of current taxonomy: 35 established species

Proposed taxonomic change(s): Addition of 1 new species

Justification: Using a coding-complete genome sequence comprising all three genomic segments, we demonstrate that a virus discovered in prairie voles (Microtus (Pedomys) ochrogaster (Wagner, 1842)) sampled in the Ozark Plateau, Arkansas, USA, Sager Creek virus (SACRV) is a genetically unique orthohantavirus. We propose a novel orthohantavirus species, *Orthohantavirus sagercreekense*, to include SACRV.

Submitted: 12/05/2024; *Revised:* -

TABLE 13 - *Orthohantavirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Orthohantavirus sagercreekense*	Sager Creek virus	S: PP905729; M: PP905731; L: PP905726

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.012M.A.v1.orthohantavirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.012M.A.v1.orthohantavirus_1nsp.xlsx

2024.013M.A.v1.Phasmaviridae_4nsp_3ab_2rn

Title: Create four new species, abolish two species, and rename two species in the family *Phasmaviridae*

Authors: Ballinger MJ (ballinger@biology.msstate.edu), Junglen S, De Coninck L

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The family *Phasmaviridae* includes 29 species organized across seven genera.

Proposed taxonomic change(s):
Create four new species, abolish three species established previously, and rename two species established previously.

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.* Three species were previously established in error due to an oversight; the available genomes are not coding-complete. Two previously established species epithets erroneously referred to places and are renamed here using appropriate suffixes.

Submitted: 06/06/2024; *Revised:* -

TABLE 14 - *Phasmaviridae*, 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Jonvirus spilikinsis*	Spilikins virus	MZ202269, MZ202270, MZ202271
New taxon	species	*Jonvirus mikadosis*	Mikado virus	MZ202272, MZ202273, MZ202274
New taxon	species	*Orthophasmavirus obscurae*	Drosophila North Esk phasmavirus	OR605709, OR605710, OR605711
New taxon	species	*Orthophasmavirus stecellulae*	Anopheles stephensi orthophasmavirus	LC775043; LC775044; LC775045

TABLE 15 - *Phasmaviridae*, 3 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	species	*Feravirus hemipterus*
Abolish taxon	species	*Orthophasmavirus flenense*
Abolish taxon	species	*Orthophasmavirus coleopterus*

TABLE 16 - *Phasmaviridae*, 2 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Orthophasmavirus miglotalis*	*Orthophasmavirus miglotasense*

Rename taxon	species	*Orthophasmavirus barstukorius*	*Orthophasmavirus barstukasense*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.013M.A.v1.Phasmaviridae.4nsp_3ab_2rn.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.013M.A.v1.Phasmaviridae.4nsp_3ab_2rn.xlsx

2024.014M.A.v2.Platrhavirus_2ng_30nsp

Title: Rename the existing genus *Platrhavirus* (as *Alphaplatrhavirus)* and create 12 new species in the renamed genus, create the new genus *Betaplatrhavirus* including 12 new species, and create the new genus *Gammaplatrhavirus* including 6 new species *(Mononegavirales: Rhabdoviridae)*

Authors: Walker PJ (peter.walker@uq.edu.au), Bejerman N, Blasdell KR, Debat H, Dietzgen RG, Fooks AR, Freitas-Astúa J, Ramos-Gonzáles PL , Kondo H, Kurath G, Shi M, Tesh RB, Tordo N, Vasilakis N , Whitfield AE

Summary:Taxonomic rank(s) affected:
Genus and species *(Mononegavirales: Rhabdoviridae)*

Description of current taxonomy:
The family *Rhabdoviridae* currently comprises four subfamilies and one additional genus *(Platrhavirus)* including 6 species.

Proposed taxonomic change(s):
Rename the existing genus *Platrhavirus* (as *Alphaplatrhavirus)* and create 12 new species in the renamed genus, and create two new genera *(Betaplatrhavirus* and *Gammaplatrhavirus)* including 18 new species for viruses detected by metagenomic sequencing in cestode or trematode worms (Platyhelminthes) or in the feces or visceral organs of animals (mammals, fish or crustaceans) that appear to have been infested with worms.

Justification:
The viruses cluster phylogenetically with others in the existing or proposed genera in ML trees inferred using L protein sequences. All new species in existing genera meet established demarcation criteria. The proposed renamed and new genera for viruses are well-separated phylogenetically from each other and from other rhabdoviruses.

Submitted: 09/06/2024; *Revised:* 24/08/2024

TABLE 17 - *Platrhavirus*, 32 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Alphaplatrhavirus dendriticum*	Dicrocoilium rhabdo-like virus 2	OP627658
New taxon	species	*Alphaplatrhavirus solidus*	Schistocephalus solidus rhabdovirus	MN803433
New taxon	species	*Alphaplatrhavirus wufeng*	Wufeng shrew rhabdovirus 5	OQ715673
New taxon	species	*Alphaplatrhavirus smithii*	Wufeng shrew rhabdovirus 7	OQ715674
New taxon	species	*Alphaplatrhavirus chodsigoa*	Wufeng shrew rhabdovirus 8	OQ715683
New taxon	species	*Alphaplatrhavirus hubei*	Wufeng shrew rhabdovirus 9	OQ715680
New taxon	species	*Alphaplatrhavirus jingmen*	Jingmen bat rhabdovirus 1	OQ715681
New taxon	species	*Alphaplatrhavirus ricketti*	Jingmen bat rhabdovirus 2	OQ715691
New taxon	species	*Alphaplatrhavirus wenzhou*	Wenzhou bat rhabdovirus 1	OQ715676
New taxon	species	*Alphaplatrhavirus langier*	Wenzhou bat rhabdovirus 3	OQ715675

New taxon	species	*Alphaplatrhavirus larvatus*	rhabdovirus sp. HLGXC14/3	OR868933
New taxon	species	*Alphaplatrhavirus acutispina*	Wenling dimarhabdovirus 8	MG600017
New taxon	genus	*Betaplatrhavirus*		
New taxon	species	*Betaplatrhavirus nodulosus*	triaenorhabdovirus 2	BK059680
New taxon	species	*Betaplatrhavirus psilotrema*	psilorhabdovirus 1	BK059745
New taxon	species	*Betaplatrhavirus simillimum*	psilorhabdovirus 2	BK059746
New taxon	species	*Betaplatrhavirus sphaeroidotrema*	sphaeridiorhabdovirus 2	BK059663
New taxon	species	*Betaplatrhavirus pseudoglobulus*	sphaeridiorhabdovirus 3	BK059664
New taxon	species	*Betaplatrhavirus himastelon*	himastelon rhabdovirus	OR553881
New taxon	species	*Betaplatrhavirus beihai*	Beihai dimarhabdovirus 1	MG600012
New taxon	species	*Betaplatrhavirus wenling*	Wenling dimarhabdovirus 1	MG600014
New taxon	species	*Betaplatrhavirus fujian*	Fujian dimarhabdovirus	MG600015
New taxon	species	*Betaplatrhavirus fuscus*	Eptesicus fuscus rhabdovirus	MT732687
New taxon	species	*Betaplatrhavirus abramus*	bat-associated rhabdovirus 2	OR951388
New taxon	species	*Betaplatrhavirus armiger*	rhabdovirus sp. HAGXC131516/2	OR869044
New taxon	genus	*Gammaplatrhavirus*		
New taxon	species	*Gammaplatrhavirus dendriticum*	Dicrocoilium rhabdo-like virus 1	OP548620
New taxon	species	*Gammaplatrhavirus orientalis*	metorhabdovirus 1	BK059675
New taxon	species	*Gammaplatrhavirus sinensis*	clonorhabdovirus 1	BK059698
New taxon	species	*Gammaplatrhavirus beihai*	Beihai barnacle virus 7	KX884411
New taxon	species	*Gammaplatrhavirus jilin*	barnaclevirus sp.	OR871063
New taxon	species	*Gammaplatrhavirus wenzhou*	Wenzhou bat rhabdovirus 2	OQ715697

TABLE 18 - *Platrhavirus*, 7 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	genus	*Alphaplatrhavirus*	*Platrhavirus*
Rename taxon	species	*Alphaplatrhavirus microphallus*	*Platrhavirus microphallus*
Rename taxon	species	*Alphaplatrhavirus nodulosis*	*Platrhavirus nodulosis*
Rename taxon	species	*Alphaplatrhavirus orientalis*	*Platrhavirus orientalis*
Rename taxon	species	*Alphaplatrhavirus pseudoglobulus*	*Platrhavirus pseudoglobulus*
Rename taxon	species	*Alphaplatrhavirus turkestanicum*	*Platrhavirus turkestanicum*
Rename taxon	species	*Alphaplatrhavirus vulpes*	*Platrhavirus vulpes*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.014M.A.v3.Platrhavirus_2ng_30nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.014M.A.v3.Platrhavirus_2ng_30nsp.xlsx

2024.015M.A.v1.Rotavirus_2nsp

Title: Create two new species *(Rotavirus kappagastroenteritidis, Rotavirus lambdagastroenteritidis)* in the genus *Rotavirus* (Family *Sedoreoviridae)*

Authors: Johne R (Reimar.Johne@bfr.bund.de)

Summary:

Taxonomic rank(s) affected:

The genus *Rotavirus*

Description of current taxonomy:

Currently, the 9 different rotavirus species *Rotavirus alphagastroenteritidisto* and *Rotavirus jotagastroenteritidis* exist.

Proposed taxonomic change(s):

Two new rotavirus species *(Rotavirus kappagastroenteritidis* and *Rotavirus lambdagastroenteritidis* should be created.

Justification:

Evolutionary analysis of complete coding regions of the RVL genomes using phylogenetic trees indicate a separate branching of all genome segments from that of the established rotavirus species. In addition, the maximum identities of deduced amino acid sequence for VP6 with that of established rotavirus species reference strains are 51% for RVK and 47% for RVL, which are lower than the cut-off value (53%) for definition of new rotavirus species.

Submitted: 14/06/2024; *Revised:* -

TABLE 19 - *Rotavirus*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Rotavirus kappagastroenteritidis*	rotavirus K	OQ934016-OQ934026
New taxon	species	*Rotavirus gastrolambdaenteritidis*	rotavirus L	OM101015-OM101025

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.015M.A.v1.Rotavirus_2nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.015M.A.v1.Rotavirus_2nsp.xlsx

2024.016M.A.v1.Sedoreoviridae_1ng_3nsp

Title: Create one new genus *(Crabreovirus)* with three new species

Authors: Zhao M (mzhao@rvc.ac.uk), Schott E (schott@umces.edu)

Summary:

Taxonomic rank(s) affected:

Sedoreoviridae family

Description of current taxonomy:

Sedoreoviridae currently has six genera, including: *Cardoreovirus, Mimoreovirus, Orbivirus, Phytoreovirus, Rotavirus,* and *Seadornavirus.*

Proposed taxonomic change(s):

A new genus, named *Crabreovirus,* should be established in the *Sedoreoviridae* family. This new genus should include three new species, including: *Crabreovirus callinectes, Crabreovirus scylla* and *Crabreovirus eriocheiris*.

Justification: Three representative viruses of the proposed new *Crabreovirus* genus exhibit less than 20% amino acid sequence identity in VP1 when compared to virus members of other established genera within *the Sedoreoviridae* family. The maximum likelihood phylogenetic tree shows that viruses in the three proposed new species form a distinct clade from members of other *Sedoreoviridae* genera, yet remain within the same clade with each other. The phylogenetic analysis supports the classification of these three species into a new genus, *Crabreovirus.*

Submitted: 14/06/2024; *Revised:* -

TABLE 20 - *Sedoreoviridae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	genus	*Crabreovirus*		
New taxon	species	*Crabreovirus callinectes*	Callinectes sapidus reovirus 1	KU311708 - KU311719
New taxon	species	*Crabreovirus scylla*	Scylla serrata reovirus SZ-2007	HQ414127 - HQ414138
New taxon	species	*Crabreovirus eriocheiris*	Eriocheir Sinensis reovirus WX-2012	KP638402 - KP638413

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.016M.A.v1.Sedoreoviridae_1ng_3nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.016M.A.v1.Sedoreoviridae_1ng_3nsp.xlsx

2024.017M.A.v1.Shilevirus_10nsp

Title: Create ten new species in genus *Shilevirus (Bunyaviricetes: Hareavirales: Leishbuviridae)*

Authors: Yurchenko, V (Vyacheslav.Yurchenko@osu.cz), Kuhn, JH, Kostygov, AYu

Summary:
Taxonomic rank(s) affected: leishbuvirid genus *Shilevirus*

Description of current taxonomy: 1 species *(Shilevirus leptomonadis*)

Proposed taxonomic change(s): Add 10 new species

Justification: Discovery of novel shileviruses in various hosts from various habitats with sufficient genetic divergence.

Submitted: 21/06/2024; *Revised:* -

TABLE 21 - *Shilevirus*, 10 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Shilevirus alphablechomonadis*	Blechmonas luni leishbunyavirus 1	S: MG967336; M: MG967335; L: MG967334
New taxon	species	*Shilevirus betablechomonadis*	Blechomonas ayalai leishbunyavirus 1	S: MG967340; M: MG967339; L: MG967338
New taxon	species	*Shilevirus puertonapoense*	Crithidia abscondita leishbunyavirus	S: KX507299; M: KX50730; L: KX507301

New taxon	species	*Shilevirus crithidiaebombi*	Crithidia bombi leishbuvirus 1	S: OR146998; M: OR146997; L: OR146996
New taxon	species	*Shilevirus otongatchiense*	Crithidia otongatchiensis leishbunyavirus	S: KX451144; M: KX683300; L: KX451145
New taxon	species	*Shilevirus alphamoraviense*	Leptomonas pyrrhocoris leishbunyavirus 3	S: OP722879; M: OP722879; L: OP722877
New taxon	species	*Shilevirus betamoraviense*	Leptomonas pyrrhocoris leishbunyavirus 4	S: OP722876; M: OP722875; L: OP722874
New taxon	species	*Shilevirus martiniquense*	Leishmania martiniquensis leishbunyavirus 1	S: MK356556; M: MK356555; L: MK356554
New taxon	species	*Shilevirus moramangoense*	Leptomonas moramango leishbunyavirus isolate LepmorLBV1b	S: KX280017; M: KX280016; L: KX280015
New taxon	species	*Shilevirus gammablechomonadis*	Blechomonas maslovi leishbunyavirus 1	S: MG967344; M: MG967343; L: MG967342

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.017M.A.v1.Shilevirus_10nsp.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.017M.A.v1.Shilevirus_10nsp.xlsx

2024.018M.A.v2.Tosoviridae_move

Title: Move free-floating negarnaviricot family *Tosoviridae* into bunyaviricete order *Hareavirales*

Authors: Kuhn JH, Koonin EV, Krupovic M, Wolf Y (wolf@ncbi.nlm.nih.gov)

Summary:
Taxonomic rank(s) affected: Family *(Tosoviridae)*

Description of current taxonomy: *Riboviria: Orthornavirae: Negarnaviricota: Tosoviridae*

Proposed taxonomic change(s): Move family *(Riboviria: Orthornavirae: Negarnaviricota: Polyploviricotina: Bunyaviricetes: Hareavirales: Tosoviridae)*

Justification: Updated RdRp phylogeny unambiguously groups tosovirids with hareavirals (sister to hareaviral families *Nairoviridae* and *Wupedeviridae)*

Submitted: 21/06/2024; *Revised:* 16/08/2024

TABLE 22 - *Tosoviridae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**Old parent taxon**	**New parent taxon**
Move taxon	family	*Tosoviridae*	*Negarnaviricota*	*Polyploviricotina*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.018M.A.v2.Tosoviridae_move.docx
https://ictv.global/system/files/proposals/pending/Animal%20dsRNA%20and%20-ssRNA%20(M)%20proposals/2024.018M.A.v2.Tosoviridae_move.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Archaeal viruses Subcommittee, 2024

Main Text

Contents

2024.001A.Uc.v2.N.v1.Apasviridae_newfam

Title: Create one new family in the order *Magrovirales* (class *Caudoviricetes)*

Authors: Prabhu A (apoorva.prabhu@uq.edu.au), Rinke C

Summary:
Taxonomic rank(s) affected: Magrovirus group A (order *Magrovirales;* class *Caudoviricetes)*

Description of current taxonomy: Recently, the order *Magrovirales* has been created for viruses associated with Marine Group II Archaea (order *Poseidoniales),* belonging to the class *Caudoviricetes.* Within *Magrovirales,* the family *Aoguangviridae,* representing the group "Magrovirus B" has been created.

Proposed taxonomic change(s): Here we propose creating the new family *'Apasviridae',* representing the group "Magrovirus A", with one new genus *'Agnivirus',* which includes the species *'Agnivirus brisbanense'.*

Please note, that the genus Savitrvirus and the species '*Savitrvirus brisbanense*', which are included in the text and the figures of this proposal, are not officially proposed at this point because complete genomes are currently not available for this virus group.

Justification: Most of the recovered magroviruses belonging to group A have not been deposited into public databases, i.e. GenBank. Hence, we propose the classification of viruses based on the demarcation criteria previously established for classification of archaeal tailed viruses (arTVs) infecting halophilic and methanogenic archaea [1].

Submitted: 24/07/2023; *Revised:* 07/10/2024

TABLE 1 - *Apasviridae*, 3 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Apasviridae*		
New taxon	genus	*Agnivirus*		
New taxon	species	*Agnivirus brisbanense*	Magrovirus_A_01	OR863078

*Source / full text:

https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.001A.Uc.v2.Apasiiviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.001A.Uc.v2.Apasiiviridae_newfam.xlsx

2024.002A.N.v1.Adrikaivirales_neworder_2newfam

Title: Create one new family in the order *Magrovirales* (class *Caudoviricetes)* and one new order, *'Adrikavirales'* within the class *Caudoviricetes*

Authors: Prabhu A (apoorva.prabhu@uq.edu.au), Rinke C

Summary:
Taxonomic rank(s) affected: Magrovirus group E (unofficially assigned to the order *Magrovirales;* class *Caudoviricetes)* and a new order within the class *Caudoviricetes*

Description of current taxonomy: Recently, the order *Magrovirales* has been created for viruses associated with Marine Group II Archaea (order *Poseidoniales*), belonging to the class *Caudoviricetes.* Within *Magrovirales,* the family *Aoguangviridae,* representing the group "Magrovirus B" has been created.

Proposed taxonomic change(s): Here we propose creating a new family *'Krittikaviridae',* representing the group "Magrovirus E", with one new genus *'Velanvirus',* which will include the species *'Velanvirus brisbanense'.* In addition, we identified a virus associated with *Poseidoniales*, which belongs to a novel order within the class *Caudoviricetes.* The new order is proposed to be named *'Adrikavirales'* and include a new family *'Satyavativiridae'.* The genus and species representative for this order is *'Vyasavirus'* and *'Vyasavirus brisbanense',* respectively.

Justification: Most of the currently available magroviruses assigned to group E are not of high quality and do not have GenBank entries. Furthermore, Poseidoniales associated viruses assigned to an order other than *Magrovirales* have not been described. Hence, we propose the classification of viruses based on the demarcation criteria previously established for classification of archaeal tailed viruses (arTVs) infecting halophilic and methanogenic archaea [1].

Submitted: 18/03/2024; *Revised:* 07/10/2024

TABLE 2 - *Adrikavirales*, 7 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Krittikaviridae*		
New taxon	genus	*Velanvirus*		
New taxon	species	*Velanvirus brisbanense*	Magrovirus_E_01	PP497039
New taxon	order	*Adrikavirales*		
New taxon	family	*Satyavativiridae*		
New taxon	genus	*Vyasavirus*		
New taxon	species	*Vyasavirus brisbanense*	Poseidoniales virus P01	PP497040

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.002A.Uc.v2,Adrikaivirales_neworder_2newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.002A.Uc.v2,Adrikaivirales_neworder_2newfam.xlsx

2024.003A.N.v1.Nipumfusiviridae_newfam

Title: Create 1 new family 'Nipumfusiviridae' with 4 genera and 10 species for archaeal viruses

Authors: Yimin Ni (Nemo.ni@outlook.com), Tianqi Xu, Shuling Yan, Lanming Chen, Yongjie Wang

Summary:

We propose a new family for Nitrosopumilaceae virus NYM1 and its relatives, the 'Nipumfusiviridae' ('Ni' and 'pum' for having sequence features similar to archaea from the family *Nitrosopumilaceae* and for being the deduced host; 'fusi' after the Latin word meaning spindles for the possible morphology). The four proposed genera are named 'Yangshanfusivirus', 'Terrafusivirus', 'Marefusivirus', and 'Baiafusivirus' after their original sampling sites, and species names are given based on the sampling locations. To be classified within this proposed family, the new members should share a minimum of 30% of average amino acid identity (AAI) with the virus genomes classified within 'Nipumfusiviridae' and share a minimum set of homologous proteins including the MCP, and the ATPase.

Submitted: 20/05/2024; *Revised:* -

TABLE 3 - *Nipumfusiviridae*, 15 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Nipumfusiviridae*		
New taxon	genus	*Marefusivirus*		
New taxon	species	*Marefusivirus pacificense*	Nitrosopumilaceae spindle-shaped virus NMP1	BK067782
New taxon	species	*Marefusivirus helgoense*	Nitrosopumilaceae spindle-shaped virus NMH1	BK067784
New taxon	species	*Marefusivirus jervisense*	Nitrosopumilaceae spindle-shaped virus NMJ1	BK067785
New taxon	species	*Marefusivirus columbiaense*	Nitrosopumilaceae spindle-shaped virus NMC1	BK067789
New taxon	species	*Marefusivirus montereyense*	Nitrosopumilaceae spindle-shaped virus NMM1	BK067790
New taxon	genus	*Terrafusivirus*		
New taxon	species	*Terrafusivirus michiganense*	Nitrosopumilaceae spindle-shaped virus NTM1	BK067788
New taxon	species	*Terrafusivirus tennesseense*	Nitrosopumilaceae spindle-shaped virus NTT1	BK067791
New taxon	genus	*Baiafusivirus*		
New taxon	species	*Baiafusivirus delawarense*	Nitrosopumilaceae spindle-shaped virus NBD1	BK067787
New taxon	species	*Baiafusivirus chesapeakense*	Nitrosopumilaceae spindle-shaped virus NBC1	BK067786
New taxon	genus	*Yangshanfusivirus*		
New taxon	species	*Yangshanfusivirus mimetica*	Nitrosopumilaceae spindle-shaped virus NYM1	BK067792

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.003A.A.v1.Nipumfusiviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.003A.A.v1.Nipumfusiviridae_newfam.xlsx

2024.004A.N.v1.Thalassapleoviridae_newphylum

Title: Create a phylum within kingdom *'Trapavirae'* (realm *Monodnaviria)* for classification of hyperthermophilic archaeal viruses with pleomorphic virions

Authors: Baquero DP, Bignon EA, Krupovic M (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected: *Monodnaviria, Trapavirae*

Description of current taxonomy: Monodnavirian kingdom *Trapavirae* currently comprises a single family, *Pleolipoviridae,* which includes haloarchaeal viruses with enveloped pleomorphic virions and single-stranded (ss) or double-stranded (ds)DNA genomes.

Proposed taxonomic change(s): Here we propose to classify viruses infecting hyperthermophilic marine archaea, distantly related to pleolipovirids, into a new family, "Thalassapleoviridae", and include it into a new phylum within the kingdom *Trapavirae.*

Justification: Whole-genome phylogenomic analysis and maximum likelihood phylogenetic analysis based on the membrane fusion protein characteristic of members of the kingdom *Trapavirae* show that members of the proposed family "Thalassapleoviridae" form a monophyletic group separate from the haloarchaeal pleolipovirids and currently unclassified related viruses of methanogenic archaea.

Submitted: - ; *Revised:* -

TABLE 4 - *Thalassapleoviridae*, 12 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	phylum	*Calorviricota*		
New taxon	class	*Caminiviricetes*		
New taxon	order	*Ageovirales*		
New taxon	family	*Thalassapleoviridae*		
New taxon	genus	*Avenivirus*		
New taxon	genus	*Aprofuvirus*		
New taxon	genus	*Geogavirus*		
New taxon	species	*Avenivirus atlanticense*	Archaeoglobus veneficus pleomorphic virus 1	BK065155
New taxon	species	*Aprofuvirus guaymasense*	Archaeoglobus profundus pleomorphic virus 1	BK065154
New taxon	species	*Geogavirus atlanticense*	Geoglobus acetivorans pleomorphic virus 1	BK065156
New taxon	species	*Geogavirus guaymasense*	Geoglobus ahangari pleomorphic virus 1	BK065157
New taxon	species	*Geogavirus pacificense*	Thalassapleovirus 2	BK065158

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.004A.A.v1.Thalassapleoviridae_newphylum_v1.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.004A.A.v1.Thalassapleoviridae_newphylum_v1.xlsx

2024.005A.N.v1.Bathyarchaeia_4newfam

Title: Create four new families for Bathyarchaeia viruses

Authors: Duan CH, Liu Y, Liu Y, Liu LR, Cai MW, Zhang R, Zeng QL, Koonin V E, Krupovic M, Li M (limeng848@szu.edu.cn)

Summary:

Bathyarchaeia is an archaeal class widespread in marine and freshwater sediments. Here we propose four new families for viruses identified by metagenomics and associated with host of the Bathyarchaeia class. The families "Fuxiviridae" and "Kunpengviridae" include head-tailed viruses of the class *Caudoviricetes* in the realm *Duplodnaviria.* The family "Chiyouviridae" consists of filamentous viruses of the archaea-specific realm *Adnaviria.* The fourth putative family, "Huangdiviridae," with only one representative genome, includes an archaea-specific spindle-shaped virus; the spindle-shaped viruses have not yet been classified at higher taxonomy ranks.

Submitted: 20/06/2024; *Revised:* 04/09/2024

TABLE 5 - *Bathyarchaeia*, 12 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	family	*Fuxiviridae*		
New taxon	family	*Kunpengviridae*		
New taxon	family	*Chiyouviridae*		
New taxon	family	*Huangdiviridae*		
New taxon	genus	*Taijivirus*		
New taxon	genus	*Dafengvirus*		
New taxon	genus	*Wargodvirus*		
New taxon	genus	*Xuanyuanvirus*		
New taxon	species	*Taijivirus yinyang*	Bathyarchaeia bifangarchaeales Fuxivirus 1	PP467601
New taxon	species	*Dafengvirus linsing*	Bathyarchaeia jinwuousiales Kupengvirus 1	PP467599
New taxon	species	*Wargodvirus xiongnu*	Bathyarchaeia bifangarchaeales Chiyouvirus 1	PP467602
New taxon	species	*Xuanyuanvirus yandi*	Bathyarchaeia baizomonadales Huangdivirus 1	QMYA01000001

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.005A.A.v2.Bathyarchaeia_4newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.005A.A.v2.Bathyarchaeia_4newfam.xlsx

2024.006A.N.v1.Usuviridae_newfam

Title: Create new family, 'Usuviridae', with two genera in the order *Methanobavirales* (class *Caudoviricetes)*

Authors: Diana P. Baquero, Sofia Medvedeva, Guillaume Borrel, SimonettaGribaldo, Mart Krupovic (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected:
Duplodnaviria, Heunggongvirae, Uroviricota, Caudoviricetes, Methanobavirales

Description of current taxonomy:
Order *Methanobavirales* (class *Caudoviricetes)* currently includes 5 families of viruses infecting methanogenic archaea.

Proposed taxonomic change(s):
Create a new family, 'Usuviridae' with two genera for classification of viruses infecting human and animal gut associated methanogenic archaea, and include this family into the existing order *Methanobavirales.*

Justification:
Whole-proteome-based phylogenomic analysis using VipTree placed MSTV1-like viruses in a distinct clade, outside of the recently established families of tailed viruses associated with methanogenic archaea or other archaeal hosts.

Submitted: 21/06/2024; *Revised:* 11/09/2024

TABLE 6 - *Usuviridae*, 5 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Usuviridae*		
New taxon	genus	*Manusuvirus*		
New taxon	genus	*Hewusuvirus*		
New taxon	species	*Manusuvirus methanobrevibacteri*	Methanobrevibacter smithii tailed virus 1	PP537965
New taxon	species	*Hewusuvirus methanobrevibacteri*	Methanobrevibacter gottschalkii virus vir075	BK068243

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.006A.Uc.v2.Usuviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.006A.Uc.v2.Usuviridae_newfam.xlsx

2024.007A.N.v1.Eurekaviridae_newfam

Title: Create a new family, "Eurekaviridae" of spindle-shaped archaeal virus

Authors: Coves M, Krupovic M, Bize A (ariane.bize@inrae.fr)

Summary:
Taxonomic rank(s) affected:
We suggest creating a new family, a new genus and a new species for classification of a spindle-shaped archaeal virus predicted to infect *Methanosarcina* species.

Description of current taxonomy:
Three families of small spindle-shaped archaeal viruses are currently defined: *Fuselloviridae, Halspiviridae and Thaspiviridae.* In addition, several spindle-shaped viruses are still unclassified. No spindle-shaped viruses infecting a methanogen has been classified so far.

Proposed taxonomic change(s):
We suggest creating a new family ("Eurekaviridae"), a new genus ("Hesperidvirus") and a new species ("Hesperidvirus aureum") to classify a newly sequenced uncultured virus, *Methanosarcina* spindle-shaped virus 1 (MetSSV1).

Justification:
MetSSV1 genome has been obtained through metavirome co-assembly, from samples collected in mesophilic anaerobic digestion batch microcosms fed with biowaste. This genome is complete and circular. It encodes several copies of the major coat proteins similar to those of previously characterized spindle-shaped viruses. However, it does not show significant genomic similarity to other archaeal spindle-shaped viruses, which justifies the creation of a new family.

Submitted: 26/06/2024; *Revised:* 02/10/2024

TABLE 7 - *Eurekaviridae*, 3 new taxa*

Operation	Rank	New taxon name	Exemplar	Exemplar
New taxon	family	*Eurekaviridae*		
New taxon	genus	*Hesperidvirus*		
New taxon	species	*Hesperidvirus aureum*	Methanosarcina spindle-shaped virus 1	PQ167755

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.007A.Uc.v2.Eurekaviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.007A.Uc.v2.Eurekaviridae_newfam.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Bacterial viruses Subcommittee, 2024

Main Text

Contents

2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns

Title: Create three new families *(Alisviridae, Ludisviridae*, and *Nixviridae)* with seven new genera and 24 new species

Authors: Matrishin CB, Kauffman KM (kmkauffm@buffalo.edu)

Summary:
Taxonomic rank(s) affected:

Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes*

Description of current taxonomy:

The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):

Creation of three new families *(Alisviridae, Ludisviridae*, and *Nixviridae)* with seven new genera *(Honmavirus, Ludisvirus, Dewhirstvirus, Nixvirus, Haasevirus*, *Excelsiorvirus,* and *Schifferlevirus)* and 24 new species.

Justification:

A comprehensive analysis of publicly available NCBI *Porphryomonas gingivalis* genomes revealed three new families of viruses, containing seven new genera and 24 new species. This discovery, using a rigorous, complementary bioinformatic approach, revealed what we believe to be precise nucleotide start and end points of the prophage genomes within bacterial contigs (see Figure 1). These novel prophages represent the first systematically described phages of *P. gingivalis.* This work, including the proposed taxonomic classifications and figures shown in this proposal, are described in Matrishin et al. (2023) {37491415} . Phage genomes are available on NCBI within BioProject PRJNA874424.

Submitted: 05/29/2024; *Revised:* -

TABLE 1 - *Alisviridae*, 34 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Alisviridae*		
New taxon	genus	*Honmavirus*		
New taxon	species	*Honmavirus pging00B*	Porphyromonas phage phage006a_EM3	BK068089
New taxon	species	*Honmavirus pging00C*	Porphyromonas phage phage007a_Bg4	PP754929
New taxon	species	*Honmavirus pging00D*	Porphyromonas phage phage008a_KCOM2795	BK068090
New taxon	species	*Honmavirus pging00E*	Porphyromonas phage phage010a_HG1691old	PP754930
New taxon	species	*Honmavirus pging00F*	Porphyromonas phage phage011a_WW2952	BK068092
New taxon	species	*Honmavirus pging00G*	Porphyromonas phage phage012a_381OKJP	BK068093
New taxon	species	*Honmavirus pging00H*	Porphyromonas phage phage013a_WW2885	BK068094
New taxon	species	*Honmavirus pging00I*	Porphyromonas phage phage014a_Kyudai4	BK068095

New taxon	family	*Ludisviridae*		
New taxon	genus	*Ludisvirus*		
New taxon	species	*Ludisvirus pging00A*	Porphyromonas phage phage005b_ATCC49417	PP754928
New taxon	family	*Nixviridae*		
New taxon	genus	*Dewhirstvirus*		
New taxon	species	*Dewhirstvirus pging00J*	Porphyromonas phage phage016a_WW2866	BK068097
New taxon	species	*Dewhirstvirus pging00K*	Porphyromonas phage phage017a_JCVISC001	BK068098
New taxon	species	*Dewhirstvirus pging00L*	Porphyromonas phage phage018a_AFR5B1	BK068099
New taxon	species	*Dewhirstvirus pging00M*	Porphyromonas phage phage019b_ATCC49417	PP754931
New taxon	genus	*Nixvirus*		
New taxon	species	*Nixvirus pging00X*	Porphyromonas phage phage032a_KCOM2801	BK068113
New taxon	genus	*Haasevirus*		
New taxon	species	*Haasevirus pging00R*	Porphyromonas phage phage025a_SJD11	BK068106
New taxon	species	*Haasevirus pging00T*	Porphyromonas phage phage027a_F0568	BK068108
New taxon	species	*Haasevirus pging00U*	Porphyromonas phage phage028a_KCOM2799	BK068109
New taxon	species	*Haasevirus pging00V*	Porphyromonas phage phage029a_Kyudai3	BK068110
New taxon	species	*Haasevirus pging00W*	Porphyromonas phage phage030a_KCOM2803	BK068111
New taxon	genus	*Excelsiorvirus*		
New taxon	species	*Excelsiorvirus pging00S*	Porphyromonas phage phage026a_KCOM2802	BK068107
New taxon	genus	*Schifferlevirus*		
New taxon	species	*Schifferlevirus pging00N*	Porphyromonas phage phage020a_SJD2	BK068101
New taxon	species	*Schifferlevirus pging00O*	Porphyromonas phage phage022a_WW2931	BK068103
New taxon	species	*Schifferlevirus pging00P*	Porphyromonas phage phage023a_KCOM2797	BK068104
New taxon	species	*Schifferlevirus pging00Q*	Porphyromonas phage phage024a_F0570	BK068105

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns.xlsx

2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns

Title: Create a new family, *Andersonviridae* for the *FelixO1-like* phages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
At present the following taxa exist as floating genera in the class *Caudoviricetes: Felixounavirus,*

Kolesnikvirus, Suspvirus, and *Mooglevirus*.

Proposed taxonomic change(s):
We propose the creation of one new *family, Andersonviridae.*
To update the genus *Felixounavirus* with 80 new species
To update the genus *Mooglevirus* with 11 new species
To add one new species to the genus *Kolesnikvirus*
To create a new genus *Daniellevirus* with two species
To create a new genus *Arnovirus* with three species

Justification:
We investigated the evolutionary relationships of 123 bacteriophages. Analysis of conserved genes revealed that these phages form a deeply branching monophyletic clade with a distance commensurate with the creation of a new family.

Submitted: 01/06/2024; *Revised:* 30/09/2024

TABLE 2 - *Andersonviridae*, 100 new taxa*. Table too large, see supplementary information sheet supp_info_tab_2

TABLE 3 - *Andersonviridae*, 6 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	genus	*Kolesnikvirus*	*Andersonviridae*
Move taxon	genus	*Felixounavirus*	*Andersonviridae*
Move taxon	genus	*Kolesnikvirus*	*Andersonviridae*
Move taxon	genus	*Mooglevirus*	*Andersonviridae*
Move taxon	genus	*Felixounavirus*	*Andersonviridae*
Move taxon	subfamily	*Ounavirinae*	*Andersonviridae*

TABLE 4 - *Andersonviridae*, 2 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old taxon name**
Move; rename taxon	species	*Mooglevirus susp1*	*Andersonviridae*	*Suspvirus SUSP1*
Move; rename taxon	species	*Mooglevirus susp2*	*Andersonviridae*	*Suspvirus SUSP2*

TABLE 5 - *Andersonviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	genus	*Suspvirus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns.xlsx

2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns

Title: Create a new family, *Berryhillviridae,* for a group of lytic *Arthrobacter* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

Summary:

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

Description of current taxonomy:
At present the following taxa exist as floating genera in the class *Caudoviricetes*:
genera *Marthavirus, Vibakivirus, Jawnskivirus* and *Ayohtrevirus*

Proposed taxonomic change(s):
We propose the created of a new family, *Berryhillviridae,* containing the existing genera *Marthavirus, Vibakivirus,* and *Ayohtrevirus* in addition to six new genera, *Jinkiesvirus, Jawnskivirus*, *Lilmacvirus, Altadenavirus, Eastwestvirus* and *Sicariusvirus*

Justification: We investigated the evolutionary relationships of 21 bacteriophages. Analysis of conserved genes and tblastx distances revealed that these phages form a deeply branching clade at a distance commensurate with the creation of a new family.

Submitted: 25/05/2024; *Revised:* -

TABLE 6 - *Berryhillviridae*, 18 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Berryhillviridae*		
New taxon	genus	*Jawnskivirus*		
New taxon	species	*Jawnskivirus king2*	Arthrobacter phage King2	MT776811
New taxon	genus	*Jinkiesvirus*		
New taxon	species	*Jinkiesvirus jinkies*	Arthrobacter phage Jinkies	MT498043
New taxon	genus	*Lilmacvirus*		
New taxon	species	*Lilmacvirus lilmac1015*	Arthrobacter phage Lilmac1015	OL742560
New taxon	species	*Lilmacvirus bolt007*	Arthrobacter phage Bolt007	OP985600
New taxon	species	*Lilmacvirus prairie*	Arthrobacter phage Prairie	MW601223
New taxon	species	*Lilmacvirus klevey*	Arthrobacter phage Klevey	MZ747522
New taxon	genus	*Altadenavirus*		
New taxon	species	*Altadenavirus altadena*	Arthrobacter phage Altadena	OR521058
New taxon	species	*Altadenavirus bumble*	Arthrobacter phage Bumble	MT498055
New taxon	genus	*Eastwestvirus*		
New taxon	species	*Eastwestvirus eastwest*	Arthrobacter phage EastWest	OK999980
New taxon	genus	*Sicariusvirus*		
New taxon	species	*Sicariusvirus sicarius2*	Arthrobacter phage Sicarius2	MW862982
New taxon	species	*Sicariusvirus wyborn*	Arthrobacter phage Wyborn	OR475274

TABLE 7 - *Berryhillviridae*, 4 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old taxon name
Move; rename taxon	species	*Jawnskivirus jawnski*	*Berryhillviridae*	*Marthavirus jawnski*
Move; rename taxon	species	*Jawnskivirus beans*	*Berryhillviridae*	*Marthavirus beans*
Move; rename taxon	species	*Jawnskivirus piccoletto*	*Berryhillviridae*	*Marthavirus piccoletto*
Move; rename taxon	species	*Jawnskivirus brent*	*Berryhillviridae*	*Marthavirus brent*

TABLE 8 - *Berryhillviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Vibakivirus*	*Berryhillviridae*
Move taxon	genus	*Ayohtrevirus*	*Berryhillviridae*
Move taxon	genus	*Marthavirus*	*Berryhillviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns.xlsx

2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns

Title: Create a new family, *Casidaviridae,* for a group of *Arthrobacter-Microbacterium* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
At present the following taxa exist as floating genera in the order *Caudoviricetes:*
Zetavirus, Baileybluvirus, Yangvirus, *Manhattanvirus* and *Liebevirus*

Proposed taxonomic change(s):
To create a new genus, *Gardenstatevirus,* with two species
To create a new genus, *Percivalvirus,* with two species
To create a new single species genus *Mabodamacavirus*
To create a new genus, *Barnstormervirus* with two species
To create a new single species genus *Honkvirus*
To create a new single species genus *Cenunavirus*
To create a new species in *Baileybluvirus*
To create seven new species in the genus *Yangvirus*
To create two new species in the genus *Manhattanvirus*
To create a new single species genus, *Emotionvirus*
To create a new single species genus, *Hilgardvirus*
To create a new single species genus, *Swepdovirus*
To create one new species in the genus *Liebevirus*
To create a new family, *Casidaviridae*

Justification:
We propose the creation of a new *family, Casidaviridae,* after examination of 21 bacteriophages related to the genera *Zetavirus, Baileybluvirus, Yangvirus*, *Manhattanvirus* and *Liebevirus* on the basis of nucleotide sequence similarity, tblastx distances and core gene phylogeny.

Submitted: 20/05/2024; *Revised:* 30/09/2024

TABLE 9 - *Casidaviridae*, 33 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Casidaviridae*		
New taxon	species	*Baileybluvirus callinallbarbz*	Arthrobacter phage CallinAllBarbz	OR553891

New taxon	species	*Yangvirus janeemi*	Arthrobacter phage Janeemi	ON970616
New taxon	species	*Yangvirus tuck*	Arthrobacter phage Tuck	OP820474
New taxon	species	*Yangvirus berrie*	Arthrobacter phage Berrie	PP208921
New taxon	species	*Yangvirus ascela*	Arthrobacter phage Ascela	OQ709218
New taxon	species	*Yangvirus cassia*	Arthrobacter phage Cassia	OQ709212
New taxon	species	*Yangvirus tfortroy*	Arthrobacter phage TforTroy	PP208923
New taxon	species	*Yangvirus nitro*	Arthrobacter phage Nitro	OR553895
New taxon	species	*Manhattanvirus vresidence*	Arthrobacter phage VResidence	OP434455
New taxon	species	*Manhattanvirus wildwest*	Arthrobacter phage Wildwest	OR521060
New taxon	species	*Liebevirus maguco*	Arthrobacter phage MaGuCo	OQ709203
New taxon	genus	*Gardenstatevirus*		
New taxon	species	*Gardenstatevirus gardenstate*	Microbacterium phage GardenState	MT952845
New taxon	species	*Gardenstatevirus iamgroot*	Microbacterium phage IAmGroot	MK880124
New taxon	genus	*Percivalvirus*		
New taxon	species	*Percivalvirus percival*	Microbacterium phage Percival	MH271308
New taxon	species	*Percivalvirus floof*	Microbacterium phage Floof	MH271298
New taxon	genus	*Mabodamacavirus*		
New taxon	species	*Mabodamacavirus mabodamaca*	Microbacterium phage Mabodamaca	OR613467
New taxon	genus	*Barnstormervirus*		
New taxon	species	*Barnstormervirus barnstormer*	Microbacterium phage Barnstormer	OQ190478
New taxon	species	*Barnstormervirus caron*	Microbacterium phage Caron	OQ190481
New taxon	genus	*Honkvirus*		
New taxon	species	*Honkvirus honk*	Microbacterium phage Honk	MW862981
New taxon	genus	*Cenunavirus*		
New taxon	species	*Cenunavirus Cen1621*	Microbacterium phage Cen1621	ON970568
New taxon	genus	*Emotionvirus*		
New taxon	species	*Emotionvirus emotion*	Arthrobacter phage Emotion	OQ709216
New taxon	genus	*Hilgardvirus*		
New taxon	species	*Hilgardvirus vroomvroom*	Arthrobacter phage VroomVroom	OQ938592
New taxon	genus	*Swepdovirus*		
New taxon	species	*Swepdovirus SWEP2*	Arthrobacter phage SWEP2	ON528933

TABLE 10 - *Casidaviridae*, 5 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	genus	*Zetavirus*	*Casidaviridae*
Move taxon	genus	*Baileybluvirus*	*Casidaviridae*
Move taxon	genus	*Yangvirus*	*Casidaviridae*
Move taxon	genus	*Manhattanvirus*	*Casidaviridae*
Move taxon	genus	*Liebevirus*	*Casidaviridae*

TABLE 11 - *Casidaviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	subfamily	*Azeevirinae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns.xlsx

2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns

Title: Create a new genus, *Cepavirus,* with two species (*Caudoviricetes*; *Autographiviridae; Slopekvirinae)* and a new species in the genera *Suseptimavirus (Caudoviricetes; Gordonclarkvirinae)* and *Uetakevirus (Caudoviricetes).*

Authors: Pas C, Fieseler L, Briers Y (yves.briers@ugent.be)

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

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

Proposed taxonomic change(s):
Creation of a new genus, *Cepavirus,* within the subfamily *Slopekvirinae,* family *Autographiviridae.*
Assign Escherichia phage vB_EcoP_PAS7 as a new species in the new genus, *Cepavirus*
Assign Escherichia phage vB_EcoP_PAS59 as a new species in the genus *Suseptimavirus,* subfamily *Gordonclarkvirinae.*
Assign Escherichia phage vB_EcoP_PAS6 as a new species within the genus *Uetakevirus.*

Justification:
These bacterial viruses fall within current genus and species demarcation criteria for inclusion within existing genera.

Submitted: 27/11/2023; *Revised:* -

TABLE 12 - *Cepavirus*, 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Cepavirus*		
New taxon	species	*Cepavirus PAS7*	Escherichia phage vB_EcoP_PAS7	OQ921331
New taxon	species	*Suseptimavirus PAS59*	Escherichia phage vB_EcoP_PAS59	OQ921332
New taxon	species	*Uetakevirus PAS61*	Escherichia phage vB_EcoP_PAS61	OQ921333

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns.xlsx

2024.007B.A.v1.Chimalliviridae_16mg

Title: Move newly classified viral genera into *Chimalliviridae* family and fix previous error

Authors: Prichard A, Pogliano J (jpogliano@ucsd.edu)

Summary:
Taxonomic rank(s) affected:
We propose to move fifteen genera into the *Chimallivirdae* family and remove one genus from this family.

Description of current taxonomy:

Last year, we submitted a proposal to create a new viral family called *Chimallivirdae* and re-assigned currently classified viruses into this family. This proposal was accepted, but in the meantime, more viruses that belong in this family have been officially recognized and classified by the ICTV. Since these proposals were submitted in the same year as ours, and there was no existing family that was appropriate for them to be assigned to at the time, these viruses were not assigned to any viral families. However, we believe that these viruses belong to the now-recognized *Chimallivirdae* family.

Proposed taxonomic change(s):

Members of the newly created genera *Miamivirus, Nimduovirus, Meadowvirus, Branisovskavirus, Ferozepurvirus, Chaoshanvirus, Ludhianavirus, Siatvirus, Maaswegvirus, Eowynvirus, Miltoncavirus, Phabiovirus, Serwervirus, Tepukevirus,* and *Pawinskivirus* should be added to the family *Chimallivirdae.* Additionally, the genus *Takahashivirus* should be removed from the family Chimallivirus, as it was included in our proposal excel sheet last year by mistake and should not belong to this family.

Justification:

We have redone the phylogenetic analysis used to support the creation of the *Chimallivirdae* family and included these newly classified genera. This shows that these new genera belong in the family *Chimallivirdae,* while *Takahashivirus PBS1,* which we included by mistake, does not.

Submitted: **-** ; *Revised:* **-**

TABLE 13 - *Chimalliviridae*, 16 move taxa*

Operation	**Rank**	**Taxon name**	**Old parent taxon**	**New parent taxon**
Move taxon	genus	*Takahashivirus*	*Chimalliviridae*	
Move taxon	genus	*Branisovskavirus*		*Chimalliviridae*
Move taxon	genus	*Chaoshanvirus*		*Chimalliviridae*
Move taxon	genus	*Eowynvirus*		*Chimalliviridae*
Move taxon	genus	*Ferozepurvirus*		*Chimalliviridae*
Move taxon	genus	*Ludhianavirus*		*Chimalliviridae*
Move taxon	genus	*Maaswegvirus*		*Chimalliviridae*
Move taxon	genus	*Meadowvirus*		*Chimalliviridae*
Move taxon	genus	*Miamivirus*		*Chimalliviridae*
Move taxon	genus	*Miltoncavirus*		*Chimalliviridae*
Move taxon	genus	*Nimduovirus*		*Chimalliviridae*
Move taxon	genus	*Pawinskivirus*		*Chimalliviridae*
Move taxon	genus	*Phabiovirus*		*Chimalliviridae*
Move taxon	genus	*Serwervirus*		*Chimalliviridae*
Move taxon	genus	*Siatvirus*		*Chimalliviridae*
Move taxon	genus	*Tepukevirus*		*Chimalliviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.007B.A.v1.Chimalliviridae_16mg.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.007B.A.v1.Chimalliviridae_16mg.xlsx

2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns

Title: Create a new family, *Colingsworthviridae,* of *Streptomyces* temperate phages (Class *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

Summary:Taxonomic rank(s) affected:

Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes*

Description of current taxonomy:

Three taxa of temperate *Streptomyces* phages exist as floating genera in the class *Caudoviricetes, Vashvirus*, *Tigunavirus* and *Lomovskayavirus.* Up to the present no effort has been made to generate higher taxa.

Proposed taxonomic change(s):

Create a new single species genus *Shadyvirus*Create a new single species genus *Sycamorevirus*
Create a new single species genus *Shaekyvirus*
Create a new genus *Sebastisaurusvirus* with three species
To add a single new species to the genus *Vashvirus*
To add a single new species to the genus *Lomovskayavirus*
To create a new family, *Colingsworthviridae,* for these genera
To transfer *Vashvirus, Tigunavirus* and *Lomovskayavirus* to this new family

Justification

As a result of detailed genomic, proteomic and phylogenetic analyses using VIRIDIC, ViPTree, VirClust we propose to create four new genera of Phi-C31-like temperate siphoviruses, in a new family named in honour of the first person to isolate a *Streptomyces* bacteriophage, Dr. Donald Colingsworth.

Submitted: 15/05/2024; *Revised:* 30/09/2024

TABLE 14 - *Colingsworthviridae*, 13 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Colingsworthviridae*		
New taxon	genus	*Shadyvirus*		
New taxon	species	*Shadyvirus shady*	Streptomyces phage Shady	MT701596
New taxon	genus	*Sycamorevirus*		
New taxon	species	*Sycamorevirus sycamore*	Streptomyces phage Sycamore	MT701593
New taxon	genus	*Shaekyvirus*		
New taxon	species	*Shaekyvirus shaeky*	Streptomyces phage Shaeky	MT701595
New taxon	genus	*Sebastisaurusvirus*		
New taxon	species	*Sebastisaurusvirus sebastisaurus*	Streptomyces phage Sebastisaurus	MK450433
New taxon	species	*Sebastisaurusvirus heather*	Streptomyces phage Heather	MK686069
New taxon	species	*Sebastisaurusvirus remusloopin*	Streptomyces phage RemusLoopin	MK686068
New taxon	species	*Vashvirus euratis*	Streptomyces phage Euratis	MK450426
New taxon	species	*Lomovskayavirus shawty*	Streptomyces phage Shawty	MK433266

TABLE 15 - *Colingsworthviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Vashvirus*	*Colingsworthviridae*
Move taxon	genus	*Lomovskayavirus*	*Colingsworthviridae*
Move taxon	genus	*Tigunavirus*	*Colingsworthviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns.xlsx

2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns

Title: Create a new family, *Connertonviridae* for a group of *Campylobacter* phages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
At present the following taxa exist as genera within the floating subfamily *Eucampyvirinae,* order *Caudoviricetes: Fletchervirus* and *Firehammervirus*.

Proposed taxonomic change(s):
To create eight new species in the genus *Fletchervirus*
To create four new species in the genus *Firehammervirus*
To create a new family *Connertonviridae* and abolish the subfamily *Eucampyvirinae.*

Justification:
We propose the abolishment of the subfamily *Eucampyvirinae* and the creation of a new family *Connertonviridae* based on analysis of the genera *Fletchervirus* and *Firehammervirus* using VIRIDIC, ViPTree, VirClust and phylogeny of 16 core proteins shared between the member species.

Submitted: 30/05/2024; *Revised:* -

TABLE 16 - *Connertonviridae*, 13 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Connertonviridae*		
New taxon	species	*Fletchervirus F341*	Campylobacter phage F341	OQ864999
New taxon	species	*Fletchervirus QDYZ*	Campylobacter phage vB_Cj_QDYZ	OQ515481
New taxon	species	*Fletchervirus PC5*	Campylobacter phage PC5	KX229736
New taxon	species	*Fletchervirus F336*	Campylobacter phage F336	MT863715
New taxon	species	*Fletchervirus CJLB7*	Campylobacter phage CJLB-7	MW057933
New taxon	species	*Fletchervirus CJLB10*	Campylobacter phage CJLB-10	MW074124
New taxon	species	*Fletchervirus F372*	Campylobacter phage F372	MT863729
New taxon	species	*Fletchervirus F207*	Campylobacter phage F207	MT863714
New taxon	species	*Firehammervirus CJLB15*	Campylobacter phage CJLB-15	MW365733
New taxon	species	*Firehammervirus F379*	Campylobacter phage F379	MT932329
New taxon	species	*Firehammervirus CJLB12*	Campylobacter phage CJLB-12	MW074125
New taxon	species	*Firehammervirus CJLB14*	Campylobacter phage CJLB-14	MW074126

TABLE 17 - *Connertonviridae*, 2 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Fletchervirus*	*Connertonviridae*
Move taxon	genus	*Firehammervirus*	*Connertonviridae*

TABLE 18 - *Connertonviridae*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	subfamily	*Eucampyvirinae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns.xlsx

2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns

Title: Create a new subfamily, *Dovevirinae,* with two genera for a group of lytic *Gordonia* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
Currently phages of this type are recognized in the genus *Lambovirus.* These are lytic siphophages with circularly permuted genomes infecting *Gordonia* species.

Proposed taxonomic change(s):
The creation of a new subfamily, *Dovevirinae,* composed of two genera, *Lambovirus* and *Xeniaduovirus* is proposed.

Justification:
Constituent species in these genera exhibit greater than 50% nucleotide sequence similarity supporting their assignment to a new subfamily

Submitted: 01/06/2024; *Revised:* -

TABLE 19 - *Dovevirinae*, 14 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	subfamily	*Dovevirinae*		
New taxon	genus	*Xeniaduovirus*		
New taxon	species	*Xeniaduovirus xenia2*	Gordonia phage Xenia2	PP725409
New taxon	species	*Lambovirus wojtek*	Gordonia phage Wojtek	OL455890
New taxon	species	*Lambovirus genamy16*	Gordonia phage Genamy16	ON755185
New taxon	species	*Lambovirus novasharks*	Gordonia phage NovaSharks	ON755187
New taxon	species	*Lambovirus zany*	Gordonia phage Zany	OL455887
New taxon	species	*Lambovirus erutan*	Gordonia phage Erutan	OR475273
New taxon	species	*Lambovirus jalebi*	Gordonia phage Jalebi	OL455895
New taxon	species	*Lambovirus birthdayboy*	Gordonia phage BirthdayBoy	OR475261
New taxon	species	*Lambovirus fulcrum*	Gordonia phage Fulcrum	OR521071
New taxon	species	*Lambovirus parvustarda*	Gordonia phage ParvusTarda	OP172868
New taxon	species	*Lambovirus otterstedtS21*	Gordonia phage OtterstedtS21	OP172870
New taxon	species	*Lambovirus patos*	Gordonia phage Patos	OP172876

TABLE 20 - *Dovevirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Lambovirus*	*Dovevirinae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns.xlsx

2024.011B.A.v2.Durnavirales_1nf_1ng_1ns

Title: Create a new family, *"Soropartitiviridae"*, within the order *Durnavirales* for classification of partiti-like virus infecting thermoacidophilic bacteria

Authors: Syun-ichi Urayama (urayama.shunichi.gn@u.tsukuba.ac.jp), Akihito Fukudome, Eugene V. Koonin, Takuro Nunoura, Mart Krupovic (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected:
Riboviria, Orthornavirae, Pisuviricota, Duplopiviricetes, Durnavirales

Description of current taxonomy:
Order *Durnavirales* includes six families of viruses with double-stranded RNA genomes. Most of the durnavirals infect fungal hosts, with the exception of partitivirids, which beside fungi, infect plants and protozoa, and picobirnavirids, which appear to infect bacteria.

Proposed taxonomic change(s):
Create a new family, *"Soropartitiviridae",* with a genus, *"Caliparnavirus", within* the order *Durnavirales* to classify partiti-like viruses discovered in the hot spring samples and infecting thermoacidophilic bacteria.

Justification:
Phylogenetic analysis based on the RNA-dependent RNA polymerase (RdRP) placed the new group of bacterial partiti-like viruses outside of the established *Partitiviridae* genera. Furthermore, unlike all other classified partititivirids, one of the two segments of "soropartitivirids" is bicistronic.

Submitted: 21/06/2024; *Revised:* -

TABLE 21 - *Durnavirales*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Soropartitiviridae*		
New taxon	genus	*Caliparnavirus*		
New taxon	species	*Caliparnavirus acidus*	hot spring partiti-like virus 1	RNA1: BTCP01000001; RNA2: BTCP01000004

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.011B.A.v3.Durnavirales_1nf_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.011B.A.v3.Durnavirales_1nf_1ng_1ns.xlsx

2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns

Title: Create a new family, *Ehrlichviridae,* for a group of *Bacillus* Andromeda-like phages (Class: *Caudoviricetes)*

Authors: Barylski J (b54026@amu.edu.pl), Moraru C, Tolstoy I, Kropinski AM

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

Description of current taxonomy:

The genus *Andromedavirus* currently exists as a floating genus in the class *Caudoviricetes*

Proposed taxonomic change(s):
To create a new genus *Suttonboningtonvirus* with one species
To create a new genus *Gettysburgvirus* with three species
To add three new species to the genus *Andromedavirus*
To create a new single species genus *Anathvirus*
To create a new single species genus *Dazunavirus*
To create a new single species genus *Chennaivirus*
To create a new single species genus *Nairobivirus*
To create a new family, *Ehrlichviridae,* for the above-mentioned taxa.

Justification:
The phages comprising these taxa form a deep branching clade using tblastx distances and single gene phylogeny. Core gene analysis shows the presence of 15 proteins conserved across all members of the proposed family.

Submitted: 19/04/2024; *Revised:* -

TABLE 22 - *Ehrlichviridae*, 16 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Ehrlichviridae*		
New taxon	species	*Andromedavirus leo2*	Bacillus phage Leo2	KU836751
New taxon	genus	*Suttonboningtonvirus*		
New taxon	species	*Suttonboningtonvirus sv1ICo2020*	Bacillus phage 1_ICo-2020	MT700412
New taxon	genus	*Gettysburgvirus*		
New taxon	species	*Gettysburgvirus gv056SW001B*	Bacillus phage 056SW001B	MN176230
New taxon	species	*Gettysburgvirus gv268TH004*	Bacillus phage 268TH004	MW394467
New taxon	species	*Gettysburgvirus gv019DV002*	Bacillus phage 019DV002	MN176220
New taxon	genus	*Anathvirus*		
New taxon	species	*Anathvirus anath*	Bacillus phage Anath	MG983742
New taxon	genus	*Dazunavirus*		
New taxon	species	*Dazunavirus DZ1*	Bacillus phage DZ1	OR338916
New taxon	genus	*Chennaivirus*		
New taxon	species	*Chennaivirus MVCVPHSA1*	Staphylococcus phage MVC_VPHSA1	OR670591
New taxon	genus	*Nairobivirus*		
New taxon	species	*Nairobivirus nv36*	Bacillus phage vB_BpsS-36	MH884513

TABLE 23 - *Ehrlichviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Andromedavirus*	*Ehrlichviridae*

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https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns.xlsx

2024.013B.A.v1.Ferrettivirinae_1nsf_3ng_38ns

Title: To create a new subfamily, *Ferrettivirinae,* for *Streptococcus* prophages [Class: *Caudoviricetes]*

Authors: Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

Summary:

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
We propose a new subfamily in the class *Caudoviricetes,* named in honour of Professor Joseph J. Ferretti, of *Streptococcus* temperate siphoprophages containing three genera: *Spinunavirus, Norfolkplacevirus* and *Hinxtonvirus.*

Justification:
Collectively these phages share ≥29.7% DNA sequence similarity and 14 homologous proteins (22.2% in common).

Submitted: 07/05/2024; *Revised:* -

TABLE 24 - *Ferrettivirinae*, 42 new taxa*. Table too large, see supplementary information sheet supp_info_tab_24*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.013B.A.v1.Ferrettivirinae_1nsf_3ng_38ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.013B.A.v2.Ferrettivirinae_1nsf_3ng_38ns.xlsx

2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns

Title: Create one new order *Grandevirales (Duplodnaviria)*

Authors: Cook R, Pye HV, Crisci MA, Telatin A, Santini JM (j.santini@ucl.ac.uk), Adriaenssens EM (Evelien.adriaenssens@quadram.ac.uk)

Summary:

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

Description of current taxonomy: The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s): We propose the creation of one new order, *Grandevirales,* comprising two new families, *Lakviridae* and *Epsomviridae,* three sub-families *(Quingentivirinae, Quadringentisvirinae* and *Sescentorumvirinae),* and four genera *(Vetruanivirus, Hatfieldvirus, Amboselivirus* and *Wendovervirus).* We also propose the creation of eight novel species within these genera.

Justification: We investigated the evolutionary relationships of 23 megaphage genomes with sizes greater than 400 kb and propose a taxonomy for their classification. Analysis of their putative proteins revealed that Lak phages formed a deeply branching monophyletic clade within the class *Caudoviricetes* that contained no other genomes, and hence justifies the creation of a new order *Grandevirales.* One of the interesting features of this clade is that all current members are characterised by an alternative genetic code, where the TAG stop codon is repurposed to an amino acid.

Submitted: 04/06/2023; *Revised:* 07/10/2024

TABLE 25 - *Grandevirales*, 18 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	order	*Grandevirales*		
New taxon	family	*Lakviridae*		
New taxon	subfamily	*Quingentivirinae*		
New taxon	genus	*Vetruanivirus*		
New taxon	species	*Vetruanivirus primi*	Prevotella phage Lak-A1	MK250015
New taxon	species	*Vetruanivirus secundi*	Prevotella phage Lak-A2	MK250019
New taxon	species	*Vetruanivirus dhakaense*	Prevotella phage Lak-C1	MK250029
New taxon	species	*Vetruanivirus porcinprimi*	uncultured phage RVC AP1_GC26	OR769218
New taxon	species	*Vetruanivirus porcinsecundi*	uncultured phage RVC AP3_GC26	OR769219
New taxon	genus	*Amboselivirus*		
New taxon	species	*Amboselivirus simi*	Prevotella phage Lak-B1	MK250020
New taxon	subfamily	*Quadringentisvirinae*		
New taxon	genus	*Hatfieldvirus*		
New taxon	species	*Hatfieldvirus porci*	uncultured phage RVC_JS4_GC31	OR769222
New taxon	family	*Epsomviridae*		
New taxon	subfamily	*Sescentorumvirinae*		
New taxon	genus	*Wendovervirus*		
New taxon	species	*Wendovervirus sonii*	uncultured phage HB1	OR769223

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https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns.xlsx

2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns

Title: To update the family *Grimontviridae* through the addition of three genera (Class: *Caudoviricetes)*

Authors: Dechesne A, Moraru C, Parra B, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

Summary:

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

Description of current taxonomy:
The C3 of podoviruses are a very rare morphotype possessing elongated capsids, the "type virus" of which is *Escherichia* phage phiEco32. The family *Grimontviridae* currently consists of five genera: *Crifsvirus,* Dalianvirus, Libingvirus, *Moazamivirus* and *Privateervirus.*

Proposed taxonomic change(s):
Create a new single species genus *Trabzonvirus*
Create a new single species genus *Lundtoftevirus*
Transfer the genus *Lahexavirus* to this family

Justification:
The family is represented by a cohesive and monophyletic group in the main predicted proteome-

based clustering tools (VirClust, ViPTree, and vConTACT2). Members of the family share 12 core proteins.

Submitted: 06/05/2024; *Revised:* 30/09/2024

TABLE 26 - *Grimontviridae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	genus	*Trabzonvirus*		
New taxon	species	*Trabzonvirus APT65*	Aeromonas phage APT65	OP491958
New taxon	genus	*Lundtoftevirus*		
New taxon	species	*Lundtoftevirus Lu221*	IncN phage Lu221	OQ829281

TABLE 27 - *Grimontviridae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	genus	*Lahexavirus*	*Grimontviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns.xlsx

2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns

Title: Create a new family, *Hodgkinviridae,* for a group of lytic *Microbacterium* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The genera *Momentomorivirus, Ouhwahvirus* and *Meganvirus* exist as floating genera in the class *Caudoviricetes*

Proposed taxonomic change(s):
To create a new single-species genus, *Fuzzbustervirus*
To add a single new species to the genus *Kozievirus*
To split the genus *Momentomorivirus* in two, creating *Margaeryvirus*
To add a single new species to the genus *Meganvirus*
To add two species to the genus *Quhwahvirus*
To create a new family, *Hodgkinviridae,* for these genera and *Metamorphovirus*

Justification:
Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Microbacterium* siphoviruses which share ≥12.2% DNA sequence similarity and 14 common proteins.

Submitted: 27/05/2024; *Revised:* 30/09/2024

TABLE 28 - *Hodgkinviridae*, 8 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**

New taxon	family	*Hodgkinviridae*		
New taxon	species	*Kozievirus MO526*	Microbacterium phage MO526	OR941552
New taxon	species	*Meganvirus nichole72*	Microbacterium phage Nicole72	OR159674
New taxon	species	*Quhwahvirus pulchra*	Microbacterium phage Pulchra	MW601217
New taxon	species	*Quhwahvirus littlefortune*	Microbacterium phage LittleFortune	OR475280
New taxon	genus	*Fuzzbustervirus*		
New taxon	species	*Fuzzbustervirus fuzzbuster*	Microbacterium phage FuzzBuster	MN062720
New taxon	genus	*Margaeryvirus*		

TABLE 29 - *Hodgkinviridae*, 5 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	genus	*Kozievirus*	*Hodgkinviridae*
Move taxon	genus	*Meganvirus*	*Hodgkinviridae*
Move taxon	genus	*Quhwahvirus*	*Hodgkinviridae*
Move taxon	genus	*Metamorphoovirus*	*Hodgkinviridae*
Move taxon	genus	*Mementomorivirus*	*Hodgkinviridae*

TABLE 30 - *Hodgkinviridae*, 2 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old taxon name**
Move; rename taxon	species	*Margaeryvirus margaery*	*Hodgkinviridae*	*Mementomorivirus margaery*
Move; rename taxon	species	*Margaeryvirus terij*	*Hodgkinviridae*	*Mementomorivirus terij*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns.xlsx

2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns

Title: Create a new family, *Jeanschmidtviridae* for a group of *Caulobacter* and *Brevundimonas* phages (Class: *Caudoviricetes)*

Authors: Millard A, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The taxa *Colossusvirus, Bertelyvirus*, *Shapirovirus* and *Poindextervirus* are floating genera in the class *Caudoviricetes*

Proposed taxonomic change(s):
To create a new genus, *Kikimoravirus,* with two species
To create a new genus, *Marchewkavirus,* with three species
To create a single-species genus, *Bajunvirus*
Abolish the subfamily *Dolichocephalovirinae*
To create a new family, *Jeanschmidtviridae,* for these genera and *Colossusvirus, Bertelyvirus*, *Shapirovirus* and *Poindextervirus.*

Justification:

The proposed members share ≥10.3% DNA sequence similarity and share 38 protein homologs.

Submitted: 10/06/2024; *Revised:* 30/09/2024

TABLE 31 - *Jeanschmidtviridae*, 10 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Jeanschmidtviridae*		
New taxon	genus	*Kikimoravirus*		
New taxon	species	*Kikimoravirus kikimora*	Brevundimonas phage vB_BpoS-Kikimora	ON529857
New taxon	species	*Kikimoravirus gurke*	Brevundimonas phage vB_BpoS-Gurke	ON529850
New taxon	genus	*Marchewkavirus*		
New taxon	species	*Marchewkavirus marchewka*	Brevundimonas phage vB_BpoS-Marchewka	ON529851
New taxon	species	*Marchewkavirus kabachok*	Brevundimonas phage vB_BpoS-Kabachok	ON529852
New taxon	species	*Marchewkavirus domovoi*	Brevundimonas phage vB_BpoS-Domovoi	ON529855
New taxon	genus	*Bajunvirus*		
New taxon	species	*Bajunvirus bajun*	Brevundimonas phage vB_BpoS-Bajun	ON529858

TABLE 32 - *Jeanschmidtviridae*, 4 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Colossusvirus*	*Jeanschmidtviridae*
Move taxon	genus	*Bertelyvirus*	*Jeanschmidtviridae*
Move taxon	genus	*Shapirovirus*	*Jeanschmidtviridae*
Move taxon	genus	*Poindextervirus*	*Jeanschmidtviridae*

TABLE 33 - *Jeanschmidtviridae*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	subfamily	*Dolichocephalovirinae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns.xlsx

2024.018B.A.v1.Kronosvirus_1ng_3ns

Title: Create one new genus *(Kronosvirus)* with three species *(Caudoviricetes).*

Authors: Ely B (ely@sc.edu)

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
Caulobacter bacteriophage Kronos is a unique siphovirus with a 50nm icosahedral head and a long (150nm) flexible tail. Aside from two phages, there are no close matches of its genome sequence to any other bacteriophage in the GenBank database. We described the phage and deposited its genome sequence in GenBank [14]. Additional phage that are closely related to Kronos can be grouped into three distinct species based on the ICTV criteria.

Justification:
The creation of the genus *Kronosvirus* complies with current demarcation criteria [10]

Submitted: 27/05/2024; *Revised:* -

TABLE 34 - *Kronosvirus*, 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Kronosvirus*		
New taxon	species	*Kronosvirus pelion*	Caulobacter phage Kronos	MH884648
New taxon	species	*Kronosvirus pomeria*	Caulobacter phage TMCBR2	OQ269668
New taxon	species	*Kronosvirus elgin*	Caulobacter phage TMCBR4	OQ330850

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.018B.A.v1.Kronosvirus_1ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.018B.A.v1.Kronosvirus_1ng_3ns.xlsx

2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns

Title: Create a new family, *Kruegerviridae,* for a group of *Gordonia* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
Vanleevirus currently exists as a floating genus in the class *Caudoviricetes*

Proposed taxonomic change(s):
To create a new genus *Cafassovirus* with four species
To create a new family, *Kruegerviridae,* for the *Cafassovirus* and *Vanleevirus.*

Justification:
By VIRIDIC analysis members of these two genera share ≥18.8% DNA sequence similarity and also share 46 protein homologs. The genera *Vanleevirus* and *Cafassovirus* form a deep-branching clade using tBLASTX distances, commensurate with the establishment of a new family of bacterial viruses.

Submitted: 28/05/2024; *Revised:* 30/09/2024

TABLE 35 - *Kruegerviridae*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Kruegerviridae*		
New taxon	genus	*Cafassovirus*		

New taxon	species	*Cafassovirus cafasso*	Gordonia phage Cafasso	MZ322021
New taxon	species	*Cafassovirus morgana*	Gordonia phage Morgana	PP537962
New taxon	species	*Cafassovirus aleemily*	Gordonia phage Aleemily	ON970578
New taxon	species	*Cafassovirus obladi*	Gordonia phage ObLaDi	OP297535

TABLE 36 - *Kruegerviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Vanleevirus*	*Kruegerviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns.xlsx

2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns

Title: Create a new family, *Lindbergviridae,* for PB1-like phages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
PB1-like phages have been classified into the following genera: *Kylevirus, Tabernariusvirus, Bcepfunavirus, Pbunavirus, Wifcevirus*, *Myosmarvirus* and *Carpasinavirus.* All these are myoviruses infecting members of the Betaproteobacteria and Gammaproteobacteria.

Proposed taxonomic change(s):
To create ten new species in the genus *Pbunavirus*
To create one new species in the genus *Myosmarvirus*
To add six new species to the genus *Wifcevirus*
To add one new species to the genus *Carpasinavirus*
To create a new single species genus *Gladiolivirus*
To create a new single species genus *Irusalimvirus*
To create a new single species genus *Plutovirus*
To create a new family, *Lindbergviridae,* for the above-mentioned taxa as well as *Kylevirus, Tabernariusvirus,* and *Bcepfunavirus.*

Justification:
All our genomic and proteomic analyses reveal that the previously established genera *Kylevirus* (2020.086B.A.v1.R.Kylevirus), *Tabernariusvirus* ((2018.099B.A.v1.A.v1.Tabernariusvirus), *Bcepfunavirus* ((2020.116B.A.v1.R.Pbunavirus), *Pbunavirus, Wifcevirus, Myosmarvirus* and *Carpasinavirus* together with the three new genera listed above belong to a new family which we have named in honour of Alf A. Lindberg. The bacteriophages share 12 common proteins.

Submitted: 27/04/2024; *Revised:* 30/09/2024

TABLE 37 - *Lindbergviridae*, 25 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Lindbergviridae*		
New taxon	species	*Pbunavirus SG1*	Pseudomonas phage SG1	OQ594965
New taxon	species	*Pbunavirus pv109*	Pseudomonas phage 109	OQ831730

New taxon	species	*Pbunavirus FBPa14*	Pseudomonas phage vB_PaeM_FBPa14	ON375839
New taxon	species	*Pbunavirus wadjak13*	Pseudomonas phage Kara-mokiny kep-wari Wadjak_13	OP310979
New taxon	species	*Pbunavirus TH15*	Pseudomonas phage TH15	MW406974
New taxon	species	*Pbunavirus PSA09*	Pseudomonas phage PSA09	MZ089730
New taxon	species	*Pbunavirus ph0031*	Pseudomonas phage PhL_UNISO_PA-DSM_ph0031	MW526258
New taxon	species	*Pbunavirus PSA25*	Pseudomonas phage PSA25	MZ089736
New taxon	species	*Pbunavirus FBPa35*	Pseudomonas phage vB_PaeM_FBPa35	ON857938
New taxon	species	*Pbunavirus victoria*	Pseudomonas phage Victoria	OR805296
New taxon	species	*Myosmarvirus SMP*	Serratia phage SMP	OP490597
New taxon	species	*Wifcevirus SP13*	Escherichia phage vB_EcoM_SP13	OP352608
New taxon	species	*Wifcevirus AV128*	Escherichia phage AV128	OR352958
New taxon	species	*Wifcevirus Ro157lw*	Escherichia phage vB_EcoM-Ro157lw	MH051335
New taxon	species	*Wifcevirus EC150*	Escherichia phage EC150	ON210137
New taxon	species	*Wifcevirus mansfield*	Escherichia phage Mansfield	MK903282
New taxon	species	*Wifcevirus ECO71P1*	Escherichia phage ECO71P1	OP172789
New taxon	species	*Carpasinavirus FoX6*	Xanthomonas phage FoX6	MT161386
New taxon	genus	*Gladiolivirus*		
New taxon	species	*Gladiolivirus maja*	Burkholderia phage Maja	MT708549
New taxon	genus	*Irusalimvirus*		
New taxon	species	*Irusalimvirus BCSR52*	Burkholderia phage BCSR52	MW460246
New taxon	genus	*Plutovirus*		
New taxon	species	*Plutovirus pluto*	Luteibacter phage vB_LflM-Pluto	ON529861

TABLE 38 - *Lindbergviridae*, 7 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Kylevirus*	*Lindbergviridae*
Move taxon	genus	*Tabernariusvirus*	*Lindbergviridae*
Move taxon	genus	*Bcepfunavirus*	*Lindbergviridae*
Move taxon	genus	*Pbunavirus*	*Lindbergviridae*
Move taxon	genus	*Myosmarvirus*	*Lindbergviridae*
Move taxon	genus	*Wifcevirus*	*Lindbergviridae*
Move taxon	genus	*Carpasinavirus*	*Lindbergviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns.xlsx

2024.021B.A.v1.Malkevirus_1ng_5ns

Title: To create a new genus, *Malkevirus,* for *Streptococcus* prophages [Class: *Caudoviricetes*]

Authors: Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
We propose a new genus, named in honour of Professor Dr. Horst Malke, comprised of temperate siphoviruses infecting *Streptococcus* spp.

Justification:
The viruses fall into a genus based on current demarcation criteria.

Submitted: 07/05/2024; *Revised:* -

TABLE 39 - *Malkevirus*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Malkevirus*		
New taxon	species	*Malkevirus ARI02853*	Streptococcus phage phiARI0285-3	KT337347
New taxon	species	*Malkevirus IPP67*	Streptococcus phage IPP67	KY065503
New taxon	species	*Malkevirus IPP45*	Streptococcus phage IPP45	KY065485
New taxon	species	*Malkevirus mv23782*	Streptococcus phage 23782	FR671408
New taxon	species	*Malkevirus mv11865*	Streptococcus phage 11865	FR671409

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.021B.A.v1.Malkevirus_1ng_5ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.021B.A.v1.Malkevirus_1ng_5ns.xlsx

2024.022B.A.v1.Markadamsvirinae_1ng_1ns

Title: Create a new genus *(Kononvirus)* with a single species to the *Markadamsvirinae* subfamily *(Caudoviricetes: Demerecviridae)*

Authors: Wójcicki M (michal.wojcicki@ibprs.pl), Shymialevich D, Średnicka P, Gientka I, Błażejak S, Sokołowska B

Summary:
Taxonomic rank(s) affected:
Proposal to create a new genus *(Kononvirus)* with a single species (tailed phages from *Caudoviricetes* class, *Demerecviridae* family and *Markadamsvirinae* subfamily).

Description of current taxonomy:
In 2022, significant changes to the taxonomy of bacterial viruses were introduced: the paraphyletic morphological families *Podoviridae, Siphoviridae,* and *Myoviridae* as well as the order *Caudovirales* were abolished, which is replaced by the class *Caudoviricetes* to group all tailed bacterial and archaeal viruses with icosahedral capsids and a double-stranded DNA genome. Moreover, a binomial system of nomenclature for species was established.
Currently, the *Demerecviridae* family includes three subfamilies *(Ermolyevavirinae, Markadamsvirinae* and *Mccorquodalevirinae)* and six separate genera *(Keyvirus, Novosibvirus, Pogseptimavirus, Priunavirus, Shenzhenvirus* and *Sugarlandvirus)* not classified at the subfamily level. The *Markadamsvirinae* subfamily currently includes two genera: *Epseptimavirus* and *Tequintavirus.*

Proposed taxonomic change(s):
We performed genomic analysis of newly isolated Enterobacter phage KKP_3711. Genome and protein analyses suggest that this bacteriophage belongs to the *Markadamsvirinae* subfamily. Still, the differences are too great to assign it to one of the two genera within this subfamily.
Therefore, we propose to create a new genus, *Kononvirus,* with one species - *Kononvirus* KKP_3711.

Justification:
Based on DNA and protein similarity this is a cohesive genus.

Submitted: 16/06/2024; *Revised:* -

TABLE 40 - *Markadamsvirinae*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	genus	*Kononvirus*		
New taxon	species	*Kononvirus KKP3711*	Enterobacter siphophage KKP_3711	PP579741

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.022B.A.v1.Markadamsvirinae_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.022B.A.v1.Markadamsvirinae_1ng_1ns.xlsx

2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns

Title: To create a new subfamily, *Mcshanvirinae,* for *Streptococcus* prophages [Class: *Caudoviricetes*]

Authors: Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
We propose a new subfamily, named in honour of Professor W. Michael McShan, of *Streptococcus* temperate siphoviruses containing three newly established genera: *Adrianbuildvirus, Medawarvirus* and *Phadecavirus.*

Justification:
The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 06/05/2024; *Revised:* -

TABLE 41 - *Mcshanvirinae*, 29 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	subfamily	*Mcshanvirinae*		
New taxon	genus	*Adrianbuildvirus*		
New taxon	species	*Adrianbuildvirus SpSL1*	Streptococcus phage SpSL1	KM882824
New taxon	species	*Adrianbuildvirus IPP5*	Streptococcus phage IPP5	KY065449
New taxon	species	*Adrianbuildvirus IPP44*	Streptococcus phage IPP44	KY065484
New taxon	species	*Adrianbuildvirus IPP42*	Streptococcus phage IPP42	KY065482
New taxon	species	*Adrianbuildvirus IPP51*	Streptococcus phage IPP51	KY065489
New taxon	species	*Adrianbuildvirus ARI0923*	Streptococcus phage phiARI0923	KT337370
New taxon	species	*Adrianbuildvirus IPP41*	Streptococcus phage IPP41	KY065481
New taxon	species	*Adrianbuildvirus IPP43*	Streptococcus phage IPP43	KY065483

New taxon	genus	*Medawarvirus*		
New taxon	species	*Medawarvirus IPP12*	Streptococcus phage IPP12	KY065454
New taxon	species	*Medawarvirus IPP22*	Streptococcus phage IPP22	KY065463
New taxon	species	*Medawarvirus IPP18*	Streptococcus phage IPP18	KY065459
New taxon	species	*Medawarvirus IPP57*	Streptococcus phage IPP57	KY065494
New taxon	species	*Medawarvirus IPP20*	Streptococcus phage IPP20	KY065461
New taxon	species	*Medawarvirus IPP21*	Streptococcus phage IPP21	KY065462
New taxon	species	*Medawarvirus IPP30*	Streptococcus phage IPP30	KY065471
New taxon	species	*Medawarvirus IPP11*	Streptococcus phage IPP11	KY065453
New taxon	species	*Medawarvirus IPP29*	Streptococcus phage IPP29	KY065470
New taxon	species	*Medawarvirus IPP19*	Streptococcus phage IPP19	KY065460
New taxon	species	*Medawarvirus ARI01312*	Streptococcus phage phiARI0131-2	KT337342
New taxon	species	*Medawarvirus IPP63*	Streptococcus phage IPP63	KY065499
New taxon	species	*Medawarvirus IPP17*	Streptococcus phage IPP17	KY065458
New taxon	species	*Medawarvirus IPP28*	Streptococcus phage IPP28	KY065469
New taxon	genus	*Phadecavirus*		
New taxon	species	*Phadecavirus PH10*	Streptococcus phage PH10	FN391954
New taxon	species	*Phadecavirus pv23TH*	Streptococcus phage 23TH	MT900487
New taxon	species	*Phadecavirus olisA1*	Streptococcus phage OlisA1	OL774868

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns.xlsx

2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns

Title: Create a new family, *Mktvariviridae,* for PhiEco32-like phages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The genera *Kuravirus, Nieuwekanaalvirus,* and *Suseptimavirus* are currently classified within the subfamily *Gordonclarkvirinae,* class *Caudoviricetes*

Proposed taxonomic change(s):
Create eight new species in the genus *Kuravirus*
Create two new species in the genus *Suseptimavirus*
Create a new family, *Mktvariviridae*

Justification:
Species classified to the genera *Kuravirus, Nieuwekanaalvirus,* and *Suseptimavirus* within the subfamily *Gordonclarkvirinae* share 12 core proteins and form a deep branching clade in ViPTree tBLASTx distance analysis.

Submitted: 06/05/2024; *Revised:* 30/09/2024

TABLE 42 - *Mktvariviridae*, 11 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Mktvariviridae*		
New taxon	species	*Kuravirus myPSH1131*	Escherichia phage myPSH1131	MG983840

New taxon	species	*Kuravirus myPSH2311*	Escherichia phage myPSH2311	MG976803
New taxon	species	*Kuravirus XT18*	Escherichia phage vB-EcoP-XT18	OR757434
New taxon	species	*Kuravirus LAMP*	Escherichia phage LAMP	MG673519
New taxon	species	*Kuravirus SDYTW1F1223*	Escherichia phage SDYTW1-F1-2-2_3	OR296290
New taxon	species	*Kuravirus pECN12032Af1*	Escherichia phage pEC-N1203-2Af.1	OQ540978
New taxon	species	*Kuravirus YF01*	Escherichia phage vB_EcoP_YF01	OQ025076
New taxon	species	*Kuravirus SR02*	Escherichia phage SR02	OQ870566
New taxon	species	*Suseptimavirus PAS59*	Escherichia phage vB_EcoP_PAS59	OQ921332
New taxon	species	*Suseptimavirus sv4E8*	Escherichia phage 4E8	OQ689734

TABLE 43 - *Mktvariviridae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	subfamily	*Gordonclarkvirinae*	*Mktvariviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns.xlsx

2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns

Title: Create a new family, *Obscuriviridae* (Class: *Caudoviricetes)*

Authors: Bartlau N (nina.bartlau@univie.ac.at), Moraru C, Wichels A, Holmfeldt K, Amann RI

Summary:Taxonomic rank(s) affected:
Family

Description of current taxonomy:
The viruses described in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
A new family, *Obscuriviridae,* is proposed, comprising two new genera, *Omtjevirus* and *Cebaduodecimvirus.*

Justification:
The *Obscuriviridae* family was delineated with two genera. The *genus Omtjevirus* has *Omtjevirus Omtje* as a species and the genus *Cebaduodecimvirus* has *Cebaduodecimvirus phi12duo* and *Cebaduodecimvirus phi12auna* as species. The proposed taxonomic assignments are based on six different methods including nucleotide-, protein-, amino acid-, and core protein-based analysis.

Submitted: 21/06/2024; *Revised:* 30/09/2024

TABLE 44 - *Obscuriviridae*, 6 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	family	*Obscuriviridae*		
New taxon	genus	*Omtjevirus*		

New taxon	species	*Omtjevirus Omtje*	Cellulophaga phage Omtje_1	MT732445
New taxon	genus	*Cebaduodecimvirus*		
New taxon	species	*Cebaduodecimvirus phi12duo*	Cellulophaga phage phi12:2	KC821606
New taxon	species	*Cebaduodecimvirus phi12auna*	Cellulophaga phage phi12a:1	KC821623

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns.xlsx

2024.026B.A.v1.Pantevenvirales_1no_3mf

Title: Create one new order *Pantevenvirales (Duplodnaviria)*

Authors: Adriaenssens EM (Evelien.adriaenssens@quadram.ac.uk), Cook R, Millard AD, Turner D

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

Description of current taxonomy: The families *Straboviridae, Kyanoviridae* and *Ackermannviridae* are unassigned at the order rank within the class *Caudoviricetes.*

Proposed taxonomic change(s): The order *Pantevenvirales* is created for these families.

Justification: The families *Straboviridae, Kyanoviridae* and *Ackermannviridae* form a monophyletic cluster in proteome-based analyses. Members of these families share a number of core orthologous genes.

Submitted: 21/06/2024; *Revised:* -

TABLE 45 - *Pantevenvirales*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	family	*Straboviridae*	*Pantevenvirales*
Move taxon	family	*Kyanoviridae*	*Pantevenvirales*
Move taxon	family	*Ackermannviridae*	*Pantevenvirales*

TABLE 46 - *Pantevenvirales*, 1 new taxon*

Operation	Rank	New taxon name
New taxon	order	*Pantevenvirales*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.026B.A.v1.Pantevenvirales_1no_3mf.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.026B.A.v1.Pantevenvirales_1no_3mf.xlsx

2024.028B.A.v1.Philemonvirus_1ns

Title: To create one (1) new species in the genus *Bifilivirus,* family *Paulinoviridae*

Authors: Deptula P (deptula@food.ku.dk), Sha Y, Potipimpanon S, Vogensen FK, Nielsen DS, Knezevic P

Summary:

Taxonomic rank(s) affected: This is a proposal for creating a new species within the genus *Bifilivirus.*

Description of current taxonomy:

Proposed taxonomic change(s): Addition of a new species *Bifilivirus philemonii*

Justification:
Filamentous phage Philemon was isolated from raw milk Emmental cheese on a dairy-associated strain of *Propionibacterium freudenreichii* PB4. The obtained TEM confirmed filamentous morphology. Philemon forms plaques on three *P. freudenreichii* strains in our collection, including the strain TL18, which was used for characterization of phage B5 (though no plaquing was reported for phage B5) {11889111}. The phage genome was sequenced with Illumina platform after formation of complementary strand with MDA technique. The genome is 5802 nt long, with 63 G+C %mol. Comparison with the only other representative of genus *Bifilivirus,* Propionibacterium virus B5 (NC_003460.1) revealed that the genome of Philemon is 92.8% identical to the genome of the Propionibacterium virus B5, thus fulfilling the criteria for creation of a separate species. The similarity of morphogenesis protein and CoaB confirms that Philemon belongs to the genus *Bifilivirus*. We propose the name of the species – *Bifivilus philemonii.*

Submitted: 23/04/2024; *Revised:* -

TABLE 47 - *Philemonvirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Bifilivirus philemonii*	Propionibacterium phage Philemon	PP693361

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.028B.A.v1.Philemonvirus_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.028B.A.v1.Philemonvirus_1ns.xlsx

2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns

Title: Create seven new genera for *Rhodococcus* siphoviruses [Class: *Caudoviricetes]*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
We propose the creation of seven new taxa for unique *Rhodococcus* siphoviruses: *Edwardsroadvirus, Wodongavirus, Reqipinevirus, Melbournevirus, Trogglehumpervirus, Mboduovirus, Reynauldvirus*

Justification:
The taxa proposed conform to demarcation criteria specified by the ICTV bacterial viruses subcommittee.

Submitted: 09/05/2024; *Revised:* -

TABLE 48 – *Rhodococcus* siphoviruses, 14 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Edwardsroadvirus*		
New taxon	species	*Edwardsroadvirus RRH1*	Rhodococcus phage RRH1	JN116822
New taxon	genus	*Wodongavirus*		
New taxon	species	*Wodongavirus REQ3*	Rhodococcus phage REQ3	JN116824
New taxon	genus	*Reqipinevirus*		
New taxon	species	*Reqipinevirus reqipine5*	Rhodococcus phage ReqiPine5	GU580943
New taxon	genus	*Melbournevirus*		
New taxon	species	*Melbournevirus REQ2*	Rhodococcus phage REQ2	JN116823
New taxon	genus	*Trogglehumpervirus*		
New taxon	species	*Trogglehumpervirus trogglehumper*	Rhodococcus phage Trogglehumper	OQ709222
New taxon	genus	*Mboduovirus*		
New taxon	species	*Mboduovirus mbo2*	Rhodococcus phage Mbo2	ON191531
New taxon	genus	*Reynauldvirus*		
New taxon	species	*Reynauldvirus reynauld*	Rhodococcus phage Reynauld	OR159659

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns.xlsx

2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns

Title: Create a new family, *Trautnerviridae,* subfamily *Polsinellivirinae* and two genera *(Rivavirus,* and *Splendidrerdvirus)* [class *Caudoviricetes*]

Authors: Cook R, Tavares P, Lurz R, Barylski J, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
The viruses classified in this proposal do not have a current taxonomic assignment.

Proposed taxonomic change(s):
To create a new genus, *Rivavirus*, with three species
To create a new genus, *Spendidredvirus*, with two species
To create a new subfamily, *Polsinellivirinae*, with these two genera (*Rivavirus* and *Spendidredvirus*)
To create a new single-species genus, *Prospektnaukivirus*
To create a new family, *Trautnerviridae,* for these taxa

Justification: *Bacillus* phage SPP1 was isolated in 1966; sequenced in 1997 (corrected in 2018); and, has been the subject of numerous morphological and physiologically studies; yet has remained unclassified. In this proposal it has been assigned to a new genus, *Rivavirus,* together with phage SplendidRed *(Splendidredvirus),* form a new subfamily, *Polsinellivirinae.* The members of this taxon are siphoviruses which have genomes of 42.8 – 46.3 kb (43.7 - 44.6 mol% G+C) and encode 74-77 proteins and no tRNAs. As a result of detailed genomic, proteomic and phylogenetic analyses using VIRIDIC, ViPTree, VirClust we further propose to create a new family named *Trautnerviridae* named in honour of Thomas A. Trautner.

Submitted: 25/05/2024; *Revised:* 30/09/2024

TABLE 49 - *Trautnerviridae*, 11 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Trautnerviridae*		
New taxon	subfamily	*Polsinellivirinae*		
New taxon	genus	*Rivavirus*		
New taxon	species	*Rivavirus SPP1*	Bacillus phage SPP1	X97918
New taxon	species	*Rivavirus rv000TH010*	Bacillus phage 000TH010	MN176219
New taxon	species	*Rivavirus rv049ML001*	Bacillus phage 049ML001	MN176227
New taxon	genus	*Splendidredvirus*		
New taxon	species	*Splendidredvirus splendidred*	Bacillus phage vB_BspS_SplendidRed	MN013088
New taxon	species	*Splendidredvirus ray17*	Bacillus phage Ray17	MH752385
New taxon	genus	*Prospektnaukivirus*		
New taxon	species	*Prospektnaukivirus sam112*	Bacillus phage vB_BcM_Sam112	MN604230

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns.xlsx

2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg

Title: Create a new family, *Sarkviridae* for the Jersey-like siphophages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
Jerseyvirus, Cornellvirus and Kagunavirus in the *subfamily Guernseyvirinae;* and, amongst the *Serratia* phages *Seretavirus* and *Otakuvirus*

Proposed taxonomic change(s):
To create a new family *Sarkviridae*

Justification:
Genomic, proteomic and phylogenetic data indicate that this group of phages is a family. In addition, Taxonomy Proposal 2023.068B.A.v1.Caudoviricetes_Serratia_3ng suggested a higher level relationship between the *Otakuvirus* and the *Guernseyvirinae.*

Submitted: 04/06/2024; *Revised:* 30/09/2024

TABLE 50 - *Sarkviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	subfamily	*Guernseyvirinae*	*Sarkviridae*
Move taxon	genus	*Seretavirus*	*Sarkviridae*
Move taxon	genus	*Otakuvirus*	*Sarkviridae*

TABLE 51 - *Sarkviridae*, 1 new taxon*

Operation	Rank	New taxon name
New taxon	family	*Sarkviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg.xlsx

2024.032B.A.v1.Sepahanvirus_1ng_2ns

Title: Create a new genus, *Seraphanvirus,* containing two species *(Caudoviricetes)*

Authors: Ganjoor MS, Bouzari M (bouzari@sci.ui.ac.ir), Soleimani-Delfan A

Summary:
Taxonomic rank(s) affected:
Genus

Description of current taxonomy:
These phages are currently unclassified.

Proposed taxonomic change(s):
To create a new genus, *Sepahanvirus,* within the class *Caudoviricetes* comprising two species, vB_Yru_GN1 and YerA41.

Justification:
Phages vB_Yru_GN1 and phage YerA41 exhibit nucleotide sequence similarity that falls within the demarcation threshold for the creation of a new genus.

Submitted: 09/12/2023; *Revised:* -

TABLE 52 - *Sepahanvirus*, 3 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Sepahanvirus*		
New taxon	species	*Sepahanvirus vB_Yru_GN1*	Yersinia phage vB_Yru_GN1	LC779065
New taxon	species	*Sepahanvirus GN1*	Yersinia phage YerA41	MW570730

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.032B.A.v1.Sepahanvirus_1ng_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.032B.A.v1.Sepahanvirus_1ng_2ns.xlsx

2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns

Title: Create a new family *(Mazoviaviridae)* and a new genus *(Dabrowskivirus)* with a single species *(Caudoviricetes* class)

Authors: Shymialevich D, Wójcicki M (michal.wojcicki@ibprs.pl), Sokołowska B

Summary:
Taxonomic rank(s) affected:
Proposal to create a new family *(Mazoviaviridae)* and a new genus *(Dabrowskivirus)* with a single species *(Caudoviricetes* class).

Description of current taxonomy:
In 2022, significant changes to the taxonomy of bacterial viruses were introduced: the paraphyletic morphological families *Podoviridae, Siphoviridae,* and *Myoviridae* as well as the order *Caudovirales* were abolished, which is replaced by the class *Caudoviricetes* to group all tailed bacterial and archaeal viruses with icosahedral capsids and a double-stranded DNA genome. Moreover, a binomial system of nomenclature for species was established. Based on the morphology and the comparative analysis of its predicted proteins, Alicyclobacillus myophage vB_Aac_IAFB_3916 was assigned to viruses with complex structures *(Caudoviricetes* class).

Proposed taxonomic change(s):
Analyses of the phylogenetic relationship of Alicyclobacillus myophage vB_Aac_IAFB_3916 prevented its unambiguous assignment to a specific family and genus. The weak similarity with other phage genomes deposited in the databases suggests that the isolated bacteriophage may be a representative of a new genus and new family of tailed bacteriophages.

Justification:
The genome of newly isolated Alicyclobacillus myophage vB_Aac_IAFB_3916 possesses no DNA homologs. At the protein level, this virus is unique. Therefore, we propose the creation of a new species *(Dabrowskivirus KKP3916),* genus *(Dabrowskivirus)* and family *(Mazoviaviridae)* for viruses of this type.

Submitted: 09/06/2024; *Revised:* 09/10/2024

TABLE 53 - *Mazoviaviridae*, 3 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Mazoviaviridae*		
New taxon	genus	*Dabrowskivirus*		
New taxon	species	*Dabrowskivirus KKP3916*	Alicyclobacillus myophage vB_Aac_IAFB_3916	OQ846916

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns.xlsx

2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns

Title: Create a new family, *Stackebrandtviridae,* for a group of *Gordonia* phages (Class: *Caudoviricetes)*

Authors: Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

Description of current taxonomy:
At present the following taxa exist as floating genera in the order *Caudoviricetes; Wizardvirus, Clownvirus, Vididuovirus, Dexdertvirus, Zitchvirus*, *Kroosvirus* and *Leonardvirus*

Proposed taxonomic change(s):
To create one new species in the genus *Wizardvirus*
To create a new subfamily, *Frickvirinae* with two genera *(Clownvirus* and *Wizardvirus)*

To add one new species to the genus *Vididuovirus*
To add one new species to the genus *Dexdertvirus*
To add four new species to the genus *Zitchvirus*
To add one new species to the genus *Leonardvirus*
To create a new subfamily, *Schenleyvirinae,* for the above four genera and *Kroosvirus.*
To create a new family, *Stackebrandtviridae,* for the above-mentioned taxa.

Justification:
Members of the Actinobacteriophage Database Cluster DC ((https://phagesdb.org/clusters/DC/) are temperate *Gordonia* phages for which we have created two genera. The related lytic viruses of Cluster DE (https://phagesdb.org/clusters/DE/) have resulted in five new genera.

Submitted: 15/06/2024; *Revised:* 30/09/2024

TABLE 54 - *Stackebrandtviridae*, 11 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Stackebrandtviridae*		
New taxon	subfamily	*Frickvirinae*		
New taxon	species	*Wizardvirus halo3*	Gordonia phage Halo3	OR521081
New taxon	subfamily	*Schenleyvirinae*		
New taxon	species	*Vividuovirus sitar*	Gordonia phage Sitar	MH153809
New taxon	species	*Dexdertvirus kwekel*	Gordonia phage Kwekel	OR521074
New taxon	species	*Zitchvirus tardus*	Gordonia phage Tardus	ON392159
New taxon	species	*Zitchvirus viaconlectus*	Gordonia phage ViaConlectus	OP068342
New taxon	species	*Zitchvirus sampson*	Gordonia phage Sampson	ON456337
New taxon	species	*Zitchvirus apunk*	Gordonia phage APunk	ON755186
New taxon	species	*Leonardvirus phauci*	Gordonia phage Phauci	ON456349

TABLE 55 - *Stackebrandtviridae*, 8 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Clownvirus*	*Stackebrandtviridae*
Move taxon	genus	*Wizardvirus*	*Stackebrandtviridae*
Move taxon	genus	*Kroosvirus*	*Stackebrandtviridae*
Move taxon	genus	*Vividuovirus*	*Stackebrandtviridae*
Move taxon	genus	*Dexdertvirus*	*Stackebrandtviridae*
Move taxon	genus	*Zitchvirus*	*Stackebrandtviridae*
Move taxon	genus	*Leonardvirus*	*Stackebrandtviridae*
Move taxon	genus	*Lilbeanievirus*	*Stackebrandtviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns.xlsx

2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections

Title: Corrections to species names in the classes *Caudoviricetes* and *Fraserviricetes*

Authors: Turner D (dann2.turner@uwe.ac.uk)

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

Description of current taxonomy:
All of these species are currently classified within the latest release of the ICTV taxonomy

Proposed taxonomic change(s):
Rename species to conform to the binomial species epithet.
Correct spelling errors
Create genus to contain floating species in *Tevenvirinae*
Change to genus and constituent species in the genus *Roskildevirus* as “Roskilde virus” refers to Norovirus in Danish
Correction of misspelt genus names in binomial species epithets.

Justification:
To ensure that the naming of viruses is consistent with the guidelines for binomial species names, to remove any names that could cause confusion in native languages and to remove any genome records that do not represent coding complete sequences.

Submitted: 19/06/2024; *Revised:* 30/09/2024

TABLE 56 - *Caudoviricetes*, 96 rename taxa*. Table too large, see supplementary information sheet supp_info_tab_56

TABLE 57 - *Caudoviricetes*, 3 move; rename taxa*

Operation	**Rank**	**New taxon name**	**Old parent taxon**	**New parent taxon**	**Old taxon name**
Move; rename taxon	species	*Centumtrigintavirus cv133*	*Tevenvirinae*	*Centumtrigintavirus*	*Acinetobacter virus 133*
Move; rename taxon	species	*Mosigvirus jaykay*	*Tequatrovirus*	*Mosigvirus*	*Tequatrovirus jaykay*
Move; rename taxon	species	*Mosigvirus efftwo*	*Tequatrovirus*	*Mosigvirus*	*Tequatrovirus efftwo*

TABLE 58 - *Caudoviricetes*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	species	*Campylobacter virus IBB35*

TABLE 59 - *Caudoviricetes*, 1 new taxon*

Operation	**Rank**	**New taxon name**
New taxon	genus	*Centumtrigintavirus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections.xlsx

2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns

Title: Create a new family, *Vandenendeviridae,* for a group of lytic *Pseudomonas* phages (Class: *Caudoviricetes)*

Authors: Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

Summary:

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

Description of current taxonomy:
Four genera are currently classified; *Baldwinvirus, Nankokuvirus, Otagovirus*, *Flaumdravirus* and *Pakpunavirus.*

Proposed taxonomic change(s):
To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus, Yunamivirus, Ventosusvirus*, *Uavernvirus,* and *Chemalvirus*
To create a new genus, *Tartuvirus,* with four species
To create two new species in the genus *Kremarvirus*
To create a new family, *Vandenendviridae,* for these genera and *Balwinvirus, Kremarvirus, Nankokuvirus, Otagovirus, Flaumdravirus*, *Pakpunavirus* and *Shenlongvirus.*

Justification:
Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Pseudomonas* myoviruses which share ≥12.2% DNA sequence similarity and 15 core proteins. The new family is named in honour of Marius van de Ende of South Africa.

Submitted: 25/05/2024; *Revised:* 30/09/2024

TABLE 60 - *Vandenendeviridae*, 20 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	family	*Vandenendeviridae*		
New taxon	genus	*Weillhallvirus*		
New taxon	species	*Weillhallvirus wv16Q*	Pseudomonas phage 16Q	OR001909
New taxon	genus	*Omahavirus*		
New taxon	species	*Omahavirus UNOG1W1*	Pseudomonas phage UNO-G1W1	PP551948
New taxon	genus	*Torinovirus*		
New taxon	species	*Torinovirus K7A1*	Pseudomonas phage phiK7A1	MT740307
New taxon	genus	*Yunamivirus*		
New taxon	species	*Yunamivirus Y1MI*	Pseudomonas phage vB_PF_Y1-MI	OR500437
New taxon	genus	*Ventosusvirus*		
New taxon	species	*Ventosusvirus ventosus*	Pseudomonas phage ventosus	MG018930
New taxon	genus	*Uavernvirus*		
New taxon	species	*Uavernvirus uavern*	Pseudomonas phage UAVern	MZ605293
New taxon	genus	*Tartuvirus*		
New taxon	species	*Tartuvirus amme3*	Pseudomonas phage vB_PpuM-Amme-3	PP496413
New taxon	species	*Tartuvirus nopa*	Pseudomonas phage vB_PpuM-NoPa	PP496415
New taxon	species	*Tartuvirus kopa4*	Pseudomonas phage vB_PpuM-KoPa-4	PP496414
New taxon	species	*Tartuvirus roomu2*	Pseudomonas phage vB_PpuM-Roomu-2	PP496417
New taxon	genus	*Chemalvirus*		
New taxon	species	*Chemalvirus PseuGes254*	Pseudomonas phage PseuGes_254	OR575930

TABLE 61 - *Vandenendeviridae*, 3 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	subfamily	*Skurskavirinae*	*Vandenendeviridae*
Move taxon	subfamily	*Gorskivirinae*	*Vandenendeviridae*
Move taxon	genus	*Nankokuvirus*	*Vandenendeviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns.xlsx

2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms

Title: Create three new families *Mestraviridae, Asemoviridae,* and *Parnassusviridae,* and move the family *Autolykiviridae* into the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria)*

Authors: Bardy P, FoggPCM, Kalatzis PG, Middelboe M, Oksanen HM (hanna.oksanen@helsinki.fi)

Summary:
Taxonomic rank(s) affected:
The taxonomic ranks affected are the genus *Corticovirus* in the family *Corticoviridae,* the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria),* and the family *Autolykiviridae (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria).* In addition, some species are affected.

Description of current taxonomy:
Currently, the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria)* contains one family *Corticoviridae* composed of one genus *Corticovirus* (2 species). The family *Autolykiviridae* belongs to the class *Tectiviricetes* but is not assigned to any order. The family *Autolykiviridae* is composed of two genera *Livvievirus* (2 *species)* and *Paulavirus* (3 species).

Proposed taxonomic change(s):
The genus *Corticovirus* (the family *Corticoviridae)* is renamed as the genus *Merivirus* and its two species are renamed accordingly. The *Vinavirales* order is rearranged so that the family *Autolykiviridae* is placed under the order along with the family *Corticoviridae.* Two new genera *Oliviavirus* and *Ameliavirus* are created in the family *Autolykiviridae.* Both genera consist of a single species *Oliviavirus viph1020o* and *Ameliavirus viph1008o* respectively*.* The genus of the virus species *Paulavirus viph1044o* is moved to the genus *Paulavirus* (the family *Autolykiviridae).* In addition, three new families *Mestraviridae, Asemoviridae,* and *Parnassusviridae* are created in the order *Vinavirales. Two* new genera *Anticleavirus* and *Polymedevirus* are created in the family *Mestraviridae.* One new species is created in each of the two genera: *Anticleavirus jorvik* and *Polymedevirus YY.* Two new genera *Elsinorevirus* and *Rumoivirus* are created in the family *Asemoviridae.* One new species is created in each of the two genera: *Elsinoreirus NO16* and *Rumoivirus VruC.* One new species *Corycianvirus MfV* is created in a new genus *Corycianvirus* in the family *Parnassusviridae.*

Justification:
The inclusion/creation of four families in the order *Vinavirales,* together with the family *Corticoviridae,* is based on the 9 signature genes shared by their members, which corresponds to approximately 50 % of their genome. This demonstrates their common evolutionary origin. Classification of *Paulavirus viph1044o* into the genus *Livvievirus* instead of *Paulavirus* was a mistake. To make the names of the family *Corticoviridae* and the genus *Corticovirus* based on a different word stem, the genus *Corticovirus* is renamed *Merivirus.*

Submitted: 20/06/2024; *Revised:* 30/09/2024

TABLE 62 - *Vinavirales*, 15 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Oliviavirus*		
New taxon	genus	*Ameliavirus*		
New taxon	family	*Mestraviridae*		
New taxon	genus	*Anticleavirus*		
New taxon	species	*Anticleavirus jorvik*	Rhodobacter phage Jorvik	OP588643
New taxon	genus	*Polymedevirus*		
New taxon	species	*Polymedevirus YY*	Marinomonas phage YY	MH105080
New taxon	family	*Asemoviridae*		
New taxon	genus	*Elsinorevirus*		
New taxon	species	*Elsinorevirus NO16*	Vibrio phage fNo16	MH730557
New taxon	genus	*Rumoivirus*		
New taxon	species	*Rumoivirus VruC*	Vibrio phage vB_VruC_PG21	OM867525
New taxon	family	*Parnassusviridae*		
New taxon	genus	*Corycianvirus*		
New taxon	species	*Corycianvirus MfV*	Marinomonas phage MfV	MW618650

TABLE 63 - *Vinavirales*, 4 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	family	*Autolykiviridae*	*Vinavirales*
Move taxon	species	*Paulavirus viph1044o*	*Vinavirales*
Move taxon	species	*Oliviavirus viph1020o*	*Vinavirales*
Move taxon	species	*Ameliavirus viph1008o*	*Vinavirales*

TABLE 64 - *Vinavirales*, 3 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	genus	*Merivirus*	*Corticovirus*
Rename taxon	species	*Merivirus Cr39582*	*Corticovirus Cr39582*
Rename taxon	species	*Merivirus PM2*	*Corticovirus PM2*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms.xlsx

2024.039D.A.v1.Artimaviricota_np

Title: Create new phylum, *"Artimaviricota"* in the kingdom *Orthornavirae* (realm *Riboviria)* for classification of a hyperthermophilic RNA virus

Authors: Syun-ichi Urayama (urayama.shunichi.gn@u.tsukuba.ac.jp), Akihito Fukudome, Eugene V. Koonin, Takuro Nunoura, Mart Krupovic (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected: *Riboviria, Orthornavirae*

Description of current taxonomy:
Realm *Riboviria* includes two kingdoms, *Orthornavirae* and *Pararnavirae,* which include highly diverse viruses that encode RNA dependent RNA polymerases (RdRP) and reverse transcriptases (RT), respectively. Kingdom *Orthornavirae* includes six phyla which were established based on

phylogenetic analysis of the RdRP and comparative analysis of the viral genomes and proteins.

Proposed taxonomic change(s):
We propose to create a new phylum in the kingdom *Orthornavirae* for classification of a group of RNA viruses discovered in hot springs that are characterized by unusual RdRPs.

Justification:
The RdRPs of HsRV1 and its relatives seem to deviate from the RdRP consensus farther than any of the other recently discovered putative phyla, with none of which they appear to be affiliated, and possess unusual structural features that appear to link them to viral RTs.

Submitted: 21/06/2024; *Revised:* -

TABLE 65 - *Artimaviricota*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	phylum	*Artimaviricota*		
New taxon	class	*Furtirnaviricetes*		
New taxon	order	*Divaquavirales*		
New taxon	family	*Hakuzoviridae*		
New taxon	genus	*Atsuirnavirus*		
New taxon	species	*Atsuirnavirus caloris*	hot spring RNA virus 1	RNA1: BTCN01000001, RNA2: BTCN01000005

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.039D.A.v1.Artimaviricota_np.docx
https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20(D)%20proposals/2024.039D.A.v1.Artimaviricota_np.xlsx

2024.040B.A.v1.Sharonstreetvirus_1ns

Title: Create a new species *Sharonstreetvirus xiamensis (Caudoviricetes)*

Authors: Liu H-T (15844493757@163.com)

Summary:

We isolated a new Aeromonas phage from aquaculture water of Xiamen named phiA034, and ViPTree analysis classified as a new species of an existing genus *Sharonstreetvirus, (Duplodnaviria Heunggongvirae, Uroviricota, Caudoviricetes*, *Casjensviridae).* Therefore, we propose a new species *Sharonstreetvirus xiamensis.* The genome of phiA034 is available under the accession number OP792756.

Submitted: 25/04/2024; *Revised:* -

TABLE 66 - *Sharonstreetvirus*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Sharonstreetvirus xiamensis*	Aeromonas phage phiA034	OP792756

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.040B.A.v1.Sharonstreetvirus_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.040B.A.v1.Sharonstreetvirus_1ns.xlsx

2024.041B.A.v1.Camvirus_2ns

Title: Create two new species **-** *Camvirus vanseggelen* and *Camvirus verabelle* [subfamily *Arquatrovirinae*, class *Caudoviricites].*

Authors: Kempff A (annabelkempff@gmail.com), van Neer V (vanneervera@gmail.com), Ongenae V (v.m.a.ongenae@biology.leidenuniv.nl), Rozen DE, Briegel A, Claessen D

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

Description of current taxonomy:
The genus *Camvirus* is classified within the subfamily *Arquatrovirinae,* class *Caudoviricetes*

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

Justification:
We have defined two new species, *Camvirus vanseggelen* and *Camvirus verabelle,* based upon phages isolated for host *Streptomyces coelicolor* from soil samples in the Netherlands at longitude N52°23'31" and latitude E4°34'49". *Camvirus vanseggelen* contains a linear dsDNA genome of 50,426 bp (65,5% G+C) encoding 73 proteins. *Camvirus verabelle* contains a linear dsDNA genome of 49,832 bp (65,0% G+C) encoding 73 proteins. These new species can be included in the genus *Camvirus* together with *Streptomyces* phage Alsaber, *Streptomyces* phage Amela, *Streptomyces* phage phiCAM, *Streptomyces* phage Endor1, *Streptomyces* phage Endor2, *Streptomyces* phage Joe, *Streptomyces* phage Saftant and *Streptomyces* phage Sitrop.

Submitted: 02/04/2024; *Revised:* -

TABLE 67 - *Camvirus*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Camvirus vanseggelen*	Streptomyces phage Vanseggelen	OQ970438
New taxon	species	*Camvirus verabelle*	Streptomyces phage Verabelle	OQ970439

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.041B.A.v1.Camvirus_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.041B.A.v1.Camvirus_2ns.xlsx

2024.042B.A.v1.Lacfervirus_1ng_1ns

Title: Create one new genus, *Lacfervirus,* in the class *Caudoviricetes*

Authors: Qiannan Wen, Xia Chen (chenxia8280@163.com)

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

Description of current taxonomy:
The virus classified in this proposal does not have a current taxonomic assignment.

Proposed taxonomic change(s):
We propose a new genus, *Lacfervirus,* comprised of a single species, *Lactobacillus* phage LFP01 in the class *Caudoviricetes.*

Justification:
The genome of *Lactobacillus* phage LFP01 has very low homology to all other bacteriophage sequences in the GenBank database. A complete genome sequence comparison using the BLASTn method revealed that the genome of *Lactobacillus* phage LFP01 had a maximum nucleotide identity of 92.83% and 55% coverage with *Lactobacillus* phage LF1. The low homology indicated that the newly sequenced bacteriophage likely represents a new genus with a single species..

Submitted: 05/06/2023; *Revised:* -

TABLE 68 - *Lacfervirus*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Lacfervirus*		
New taxon	species	*Lacfervirus LFP01*	Lactobacillus virus LFP01	OR048821

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.042B.A.v1.Lacfervirus_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.042B.A.v1.Lacfervirus_1ng_1ns.xlsx

2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp

Title: Rename and split an existing genus of the family *Cystoviridae (Vidaverviricetes: Mindivirales),* rename seven virus species, create two new species and genera

Authors: Poranen MM (minna.poranen@helsinki.fi), Mäntynen S

Summary:
Taxonomic rank(s) affected: The proposal affects species and genus ranks under the *Cystoviridae* family.

Description of current taxonomy: The *Cystoviridae* family currently includes one *genus Cystovirus* and seven species, *Cystovirus phi6, Cystovirus phi8, Cystovirus phi12, Cystovirus phi13, Cystovirus phi2954, Cystovirus phiNN* and *Cystovirus phiYY. Cystoviridae* is the only family of the order *Mindivirales* and the class *Vidaverviricetes* that belongs to the phylum *Duplornaviricota (Orthornavirae, Riboviria)* together with classes *Resentoviricetes* and *Chrymotiviricetes.*

Proposed taxonomic change(s): We propose a new name for the genus *Cystovirus* and its splitting into five genera*.* Due to the introduction of the new genera, we propose renaming of all the current species. In addition, we propose to create two new species and two additional new genera in the family *Cystoviridae.*

Justification: Seven new dsRNA bacteriophage isolates have been identified and now proposed to be taxonomically classified to create two new species. Sequence comparisons of these viruses and previously classified dsRNA bacteriophages of the genus *Cystovirus* justify splitting of the *Cystovirus* genus and creation of all together seven genera under the *Cystoviridae.* The genus *Cystovirus* is renamed to distinguish the name stems of genus and family rank.

Submitted: 21/06/2024; *Revised:* 30/09/2024

TABLE 69 - *Cystoviridae*, 5 move; rename taxa*

Operation	Rank	New taxon name	Old parent taxon	New parent taxon	Old taxon name
Move; rename taxon	species	*Alphacystovirus phi8*	*Cystovirus*	*Alphacystovirus*	*Cystovirus phi8*
Move; rename taxon	species	*Betacystovirus phi12*	*Cystovirus*	*Betacystovirus*	*Cystovirus phi12*
Move; rename taxon	species	*Gammacystovirus phi13*	*Cystovirus*	*Gammacystovirus*	*Cystovirus phi13*
Move; rename taxon	species	*Gammacystovirus phiYY*	*Cystovirus*	*Gammacystovirus*	*Cystovirus phiYY*
Move; rename taxon	species	*Deltacystovirus phi2954*	*Cystovirus*	*Deltacystovirus*	*Cystovirus phi2954*

TABLE 70 - *Cystoviridae*, 4 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Epsiloncystovirus*		
New taxon	species	*Epsiloncystovirus phiNY*	Microvirgula phage phiNY	MW471133; MW471134; MW471135
New taxon	genus	*Zetacystovirus*		
New taxon	species	*Zetacystovirus CAP*	Acinetobacter phage CAP7	MZ558516; MZ558517; MZ558518

TABLE 71 - *Cystoviridae*, 3 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	genus	*Orthocystovirus*	*Cystovirus*
Rename taxon	species	*Orthocystovirus phi6*	*Cystovirus phi6*
Rename taxon	species	*Orthocystovirus phiNN*	*Cystovirus phiNN*

TABLE 72 - *Cystoviridae*, 2 split taxa*

Operation	Rank	Old taxon	New taxon 1	New taxon 2
Split taxon	genus	Cystovirus	Alphacystovirus	Betacystovirus
Split taxon	genus	Cystovirus	Gammacystovirus	Deltacystovirus

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp.xlsx

2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns

Title: Create one (1) new family *(Felixviridae),* including one (1) new subfamily *(Maevirinae),* three (3) genera (two new: *Nakavirus, Chronisvirus;* one existent*: Certevirus),* including two (2) new species *(Nakavirus sapi* and *Chronisvirus chronis).*

Authors: Nobrega F.L. (f.nobrega@soton.ac.uk), Rothschild-Rodriguez, D., Lambon, K.

Summary:
Taxonomic rank(s) affected:
Viruses; Duplodnaviria; Heunggongvirae; Uroviricota; Caudoviricetes

Description of current taxonomy:
Unclassified *Caudoviricetes.*

Proposed taxonomic change(s):
We propose a new family, *Felixviridae,* which includes at least one new subfamily, *Maevirinae,* and at least three genera, *Nakavirus* (new), *Chronisvirus* (new) and *Certevirus* (already existent). The *Nakavirus* and *Chronisvirus* genera include at least one newly proposed species each, *Nakavirus sapi* (for phages RothC and RothD), and *Chronisvirus chronis* (for phage vB_Kpn_Chronis), respectively.

Justification:
This family has not been taxonomically characterised, with only one previously cultured *Klebsiella* phage relative, vB_Kpn_Chronis, and a Protoea phage, PdC23. We isolated 53 phages as part of the Klebsiella Phage Collection, two of which, RothC and RothD were not able to be assigned to any existing viral families, leading us to propose a new family, *Felixviridae.* We additionally found this family of phages to be present in metagenomes coming from human stool, a proxy for the human gut microbiota, which are also currently unclassified, but previously identified by the Gut Phage Database (GPD). Genomic analyses provide sufficient evidence to suggest the *Felixviridae* family is currently composed of at least one subfamily, *Maevirinae,* comprising RothC, D and Chronis; at least three genera, *Nakavirus, Chronisvirus,* and previously existent *Certevirus.* The *Nakavirus* genus holds phages RothC and RothD. High similarity between RothC and RothD places them under the same species proposed to be *Nakavirus sapi.* The *Chronisvirus* genus holds the phage vB_Kpn_Chronis, forming the *Chronisvirus chronis* species.

Submitted: 19/06/2024; *Revised:* 27/06/2024

TABLE 73 - *Felixviridae*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Felixviridae*		
New taxon	subfamily	*Maevirinae*		
New taxon	genus	*Chronisvirus*		
New taxon	species	*Chronisvirus chronis*	vB_Kpn_Chronis	MN013086
New taxon	genus	*Nakavirus*		
New taxon	species	*Nakavirus sapi*	Klebsiella phage RothC	PP934563

TABLE 74 - *Felixviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	genus	*Certevirus*	*Felixviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns.xlsx

2024.045B.A.v2.Autographivirales

Title: Promoting the family *Autographiviridae* to create one new order, *Autographivirales,* with four new families, four new subfamilies, 93 new genera and 607 new species *(Duplodnaviria, Caudoviricetes).*

Authors: Turner D (dann2.Turner@uwe.ac.uk), Carrillo D, Lood C, Ely B, Lehman SM, Dutilh B, Kropinski AM, Lavigne R, Adriaenssens EM, Millard AD

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

Description of current taxonomy:
The family *Autographiviridae* was established under taxonomic proposal

Proposed taxonomic change(s):
We propose;
The establishment of a new order, *Autographivirales,* containing four new families.
The creation of four new subfamilies
The creation of 93 new genera
The creation of 610 new species
Abolition of 21 species

Justification:
The proposed order forms a single deep-branching clade in tBLASTx distance analysis, reflected in core gene maximum-likelihood phylogeny. The proposed families form monophyletic clusters in proteome-based analyses and each share a number of core orthologous genes.

Submitted: 21/06/2024; *Revised:* 30/09/2024

TABLE 75 - *Autographivirales*, 708 new taxa*. Table too large, see supplementary information sheet supp_info_tab_75

TABLE 76 - *Autographivirales*, 60 move taxa*. Table too large, see supplementary information sheet supp_info_tab_76

TABLE 77 - *Autographivirales*, 21 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	species	*Friunavirus SWHAb1*
Abolish taxon	species	*Friunavirus SWHAb3*
Abolish taxon	species	*Phikmvvirus NFS*
Abolish taxon	species	*Phikmvvirus PT2*
Abolish taxon	species	*Vectrevirus cee*
Abolish taxon	species	*Maculvirus OWB*
Abolish taxon	species	*Murciavirus CB5A*
Abolish taxon	species	*Kaohsiungvirus AS51*
Abolish taxon	species	*Cuernavacavirus RHEph09*
Abolish taxon	species	*Atuphduovirus atuph03*
Abolish taxon	species	*Przondovirus KpV766*
Abolish taxon	species	*Teseptimavirus YpsPG*
Abolish taxon	species	*Teseptimavirus YpPY*
Abolish taxon	species	*Helsettvirus fPS53*
Abolish taxon	species	*Teetrevirus T7M*
Abolish taxon	species	*Berlinvirus Yepe2*
Abolish taxon	species	*Berlinvirus Yepf*
Abolish taxon	species	*Kayfunavirus EcpYZU01*
Abolish taxon	species	*Pektosvirus PP81*
Abolish taxon	species	*Ghunavirus Psa17*

Abolish taxon	species	*Friunavirus AB3*

TABLE 78 - *Autographivirales*, 14 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old taxon name
Move; rename taxon	species	*Rodentiumvirus LL11*	*Autographivirales*	*Vectrevirus LL11*
Move; rename taxon	species	*Rodentiumvirus CrRp3*	*Autographivirales*	*Vectrevirus CrRp3*
Move; rename taxon	species	*Nerthusvirus achelous*	*Autographivirales*	*Uliginvirus achelous*
Move; rename taxon	species	*Nerthusvirus nerthus*	*Autographivirales*	*Uliginvirus nerthus*
Move; rename taxon	species	*Nerthusvirus alpheus*	*Autographivirales*	*Uliginvirus alpheus*
Move; rename taxon	species	*Njordvirus njord*	*Autographivirales*	*Uliginvirus njord*
Move; rename taxon	species	*Ebriosvirus ebrios*	*Autographivirales*	*Teseptimavirus ebrios*
Move; rename taxon	species	*Ebriosvirus IME15*	*Autographivirales*	*Teseptimavirus IME15*
Move; rename taxon	species	*Hennigervirus shl2*	*Autographivirales*	*Ghunavirus shl2*
Move; rename taxon	species	*Hennigervirus PPPL1*	*Autographivirales*	*Ghunavirus PPPL1*
Move; rename taxon	species	*Hennigervirus henninger*	*Autographivirales*	*Ghunavirus henninger*
Move; rename taxon	species	*Unosvirus UNOSLW1*	*Autographivirales*	*Pifdecavirus UNOSLW1*
Move; rename taxon	species	*Pfluvirus PFP1*	*Autographivirales*	*Pifdecavirus PFP1*
Move; rename taxon	species	*Pfluvirus pv22PfluR64PP*	*Autographivirales*	*Pifdecavirus pv22PfluR64PP*

TABLE 79 - *Autographivirales*, 2 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Ghunavirus gv17A*	*Ghunavirus 17A*
Rename taxon	species	*Warsawvirus wv3MF5*	*Warsawvirus 3MF5*

TABLE 80 - *Autographivirales*, 1 promote taxon*

Operation	New taxon name	Old rank	New rank
Promote taxon	*Autographivirales*	order	order

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.045B.A.v2.Autographivirales.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.045B.A.v2.Autographivirales.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Fungal and Protist Viruses Subcommittee, 2024

Main Text

Contents

2024.001F.N.v1.Botourmiaviridae_spren

Title: Change the name of 32 species of six genera of the family *Botourmiaviridae*

Authors: Ayllón MA (mariaangeles.ayllon@upm.es), Turina M, Donaire L, Nerva L, Marzano SYL, Xie J, Jiang D

Summary:
Taxonomic rank(s) affected: Species.

Description of current taxonomy: Species correctly classified inside the genus but with outdated names.

Proposed taxonomic change(s): We propose to change the name of 32 species in the genera *Botoulivirus, Magoulivirus, Ourmiavirus, Penoulivirus, Rhizoulivirus* and *Scleroulivirus* of the family *Botourmiaviridae.*

Justification: The name of 32 species of *Botoulivirus, Magoulivirus, Ourmiavirus, Penoulivirus, Rhizoulivirus* and *Scleroulivirus* of the family *Botourmiaviridae* were not compliant to the binomial format, so in this proposal we made changes to meet the ICTV criteria in naming species.

Submitted: **-** ; *Revised:* **-**

TABLE 1 - *Botourmiaviridae*, 32 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Botoulivirus botrytidis*	*Botrytis botoulivirus*
Rename taxon	species	*Botoulivirus epicocci*	*Epicoccum botoulivirus*
Rename taxon	species	*Botoulivirus alphasclerotiniae*	*Sclerotinia botoulivirus 2*
Rename taxon	species	*Botoulivirus betasclerotiniae*	*Sclerotinia botoulivirus 3*
Rename taxon	species	*Magoulivirus acremonii*	*Acremonium magoulivirus*
Rename taxon	species	*Magoulivirus plasmoparae*	*Cladosporium magoulivirus 1*

Rename taxon	species	*Magoulivirus cladosporii*	*Cladosporium magoulivirus 2*
Rename taxon	species	*Magoulivirus colletotrichi*	*Colletotrichum magoulivirus*
Rename taxon	species	*Magoulivirus oryzae*	*Magnaporthe magoulivirus 1*
Rename taxon	species	*Magoulivirus penicillii*	*Penicillium magoulivirus*
Rename taxon	species	*Magoulivirus phaeoacremonii*	*Phaeoacremonium magoulivirus*
Rename taxon	species	*Magoulivirus rhizoctoniae*	*Rhizoctonia magoulivirus 1*
Rename taxon	species	*Ourmiavirus manihoti*	*Cassava virus C*
Rename taxon	species	*Ourmiavirus pruni*	*Epirus cherry virus*
Rename taxon	species	*Ourmiavirus cucurbitae*	*Ourmia melon virus*
Rename taxon	species	*Penoulivirus aspergilli*	*Aspergillus penoulivirus*
Rename taxon	species	*Penoulivirus cladosporii*	*Cladosporium penoulivirus*
Rename taxon	species	*Penoulivirus epicocci*	*Epicoccum penoulivirus*
Rename taxon	species	*Penoulivirus oryzae*	*Magnaporthe penoulivirus*
Rename taxon	species	*Penoulivirus neofusicocci*	*Neofusicoccum penoulivirus*
Rename taxon	species	*Penoulivirus penicillii*	*Penicillium penoulivirus*
Rename taxon	species	*Penoulivirus phaeoacremonii*	*Phaeoacremonium penoulivirus*
Rename taxon	species	*Penoulivirus phomae*	*Phoma penoulivirus*
Rename taxon	species	*Penoulivirus phomopsis*	*Phomosis penoulivirus*
Rename taxon	species	*Penoulivirus pyriculariae*	*Pyricularia penoulivirus*
Rename taxon	species	*Penoulivirus sclerotiniae*	*Sclerotinia penoulivirus*
Rename taxon	species	*Rhizoulivirus rhizoctoniae*	*Rhizoctonia rhizoulivirus*
Rename taxon	species	*Scleroulivirus cladosporii*	*Cladosporium scleroulivirus*
Rename taxon	species	*Scleroulivirus pyriculariae*	*Pyricularia scleroulivirus 3*
Rename taxon	species	*Scleroulivirus sclerotiniae*	*Sclerotinia scleroulivirus 1*
Rename taxon	species	*Scleroulivirus alphaglycinae*	*Soybean scleroulivirus 1*
Rename taxon	species	*Scleroulivirus betaglycinae*	*Soybean scleroulivirus 2*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.001F.A.v1.Botourmiaviridae_spren.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.001F.A.v1.Botourmiaviridae_spren.xlsx

2024.002F.Uc.v3.Marnaviridae_spren

Title: Rename 20 species within family *Marnaviridae*

Authors: Lang AS (aslang@mun.ca)

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy: Family *Marnaviridae* is currently composed of seven genera containing a total of 20 species with an inadequate nomenclature.

Proposed taxonomic change(s): Changes in names of all 20 currently classified species are proposed to adhere to newly adopted binomial nomenclatural standards/formats.

Justification:

Proposed changes are required to comply with binomial species nomenclature mandated by the ICTV.

Submitted: 18/04/2024; *Revised:* 17/10/2024

TABLE 2 - *Marnaviridae*, 20 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	species	*Bacillarnavirus yujii*	*Chaetoceros socialis forma radians RNA virus 1*
Rename taxon	species	*Bacillarnavirus setoensis*	*Chaetoceros tenuissimus RNA virus 01*
Rename taxon	species	*Bacillarnavirus nagasakii*	*Rhizosolenia setigera RNA virus 01*
Rename taxon	species	*Kusarnavirus tomaruii*	*Astarnavirus*
Rename taxon	species	*Labyrnavirus takaoii*	*Aurantiochytrium single-stranded RNA virus 01*
Rename taxon	species	*Locarnavirus jerichoensis*	*Jericarnavirus B*
Rename taxon	species	*Locarnavirus greningerii*	*Sanfarnavirus 1*
Rename taxon	species	*Locarnavirus derisii*	*Sanfarnavirus 2*
Rename taxon	species	*Locarnavirus rohweri*	*Sanfarnavirus 3*
Rename taxon	species	*Marnavirus taichanarum*	*Heterosigma akashiwo RNA virus*
Rename taxon	species	*Salisharnavirus vlokiae*	*Britarnavirus 1*
Rename taxon	species	*Salisharnavirus britensis*	*Britarnavirus 4*
Rename taxon	species	*Salisharnavirus mirandaeae*	*Palmarnavirus 128*
Rename taxon	species	*Salisharnavirus stewardii*	*Palmarnavirus 473*
Rename taxon	species	*Sogarnavirus gustavseniae*	*Britarnavirus 2*
Rename taxon	species	*Sogarnavirus kitsilanoensis*	*Britarnavirus 3*
Rename taxon	species	*Sogarnavirus tomaruii*	*Chaetarnavirus 2*
Rename taxon	species	*Sogarnavirus kimuraei*	*Chaetenuissarnavirus II*
Rename taxon	species	*Sogarnavirus culleyi*	*Jericarnavirus A*
Rename taxon	species	*Sogarnavirus palmerensis*	*Palmarnavirus 156*

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https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.002F.Uc.v3.Marnaviridae_spren.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.002F.Uc.v3.Marnaviridae_spren.xlsx

2024.003F.A.v1.Splipalmiviridae_newfam

Title: Create one new family, including three new genera and 16 new species, in the order *Wolframvirales* (class *Amabiliviricetes,* phylum *Lenarviricota,* Kingdom *Orthornavirae,* Realm *Riboviria)*

Authors: Sato Y, Daghino S, Chiba Y, Urayama S, Xie J, Ayllón MA, Suzuki N, Turina M (massimo.turina@ipsp.cnr.it)

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

Description of current taxonomy: Currently unclassified

Proposed taxonomic change(s): We propose to create a new family “Splipalmiviridae”, including three new genera which collectively accommodates 16 new species, in the order *Wolframvirales.*

Justification: The order *Wolframvirales* currently consists of one family *Narnaviridae.* Members of the *family Narnaviridae* have non-segmented (+)RNA genomes each encoding an RNA-dependent RNA polymerase (RdRP) in an open reading frame. Recently found unclassified “splipalmiviruses” are phylogenetically close to narnavirids, but carry divided RdRPs encoded by two independent genomic segments. Considering the phylogenetic proximity but the different RdRP-encoding strategy compared to narnavirids, we propose to create the new family “Splipalmiviridae” for “splipalmiviruses”, in the order *Wolframvirales.*

Submitted: 20/06/2024; *Revised:* -

TABLE 3 - *Splipalmiviridae*, 20 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Splipalmiviridae*		
New taxon	genus	*Jakapalmivirus*		
New taxon	species	*Jakapalmivirus sclerotiniae*	Botrytis cinerea binarnavirus 5	RNA1: MN619799; RNA2: MT711187
New taxon	species	*Jakapalmivirus bremiae*	Bremia lactucae associated splipalmivirus 1	RNA1: MN565689; RNA2: MZ926717; RNA3: OR060921
New taxon	species	*Jakapalmivirus cinereae*	Botrytis cinerea binarnavirus 1	RNA1: MN619795; RNA2: MT711186
New taxon	species	*Jakapalmivirus botritidis*	Botrytis cinerea binarnavirus 2	RNA1: MN619796; RNA2: MT119676
New taxon	species	*Jakapalmivirus ibericum*	Downy mildew lesion associated splipalmivirus 3	RNA1: MN539820; RNA2: OQ980200; RNA3: OQ980201
New taxon	species	*Jakapalmivirus italiense*	Downy mildew lesion associated splipalmivirus 4	RNA1: MN539821; RNA2: OQ980202; RNA3: OQ980203
New taxon	genus	*Divipalmivirus*		
New taxon	species	*Divipalmivirus italiense*	Downy mildew lesion associated splipalmivirus 7	RNA1: MN539824; RNA2: OQ990757
New taxon	species	*Divipalmivirus aspergilli*	Aspergillus fumigatus narnavirus 2	RNA1: LC553684; RNA2: LC553685; RNA3: LC553686
New taxon	species	*Divipalmivirus cryphonectriae*	Cryphonectria naterciae splipalmivirus 1	RNA1: LC634419; RNA2: LC634420; RNA3: LC634421; RNA4: LC649880
New taxon	species	*Divipalmivirus diplodiae*	Diplodia seriata splipalmivirus 1	RNA1: OM837803; RNA2: OM837804; RNA3: OM837805
New taxon	species	*Divipalmivirus suilli*	Suillus luteus narnavirus 4	RNA1: OQ862540; RNA2: OQ862539

New taxon	species	*Divipalmivirus japonicum*	Aspergillus flavus narnavirus 1	RNA1: LC763252; RNA2: LC763253; RNA3: LC763254; RNA4: LC763255
New taxon	genus	*Delepalmivirus*		
New taxon	species	*Delepalmivirus ibericum*	Downy mildew lesion associated splipalmivirus 20	RNA1: MN539837; RNA2: OQ990758; RNA3: OQ990759
New taxon	species	*Delepalmivirus oidiodendri*	Oidiodendron maius splipalmivirus 1	RNA1: MN736964; RNA2: MN736965; RNA3: MW988098
New taxon	species	*Delepalmivirus magnaporthae*	Magnaporthe oryzae narnavirus 1	RNA1: LC553711; RNA2: LC553710
New taxon	species	*Delepalmivirus sclerotiniae*	Sclerotinia sclerotiorum narnavirus 5	RNA1: OK573450; RNA2: OK573451

*Source / full text:
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.003F.A.v1.Splipalmiviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.003F.A.v1.Splipalmiviridae_newfam.xlsx

2024.004F.Uc.v2.Oomyviridae_newfam

Title: Create a new order, Lineavirales, and a new family, the Oomyviridae, with 3 genera and 38 species in the class *Arfiviricetes* of the phylum *Cressdnaviricota*

Authors: Canuti M (marta.canuti@gmail.com), Pénzes J (Judycash08@gmail.com)

Summary:
Taxonomic rank(s) affected: Phylum *Cressdnaviricota* and class *Arfiviricetes.*

Description of current taxonomy: Currently unclassified.

Proposed taxonomic change(s): Create a new order, Lineavirales, and a new family, the Oomyviridae, with 3 genera (Nicoomyvirus, Avoomyvirus, and Swoomyvirus) and 38 species, in the class *Arfiviricetes* of the phylum *Cressdnaviricota.*

Justification: In 2013 a novel virus that was considered to be a "hybrid" between a parvovirus and a circovirus ("parvovirus-like hybrid virus) was discovered. With the increased use of metagenomics, several recent publications described similar viruses, proposing their classification as parvoviruses and erroneously labeling them in GenBank as parvoviruses. This misclassification issue is continuously increasing and is in dire need to be rectified. Here, we show that these viruses comprise a distinct linear ssDNA virus family (Oomyviridae) within the *Cressdnaviricota* and that their unique features and phylogenetic relationships with other members of the *class Arfiviricetes,* are strong reasons to include these viruses in a distinct order, for which we propose the name Lineavirales, owning to the linear genome organization these viruses were found to possess thus far. We also show that, although most of these viruses were identified in samples collected from animals, their likely hosts are organisms of the eukaryotic clade Stramenopiles (SAR supergroup).

Submitted: 09/06/2024; *Revised:* 28/10/2024

TABLE 4 - *Oomyviridae*, 43 new taxa*. Table too large, see supplementary information sheet

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https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.004F.Uc.v2.Oomyviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.004F.Uc.v2.Oomyviridae_newfam.xlsx

2024.005F.A.v2.Pimascovirales_reorg

Title: Creation of a new suborder within the *Pimascovirales* to position and name Pithovirus-related isolates

Authors: Claverie JM (Claverie@igs.cnrs-mrs.fr), Legendre M, Rigou S, Abergel C

Summary:Taxonomic rank(s) affected:
A new suborder, the *Ocovirineae* within the *Pimascovirales,*
3 distinct families: *Pithoviridae, Orpheoviridae,* and *Hydriviridae,*
One family, the *Cedratviridae* demoted as the new *Orthocedratvirinae* subfamily
Two subfamilies: *Orthopithovirinae* and *Orthocedratvirinae* splitting the *Pithoviridae* family

Description of current taxonomy: Previously proposed in proposal #2023.011F by Abrahão and colleagues: two different families: *Pithoviridae* & *Cedraviridae* within *the Pimascovirales* order

Proposed taxonomic change(s): a new suborder, the *Ocovirineae* within the *Pimascovirales,* justified by the need to separate them from the other more distant *families* (*Marseilleviridae, Ascoviridae, Iridoviridae)* in the same order*.*

The creation of 3 distinct families: *Pithoviridae, Orpheoviridae,* and *Hydriviridae* to acknowledge their large differences in genome sizes and gene contents (and accommodate new isolates)
The split of the *Pithoviridae* into two *subfamilies: Orthopithovirinae* and *Orthocedratvirinae* to acknowledge their closer proximity compared to members of the other families listed above.

Justification: see above

Submitted: 13/03/2024; *Revised:* 09/10/2024

TABLE 5 - *Pimascovirales*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	suborder	*Ocovirineae*		
New taxon	subfamily	*Orthopithovirinae*		
New taxon	family	*Hydriviridae*		
New taxon	genus	*Alphahydrivirus*		
New taxon	species	*Alphahydrivirus permafrostis*	R_bin116_k1, metagenomics	OW988864

TABLE 6 - *Pimascovirales*, 3 move taxa*

Operation	**Rank**	**Taxon name**	**Old parent taxon**	**New parent taxon**
Move taxon	family	*Pithoviridae*	*Pimascovirales*	*Ocovirineae*
Move taxon	family	*Orpheoviridae*	*Pimascovirales*	*Ocovirineae*
Move taxon	genus	*Alphapithovirus*	*Pimascovirales*	*Ocovirineae*

TABLE 7 - *Pimascovirales*, 2 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	species	*Alphacedratvirus aljazairmassiliense*	*Alphacedratvirus aljazairense*

Rename taxon	species	*Alphacedratvirus francolausannense*	*Alphacedratvirus franciense*

TABLE 8 - *Pimascovirales*, 1 demote taxon*

Operation	**New taxon name**	**Old rank**	**New rank**
Demote taxon	*Orthocedratvirinae*	subfamily	subfamily

*Source / full text:

https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.005F.A.v2.Pimascovirales_reorg.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.005F.A.v2.Pimascovirales_reorg.xlsx

2024.006F.A.v1.Amalgaviridae_newgen

Title: Create a new genus Unirnavirus to accommodate 13 new species within family *Amalgaviridae*

Authors: Kotta-Loizou I (i.kotta-loizou13@imperial.ac.uk), Coutts RHA

Summary:
Taxonomic rank(s) affected: Family *Amalgaviridae*

Description of current taxonomy: Family *Amalgaviridae* accommodates 2 genera, *Amalgavirus* and *Zybavirus*

Proposed taxonomic change(s): Within family *Amalgaviridae,* establishing a new genus Unirnavirus to accommodate 13 new species

Justification: Sequence demarcation and phylogenetic analysis, genome organization and host range

Submitted: 20/06/2024; *Revised:* -

TABLE 9 - *Amalgaviridae*, 14 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	genus	*Unirnavirus*		
New taxon	species	*Unirnavirus aldianthicolae*	Alternaria dianthicola dsRNA virus 1	MT241326
New taxon	species	*Unirnavirus allongipei*	Alternaria longipes non-segmented mycovirus 1	KJ817371
New taxon	species	*Unirnavirus aspergilli*	Aspergillus lentulus non-segmented dsRNA virus 1	LC553704
New taxon	species	*Unirnavirus beauveriae*	Beauveria bassiana non-segmented RNA virus 1	LN610699
New taxon	species	*Unirnavirus cogleosporioidei*	Colletotrichum gloeosporioides RNA virus 1	ON887156
New taxon	species	*Unirnavirus cohigginsiani*	Colletotrichum higginsianum non-segmented dsRNA virus 1	KM923925
New taxon	species	*Unirnavirus combuense*	Combu double-strand RNA mycovirus	MH990637
New taxon	species	*Unirnavirus fusarii*	Fusarium culmorum virus 1	MN187541
New taxon	species	*Unirnavirus pripenicillii*	Penicillium janczewskii Beauveria bassiana-like virus 1	KT601106
New taxon	species	*Unirnavirus prustilaginoideae*	Ustilaginoidea virens unassigned RNA virus HNND 1	KR106133
New taxon	species	*Unirnavirus secupenicillii*	Penicillium citrinum non-segmented RNA virus 1	OP103962

New taxon	species	*Unirnavirus secustilaginoideae*	Ustilaginoidea virens RNA virus M-A	ON791647
New taxon	species	*Unirnavirus trichodermae*	Trichoderma harzianum mycovirus 1	MH155602

*Source / full text:
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.006F.A.v1.Amalgaviridae_newgen.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.006F.A.v1.Amalgaviridae_newgen.xlsx

2024.007F.Uc.v2.Mycoalphaviridae_newfam

Title: Create one new family (Mycoalphaviridae) including two new genus (Alphasclernavirus, Betasclernavirus) and seven new species

Authors: Xie J (jiataoxie@mail.hzau.edu.cn), Mu F, Jia J, Jiang D, Sabanadzovic S

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

Description of current taxonomy: The order including four families and twenty-seven species.

Proposed taxonomic change(s): Create one new family (Mycoalphaviridae) including two new genera (Alphasclernavirus, Betasclernavirus) and seven new species.

Justification: Members in the proposed family Mycoalphaviridae have a single-stranded positive-sense RNA genome ranging from 6.0 to 10.1 kb and encoding either one or more open reading frames. Members of the proposed family are only identified in fungi and oomycetes. The RNA-depended RNA polymerase of viruses in the family Mycoalphaviridae has the closest similarity to viruses of the order *Hepelivirales,* though the identity is lower than 20%. These low-level amino acid sequence identities, the different host ranges, and the result of phylogenetic analysis both support the establishment of the new family. The proposed family Mycoalphaviridae includes two proposed genera Alphasclernavirus and Betasclernavirus that accommodate three and seven species, respectively. The identity between genus and between species is lower than 26% and 50%, respectively, in the family.

Submitted: - ; *Revised:* 18/10/2024

TABLE 10 - *Mycoalphaviridae*, 10 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Mycoalphaviridae*		
New taxon	genus	*Alphasclernavirus*		
New taxon	species	*Alphasclernavirus alphasclerotiniae*	Sclerotinia sclerotiorum mycoalphavirus virus 1	MT706025
New taxon	species	*Alphasclernavirus betasclerotiniae*	Sclerotinia sclerotiorum RNA virus L	EU779934
New taxon	genus	*Betasclernavirus*		
New taxon	species	*Betasclernavirus alphafusarii*	Fusarium graminearum alphavirus-like virus 1	MN400076
New taxon	species	*Betasclernavirus botrytidis*	Botrytis cinerea alpha-like virus 1	MN625250
New taxon	species	*Betasclernavirus betafusarii*	Fusarium sacchari alphavirus-like virus 1	MN295968
New taxon	species	*Betasclernavirus betasclerotii*	Sclerotium rolfsii alphavirus-like virus 1	MH766488

New taxon	species	*Betasclernavirus alphasclerotii*	Sclerotium rolfsii alphavirus-like virus 3	MH766490

*Source / full text:
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.007F.Uc.v2.Mycoalphaviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.007F.Uc.v2.Mycoalphaviridae_newfam.xlsx

2024.008F.Uc.v2.Orpoviricetes_newclass

Title: Create a new class, *Orpoviricetes,* including two new orders, four families, seven genera and 26 new species in kingdom *Orthornavirae* (realm *Riboviria)*

Authors: Botella L, Turina M, Hejna O, Krupovic M, Neri U, Poimala A , Shamsi W, Sabanadzovic S, Sutela S, Vainio E, Forgia M (marco.forgia@ipsp.cnr.it)

Summary:

“Ormycoviruses” are recently identified RNA viruses that infect fungi and oomycetes. Their genomes consist of two monocistronic single-stranded (ss) RNA segments, with RNA1 encoding a putative RNA-directed RNA polymerase (RdRP) and RNA2 encoding a hypothetical protein with an unknown function. Ormycoviruses are unique in that they exhibit variations in the conserved motif C of the RdRP, such as NDD, GDQ, and HDD, which are not commonly found in other RNA viruses. This variation, coupled with their significant evolutionary divergence from other RNA viruses, supports the classification of ormycoviruses into a new class within the kingdom *Orthornavirae.* Therefore, we propose the establishment of the floating class "Orpoviricetes," which includes two orders, and four families, encompassing seven genera and 26 new species to initiate official classification of this group of *viruses.*

Taxonomic rank(s) affected: *Riboviria, Orthornavirae*

Description of current taxonomy: Kingdom *Orthornavirae* includes six phyla which were established based on phylogenetic analysis of the RdRP and comparative analysis of the viral genomes and encoded proteins.

Proposed taxonomic change(s): Creation of a new class *“Orpoviricetes”,* two new orders, five families and seven genera which collectively accommodates 26 new species.

Justification: Viruses from the kingdom *Orthornavirae,* which encompasses RNA viruses that encode RNA-directed RNA polymerases (RdRPs), generally have highly conserved motif C. This motif, often containing the core triplet GDD, is critical for the catalytic activity of the RdRP enzyme. Other triplets more rarely occurring are NDD, SDD, GDN, IDD, ADN, and ADD (in order of frequency; Olendraite et al. 2023). However, “ormycoviruses” exhibit unique variations in the core amino acid triad of motif C (e.g., NDD, GDQ, and HDD, shown in Figure 1 and 2) not found in other RNA viruses. Based on the significant variations in the conserved motif C and the high divergence from other RNA viruses (not conserved enough to be retrieved by BLAST searches using any of the RdRP encoded by viruses classified in the six currently recognized phyla), there is a strong case for considering “ormycoviruses” as members of, at least, a distinct class. Variations within the C motifs are rare but not unprecedented in other RNA viruses, so there is still a need to carry out phylogenetic and structural analyses to confirm whether ormycoviruses have diverged from viruses within existing phyla or have diverged prior to the radiation of viruses classified in the six currently established phyla. Therefore, as an initial step in the official classification of these viruses, we propose to classify them within a new class non-assigned to an existing phylum within the kingdom *Orthornavirae.* This classification would reflect their unique evolutionary pathway and potentially distinct biological characteristics.

Submitted: 20/06/2024; *Revised:* 17/10/2024

TABLE 11 - *Orpoviricetes*, 40 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	class	*Orpoviricetes*		
New taxon	order	*Formycovirales*		
New taxon	family	*Gammaormycoviridae*		
New taxon	genus	*Hormycovirus*		
New taxon	species	*Hormycovirus hortiboleti*	Hortiboletus rubellus ormycovirus 1	RNA1: PP260025; RNA2: PP260026
New taxon	genus	*Tormycovirus*		
New taxon	species	*Tormycovirus erysiphe*	Erysiphe lesion associated ormycovirus 4	RNA1:OM272933; RNA2: OM272934
New taxon	species	*Tormycovirus thrichodermae*	Trichoderma tomentosum ormycovirus 1	RNA1: OQ463855; RNA2: OQ463856
New taxon	species	*Tormycovirus fusarii*	Fusarium graminearum ormycovirus 1	RNA1: PP658032; RNA2: PP658033
New taxon	species	*Tormycovirus unplasmoparae*	Downy mildew lesion associated ormycovirus 4	RNA1:OM272935; RNA2:OM272936
New taxon	species	*Tormycovirus duaplasmoparae*	Downy mildew lesion associated ormycovirus 5	RNA1: OM272937; RNA2: OM272938
New taxon	family	*Betaormycoviridae*		
New taxon	genus	*Vormycovirus*		
New taxon	species	*Vormycovirus unerysiphe*	Erysiphe lesion associated ormycovirus 2	RNA1:OM272931; RNA2: OM272932
New taxon	species	*Vormycovirus duerysiphe*	Erysiphe lesion associated ormycovirus 3	RNA1:OM363731; RNA2: OM363732
New taxon	species	*Vormycovirus plasmoparae*	Downy mildew lesion associated ormycovirus 3	RNA1:OM363729; RNA2: OM363730
New taxon	species	*Vormycovirus verticilli*	Verticillium dahliae ormycovirus 2	RNA1: OR734292; RNA2: OR734293
New taxon	species	*Vormycovirus ophiocordyceps*	Ophiocordyceps sinensis ormycovirus 1	RNA1: PP623130; RNA2: PP623131
New taxon	genus	*Stormycovirus*		
New taxon	species	*Stormycovirus starmellariae*	Starmerella bacillaris ormycovirus 1	RNA1: OM272929; RNA2: OM272930
New taxon	species	*Stormycovirus alariae*	Alaria esculenta RNA virus 1	RNA1: PP793779; RNA2: PP793780
New taxon	order	*Bormycovirales*		
New taxon	family	*Alphaormycoviridae*		
New taxon	genus	*Phormycovirus*		
New taxon	species	*Phormycovirus phytophthorae*	Phytophthora cinnamomi ormycovirus 7-5	RNA1: PP891879; RNA2: PP891862
New taxon	species	*Phormycovirus unphytophthorae*	Phytophthora cinnamomi ormycovirus 4-1	RNA1: PP891842; RNA2: PP891839
New taxon	species	*Phormycovirus duphytophthorae*	Phytophthora cinnamomi ormycovirus 5-2	RNA1: PP891849; RNA2: PP891846
New taxon	species	*Phormycovirus trephytophthorae*	Phytophthora cinnamomi ormycovirus 6-4	RNA1: PP891858; RNA2: PP891851
New taxon	species	*Phormycovirus quaphytophthorae*	Phytophthora cinnamomi ormycovirus 11-3	RNA1: PP891940; RNA2: PP891934
New taxon	species	*Phormycovirus plasmoparae*	Downy mildew lesion associated ormycovirus 2	RNA1: OM262448; RNA2: PP940184
New taxon	genus	*Dormycovirus*		
New taxon	species	*Dormycovirus erysiphe*	Erysiphe lesion associated ormycovirus 1	RNA1: OM272927; RNA2: OM272928

New taxon	species	*Dormycovirus plasmoparae*	Downy mildew lesion associated ormycovirus 1	RNA1: OM363727; RNA2: OM363728
New taxon	species	*Dormycovirus phytophthorae*	Phytophthora cinnamomi ormycovirus 9-16	RNA1: PP891926; RNA2: PP891910
New taxon	family	*Deltanormycoviridae*		
New taxon	genus	*Bormycovirus*		
New taxon	species	*Bormycovirus verticilli*	Verticillium dahliae ormycovirus 1	RNA1: OR734290; RNA2: OR734291
New taxon	species	*Bormycovirus unphytophthorae*	Phytophthora cinnamomi ormycovirus 1-1	RNA1: PP891751; RNA2: PP891713
New taxon	species	*Bormycovirus duphytophthorae*	Phytophthora cinnamomi ormycovirus 2-25	RNA1: PP891801; RNA2: PP891774
New taxon	species	*Bormycovirus trephytophthorae*	Phytophthora cinnamomi ormycovirus 3-7	RNA1: PP891825; RNA2: PP891808

*Source / full text:
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.008F.Uc.v2.Orpoviricetes_newclass.docx
https://ictv.global/system/files/proposals/pending/Fungal%20and%20protist%20virus%20(F)%20proposals/2024.008F.Uc.v2.Orpoviricetes_newclass.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) from the Plant viruses Subcommittee, 2024

Main Text

Contents

2024.001P.A.v1.Fimoviridae_1nsp

Title: Create *Emaravirus clematis* as a new species in the genus *Emaravirus,* family *Fimoviridae*

Authors: Yang C, An W, Li C, Zhang S, Cao M, Digiaro M (digiaro@iamb.it), Elbeaino T, Kubota K, Ochoa Corona FM, von Bargen S

Summary:
The creation of the new species *Emaravirus clematis* in the genus *Emaravirus,* family *Fimoviridae,* is proposed to accommodate Clematis yellow mottle-associated virus (CYMaV), identified in China on *Clematis brevicaudata* DC, as its exemplar virus isolate. The new species consists of five segmented, linear, single-stranded (ss), negative-sense RNA genomes (of which two RNA3s encode the nucleocapsid protein), fully sequenced, which show features common to homologous RNAs of other known emaravirus species, but from which it differs significantly in nucleotide and amino acid sequences.

Submitted: 30/04/2024; *Revised:* 16/09/2024

TABLE 1 - *Fimoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Emaravirus clematis*	Clematis yellow mottle-associated virus	RNA1: OP807964; RNA2: OP807965; RNA3a: OP807966; RNA3b: OP807967; RNA4: OP807968

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.001P.A.v2.Fimoviridae_1nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.001P.A.v2.Fimoviridae_1nsp.xlsx

2024.002P.A.v1.Alphaflexiviridae_7nsp

Title: Create eight new species in the family *Alphaflexiviridae*

Authors: Abrahamian P, Donaire L, Candresse T, Fox A, Hammond J, Hasiów-Jaroszewska B , Kreuze J, Rubino L, Aranda MA (m.aranda@cebas.csic.es)

Summary:
Taxonomic rank affected: Species.

Description of current taxonomy: The *family Alphaflexiviridae* currently includes 65 virus species in genera *Allexivirus* (13), *Botrexvirus* (1), *Lolavirus* (1), *Platypuvirus* (1), *Potexvirus* (48) and *Sclerodarnavirus* (1).

Proposed taxonomic changes: This taxonomic proposal considers the recognition of 7 new virus species belonging to genera *Allexivirus* (1), *Botrexvirus* (2) and *Potexvirus* (4) 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 or amino acid sequences of viruses belonging to the seven newly proposed species fit well within these demarcation criteria.

Submitted: 14/06/2024; *Revised:* -

TABLE 2 - *Alphaflexiviridae*, 7 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Allexivirus rehmanniae*	Rehmannia allexivirus	PP097219
New taxon	species	*Botrexvirus unosclerotiniae*	Sclerotinia sclerotiorum alphaflexivirus 1	ON993219
New taxon	species	*Botrexvirus duosclerotiniae*	Sclerotinia sclerotiorum alphaflexivirus 2	OQ865609
New taxon	species	*Potexvirus ecsadenii*	Adenium obesum virus X; desert rose mottle virus	OR039325; OR240084
New taxon	species	*Potexvirus chaenostomae*	Chaenostoma potexvirus	OL979628
New taxon	species	*Potexvirus ecshibisci*	Hibiscus virus X	PP115950
New taxon	species	*Potexvirus ecscaricae*	Papaya virus X	MN265368

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.002P.A.v1.Alphaflexiviridae_7nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.002P.A.v1.Alphaflexiviridae_7nsp.xlsx

2024.003P.A.v1.Tospoviridae_2nsp

Title: Create two new species in the genus *Orthotospovirus (Elliovirales: Tospoviridae)*

Authors: Tomitaka Y, Shimomoto Y, Sasaya T (tsasaya@affrc.go.jp)

Summary:
We propose the classification of two newly discovered tospovirids into new species in the genus *Orthotospovirus,* on the base of a species demarcation criteria in the amino acid sequence of the RNA-directed RNA polymerase (RdRp) and nucleocapsid protein (N).

Submitted: 13/06/2024; *Revised:* -

TABLE 3 - *Tospoviridae*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Orthotospovirus eustomae*	lisianthus necrotic ringspot virus	MF469045; MF469046; MF469047
New taxon	species	*Orthotospovirus fatsiae*	Fatsia japonica ringspot-associated virus	LC626335; LC626336; LC626337

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.003P.A.v1.Tospoviridae_2nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.003P.A.v1.Tospoviridae_2nsp.xlsx

2024.004P.A.v1.Konkoviridae_1nsp

Title: Create one new species in the genus *Olpivirus (Hareavirales: Konkoviridae)*

Authors: Neriya Y , Schravesande WEW, van den Burg HA , Verhage A, Tomitaka Y, Sasaya T (tsasaya@affrc.go.jp)

Summary:

We propose the classification of one newly discovered konkovirid into a new species in the genus *Olpivirus,* on the base of a species demarcation criterion of <95% identity in the amino acid sequence of the RNA-directed RNA polymerase (RdRP).

Submitted: 13/06/2024; *Revised:* 07/10/2024

TABLE 4 - *Konkoviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Olpivirus lactucae*	Lactuca big vein associated phlebovirus	RNA1: OR610326; RNA2: OR610327; RNA3: OR610328; RNA4: OR610329

*Source / full text: https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.004P.A.v2.Konkoviridae_1nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.004P.A.v2.Konkoviridae_1nsp.xlsx

2024.005P.A.v1.Caulimoviridae_3nsp

Title: Create three new species in the genus *Badnavirus (Ortervirales: Caulimoviridae)*

Authors: Umber M, Dasgupta I, Geering ADW, Hafrén A, Hull R, Kreuze J, Leisner S, Muller E, Pappu H, Pooggin M, Richer-Pöggeler K, Seal S, Stavolone L, Teycheney PY (teycheney@cirad.fr)

Summary:
Taxonomic rank(s) affected:
Genus *Badnavirus.*

Description of current taxonomy:
The family *Caulimoviridae* [1] currently comprises 11 genera whose members share similar genome organization. The molecular species demarcation criteria are <80% identity of nucleotide sequences in the reverse transcriptase (RT) / ribonuclease H (RNase H) region of the polymerase. Genus *Badnavirus* [2] currently includes 71 species and is the largest genus within the family *Caulimoviridae.*

Proposed taxonomic change(s):
We propose the creation of three new species in the genus *Badnavirus*: *Badnavirus fatsiae, Badnavirus tetainflatheobromae* and *Badnavirus ziziphi*.

Justification:
Complete genomes of the exemplar members of the three proposed new species were sequenced and published recently. Their organizations are similar to those of other members of genus *Badnavirus.* Phylogenetic analyses place them in this genus as distinct representatives of novel species.

Submitted: 14/06/2024; *Revised:* -

TABLE 5 - *Caulimoviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Badnavirus fatsiae*	Fatsia badnavirus 1	OM540428
New taxon	species	*Badnavirus tetainflatheobromae*	cacao swollen shoot GhanaT virus	MN179342
New taxon	species	*Badnavirus ziziphi*	jujube badnavirus WS	OL739567

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.005P.A.v1.Caulimoviridae_3nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.005P.A.v1.Caulimoviridae_3nsp.xlsx

2024.006P.A.v1.Kitaviridae_3nsp

Title: Create a new species in the genus *Cilevirus and* two in the genus *Higrevirus,* family *Kitaviridae (Martellivirales).*

Authors: Li C, An W, Zhang S, Cao M, Yang C (xueyang27@126.com), Mohammadi M, Hosseini A, Nasrollanejad S, Roy A , Freitas-Astua J , Tiberini A, Jun-Min L, Ramos-González PL

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy:
Family *Kitaviridae,* order *Martellivirales,* includes plant-infecting viruses having linear single-stranded (ss) positive-sense (+) split RNA genomes. Viruses in this family are assigned to the genera *Cilevirus, Higrevirus,* or *Blunervirus* (Quito-Avila *et al., 2021;* Ramos-González et al., 2023).

Proposed taxonomic change(s):
Create three new species in the family *Kitaviridae*; one in the genus *Cilevirus,* and two in the genus *Higrevirus.*

Justification:
The genomes of the three novel viruses show an arrangement that resembles that of kitavirids, and their core conserved proteins share relatively low amino acid (aa) sequence identities (<85%) with recognized members of the family *Kitaviridae.* In phylogenetic analyses, the three viruses grouped with characterized members of the genera *Cilevirus* and *Higrevirus,* but they are well-separated and supported by bootstrap values higher than 95%. All new species meet the already established or the demarcation criteria defined in this proposal.

Submitted: 11/06/2024; *Revised:* -

TABLE 6 - *Kitaviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Higrevirus amurense*	Phellodendron-associated higre-like virus	RNA1: OP324809; RNA2: OP324810; RNA3: OP324811
New taxon	species	*Higrevirus pistaciae*	Pistachio virus X	RNA1: MT334620; RNA2: MT334619; RNA3: MT334618
New taxon	species	*Cilevirus pistaciae*	Pistachio virus Y	RNA1: MT362606; RNA2: MT362605

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.006P.A.v1.Kitaviridae_3nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.006P.A.v1.Kitaviridae_3nsp.xlsx

2024.007P.A.v1.Geminiviridae_Capulavirus_1nsp

Title: Create one new species in the genus *Capulavirus* (*Geplafuvirales*: *Geminiviridae*)

Authors: Roumagnac, Philippe (philippe.roumagnac@cirad.fr), Ascencio-Ibanez, Jose, Lett, Jean-Michel, López-Lambertini, Paola M., Martin, Darren P., Navas-Castillo, Jesús, Ribeiro, Simone, Urbino, Cica, Varsani, Arvind, Zerbini, F. Murilo

Summary:
Proposed changes*:*
Add one species in the *Capulavirus* genus

Taxonomic rank(s) affected:
Capulavirus genus in the *Geminiviridae* family

Description of current taxonomy:
Monodnaviria / Shotokuvirae / Cressdnaviricota / Repensiviricetes / Geplafuvirales / Geminiviridae / Capulavirus

Proposed taxonomic change(s):
We proposed to add one new species to the *Capulavirus* genus: *Capulavirus trifolii*

Justification:
Similar to members of the *Capulavirus* genus, members of the proposed new species *Capulavirus trifolii* 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 *Capulavirus trifolii* shares 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 *Capulavirus trifolii* represents a new species in the genus *Capulavirus.*

Submitted: 10/06/2024; *Revised:* -

TABLE 7 - *Geminiviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Capulavirus trifolii*	Trifolium virus 1	MW698813

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.007P.A.v1.Geminiviridae_Capulavirus_1nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.007P.A.v1.Geminiviridae_Capulavirus_1nsp.xlsx

2024.008P.A.v1.Geminiviridae_Citlodavirus_2nsp

Title: Create two new species in the genus *Citlodavirus* (*Geplafuvirales*: *Geminiviridae)*

Authors: Roumagnac, Philippe (philippe.roumagnac@cirad.fr), Ascencio-Ibanez, Jose, Lett, Jean-Michel, López-Lambertini, Paola M., Martin, Darren P., Navas-Castillo, Jesús, Ribeiro, Simone, Urbino, Cica, Varsani, Arvind, Zerbini, F. Murilo

Summary:
Proposed changes*:*
Add two species in *the Citlodavirus* genus

Taxonomic rank(s) affected:
Citlodavirus genus in the *Geminiviridae* family

Description of current taxonomy:
Monodnaviria / Shotokuvirae / Cressdnaviricota / Repensiviricetes / Geplafuvirales / Geminiviridae / Citlodavirus

Proposed taxonomic change(s):
We proposed to add two new species to the *Citlodavirus* genus, *Citlodavirus apijamaicaense* and *Citlodavirus myricae*.

Justification:
Similar to members of the *Citlodavirus* genus, members of the proposed new species *Citlodavirus apijamaicaense* and *Citlodavirus myricae* have the virion-strand origin of replication nonanucleotide

motif ‘TAA TAT TAC’, a relatively large genome (3918 nt and 3775 nt, respectively) and unique genome arrangements that, in both cases, include the putative *mp* gene (888 nt and 912 nt, respectively) that is similar in size to the *mp* gene in the DNA-B of bipartite begomoviruses. Genome-wide pairwise analysis of the representative genomes of citlodaviruses showed that *Citlodavirus apijamaicaense* and *Citlodavirus myricae* share less than 78% identity with all representative genomes of citlodaviruses and between each other. Since 78% nucleotide identity is the genome-wide species demarcation threshold for citlodaviruses, we conclude that *Citlodavirus apijamaicaense* and *Citlodavirus myricae* represent two new species in the genus *Citlodavirus.*

Submitted: 10/06/2024; *Revised:* -

TABLE 8 - *Geminiviridae*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Citlodavirus apijamaicaense*	apiscitlodal virus	PP467584
New taxon	species	*Citlodavirus myricae*	Myrica rubra citlodavirus 1	OP374189

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.008P.A.v1.Geminiviridae_Citlodavirus_2nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.008P.A.v1.Geminiviridae_Citlodavirus_2nsp.xlsx

2024.009P.A.v1.Geminiviridae_Mastrevirus_5nsp

Title: Establish five new species in the genus *Mastrevirus*

Authors: Varsani, Arvind (Arvind.varsani@asu.edu), Martin, Darren P., Roumagnac, Philippe, Ascencio-Ibanez, Jose, Lett, Jean-Michel, López-Lambertini, Paola M., Navas-Castillo, Jesús, Ribeiro, Simone, Urbino, Cica, Zerbini, F. Murilo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Mastreviruses are currently classified according to the following hierarchy:
Monodnaviria; *Shotokuvirae*; *Cressdnaviricota*; *Repensiviricetes*; *Geplafuvirales*; *Geminiviridae*; *Mastrevirus.*

Within the genus *Mastrevirus,* viruses are classified into species based on a 78% genome-wide pairwise identity threshold [1].

Proposed taxonomic change(s):
We propose the establishment of five new species to classify a suite of new mastreviruses that have been identified over the last year or so.

Justification:
The members of the five new proposed species in the genus *Mastrevirus* share < 78% genome-wide pairwise identity with sequences of members of currently established mastrevirus species.

Submitted: 10/06/2024; *Revised:* -

TABLE 9 - *Geminiviridae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**

New taxon	species	*Mastrevirus urochloareunionense*	Urochloa decumbens associated virus	OQ451139
New taxon	species	*Mastrevirus nomiae*	Nomiamastrel virus	PP467585
New taxon	species	*Mastrevirus brachypodiumprimi*	Brachypodium phoenicoides associated virus 1	OR596402
New taxon	species	*Mastrevirus bothriochloae*	Bothriochloa barbinodis associated virus	OR596403
New taxon	species	*Mastrevirus brachypodiumsecundi*	Brachypodium phoenicoides associated virus 2	OR596405

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.009P.A.v1.Geminiviridae_Mastrevirus_5nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.009P.A.v1.Geminiviridae_Mastrevirus_5nsp.xlsx

2024.010P.A.v1.Begomovirus_19nsp

Title: Create 19 new species in the genus *Begomovirus (Geplafuvirales: Geminiviridae)*

Authors: Zerbini FM (zerbini@ufv.br), Ascencio-Ibanez J, Lett JM, Navas-Castillo J, Urbino C, López-Lambertini P, Martin DP, Ribeiro SG, Roumagnac P, Varsani A

Summary:
Taxonomic rank affected: Species in the genus *Begomovirus*

Description of current taxonomy: *Monodnaviria* -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus*
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: We propose the establishment of 19 new species to classify new begomoviruses that have been identified and described in the literature over the last three years.

Justification: All 19 proposed new species have <91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity with sequences of members of currently established begomovirus species.

Submitted: 10/06/2024; *Revised:* -

TABLE 10 - *Begomovirus*, 19 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Begomovirus chuxiongense*	tomato leaf curl Chuxiong virus	OR543988
New taxon	species	*Begomovirus solanumaureusreti*	tomato golden net virus	MT214095
New taxon	species	*Begomovirus solanumflavusreti*	tomato yellow net viurs	MT214096
New taxon	species	*Begomovirus whitaniae*	Withania leaf curl virus	OP617239
New taxon	species	*Begomovirus sidaflavusfolii*	sida chlorotic leaf vrius	MN013784; MN013785
New taxon	species	*Begomovirus cajani*	Cajanus scarabaeoides yellow mosaic virus	OM397101; OM397102
New taxon	species	*Begomovirus hortuscrotoni*	garden croton enation leaf curl virus	MW816855; MW816857
New taxon	species	*Begomovirus jatrophagunturense*	Jatropha leaf curl Guntur virus	MZ217773

New taxon	species	*Begomovirus hyptidis*	Hyptis golden mosaic virus	ON073795; ON073796
New taxon	species	*Begomovirus galii*	Galium leaf distortion virus	OL689630
New taxon	species	*Begomovirus myanmarense*	tobacco curly shoot Myanmar virus	MK920410
New taxon	species	*Begomovirus caboniensis*	Cnidoscolus mild mosaic virus	MZ465527; MZ465585
New taxon	species	*Begomovirus pyrenacanthae*	Pyrenacantha yellow mosaic virus	MZ390982; MZ390984
New taxon	species	*Begomovirus puerense*	tobacco leaf curl Puer virus	MZ465370
New taxon	species	*Begomovirus solanumdistorsionis*	tomato mottle leaf distortion virus	MW561191; MW650837
New taxon	species	*Begomovirus alceacrispi*	hollyhock vein yellowing virus	LK028571
New taxon	species	*Begomovirus muntiflavi*	Muntingia yellow spot virus	MW032664; MW032665
New taxon	species	*Begomovirus flavintervenae*	tomato interveinal yellowing virus	MW057360
New taxon	species	*Begomovirus sidaflavitessellati*	sida yellow mosaic Gujarat virus	KX513859

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.010P.A.v1.Geminiviridae_Begomovirus_19nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.010P.A.v1.Geminiviridae_Begomovirus_19nsp.xlsx

2024.011P.A.v1.Bromoviridae_4nsp

Title: Create four (4) new species in the genus *Ilarvirus (Martellivirales: Bromoviridae)*

Authors: Thompson JR (jeremy.thompson@mpi.govt.nz), Canto T, Carr JP, Pallás V, Šafářová D

Summary:
This taxonomic proposal considers the recognition of the following four new virus species (Table 1) based on species demarcation criteria in the family *Bromoviridae* genus *Ilarvirus* of “serology, host range and sequence similarity”. In the absence of biological information, we propose to include a refinement of the “sequence similarity” criterion to require less than 85% identity for the complete RNA2 2a protein.

Submitted: 10/06/2024; *Revised:* 07/10/2024

TABLE 11 - *Bromoviridae*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Ilarvirus ApNMV*	apple necrotic mosaic virus	LC108993; LC108994; LC108995
New taxon	species	*Ilarvirus BabIV1*	babaco ilarvirus 1	OQ256238; OQ256239; OQ256240
New taxon	species	*Ilarvirus TIV1*	tomato ilarvirus 1	OL472057; OL472058; OL472059
New taxon	species	*Ilarvirus ToNSV*	tomato necrotic spot virus	MH780154; MH780155; MH780156

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.011P.A.v2.Bromoviridae_4nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.011P.A.v2.Bromoviridae_4nsp.xlsx

2024.012P.Uc.v1.Potyviridae_1ng_10nsp

Title: Create 1 new genus *(Phragmivirus)* with 2 species, and 8 new species in the genus *Potyvirus (Patatavirales: Potyviridae)*

Authors: Inoue-Nagata AK (alice.nagata@embrapa.br), Jordan R, Kreuze JF, Li F, Lopez-Moya JJ, Makinen K, Ohshima K, Wylie SJ

Summary:
Taxonomic rank(s) affected: Genus within the family *Potyviridae* and species within the genus *Potyvirus* and the newly proposed *Phragmivirus*

Description of current taxonomy: According to the ICTV Report chapter on *Potyviridae,* twelve genera are differentiated by biological criteria, mainly transmission by specific vectors, and by molecular data, in which members of different genera are <46% identical in nucleotide sequence. Members of different species have complete ORF sequences that are generally <76% identical in nucleotide sequence and <82% identical in amino acid sequence. In considering the evidence for new species or genera in the family *Potyviridae,* the Study Group will evaluate each new case based on complete or near-complete genome sequence(s) together with host and biological characteristics.

Proposed taxonomic changes: Creation of one new genus *(Phragmivirus),* two new species in the genus *Phragmivirus* and eight new species in the genus *Potyvirus:*
Genus *Phragmivirus*
Phragmivirus phragmii
Phragmivirus spatinae

Genus *Potyvirus*
Potyvirus aconiti
Potyvirus puerariae
Potyvirus alilii
Potyvirus parisflavitessellati
Potyvirus catharanthiflavitessellati
Potyvirus polygonatimaculae
Potyvirus crocitessellati
Potyvirus galanthi

Justification: the genomes of the proposed members in the new genus *Phragmivirus* share sequence identity below the threshold for genera differentiation in the family *Potyviridae;* the proposed species have a genome strategy typical of members of genus *Phragmivirus* (2 species) and *Potyvirus* (8 species), and their nucleotide and amino acid sequences are below the threshold for species demarcation criteria for the genera. The characteristics of each new species and the new genus are described below.

Submitted: 11/06/204; *Revised:* 21/09/2024

TABLE 12 - *Potyviridae*, 11 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Potyvirus aconiti*	Aconitum virus 2	MZ389235
New taxon	species	*Potyvirus puerariae*	Kudzu chlorotic ring blotch virus	OQ148665
New taxon	species	*Potyvirus alilii*	Lily virus A	OR879085
New taxon	species	*Potyvirus parisflavitessellati*	Paris yunnanensis mosaic chlorotic virus	ON871824
New taxon	species	*Potyvirus catharanthiflavitessellati*	Periwinkle mild yellow mosaic virus	PP382205
New taxon	species	*Potyvirus polygonatimaculae*	Polygonatum kingianum mottle virus	ON428226
New taxon	species	*Potyvirus crocitessellati*	Saffron yellow mosaic virus	OK632024
New taxon	species	*Potyvirus galanthi*	Snowdrop virus Y	OP871788

New taxon	genus	*Phragmivirus*		
New taxon	species	*Phragmivirus phragmii*	Common reed chlorotic stripe virus	KY612317
New taxon	species	*Phragmivirus spartinae*	Spartina mottle virus	MN788417

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https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.012P.Uc.v2.Potyviridae_1ng_10nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.012P.Uc.v2.Potyviridae_1ng_10nsp.xlsx

2024.013P.Uc.v1.Secoviridae_1ng_2nsg_39nsp

Title: Create a new genus, two new subgenera, and 34 new species in the family *Secoviridae* (*Picornavirales*)

Authors: Fuchs M (mf13@cornell.edu), Hily J-M, Petrzik K, Sanfaçon H, Stewart L, Thompson J, Van der Vlugt R, Wetzel T

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

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 a new genus in the family*: Mersevirus*
Create two new subgenera in the genus *Waikavirus*: *Ritunrivirus*, *Actinidivirus*
Create two new species in the genus *Fabavirus*: *Fabavirus betavitis*, *Fabavirus cirsii*
Create four new species in the proposed new genus *Mersevirus*: *Mersevirus merculiaris*, *Mersevirus paris, Mersevirus boehmeriae, Mersevirus jujubae*
Create two new species in the genus *Nepovirus: Nepovirus betaparis, Nepovirus mirae*
Create three new species in the genus *Sadwavirus: Sadwavirus cattleyae, Sadwavirus gymnemae, Sadwavirus chrysanthemi*
Create three new species in the genus *Torradovirus: Torradovirus physalis, Torradovirus nanorugosum, Torradovirus arctii*
Create 20 new species in the genus *Waikavirus: Waikavirus ajugae, Waikavirus anacycli, Waikavirus betacamelliae, Waikavirus eleocharis, Waikavirus hirtae, Waikavirus juglandis, Waikavirus ligustici, Waikavirus mertensiae, Waikavirus populi, Waikavirus pedicularis, Waikavirus primulae, Waikavirus querci, Waikavirus ranunculi, Waikavirus thymi, Waikavirus trifoccidentale, Waikavirus thapsiae, Waikavirus violae, Waikavirus carotae, Waikavirus celtis, Waikavirus pittospori*

Justification:
The creation of the proposed new genus *Mersevirus* is justified based on the distinct genome organization of *Mersevirus merculiaris, Mersevirus paris, Mersevirus boehmeriae*, and *Mersevirus jujubae* with a Ham1 domain with predicted inosine triphosphate pyrophosphatase activity at the C-terminus of the RNA-dependent RNA polymerase -a feature unique among members of the family *Secoviridae*- and a grouping on a monophyletic clade of the amino acid sequence of the CPs and conserved Pro-Pol region.
The creation of the proposed new subgenus *Ritunrivirus* is justified based on a statistically supported single lineage of 22 distinct species in the genus *Waikavirus* defined by the amino acid sequence of the combined three CPs and the conserved Pro-Pol region.
The creation of the proposed new subgenus *Actinidivirus* is justified based on a statistically supported single lineage of 16 distinct species in the genus *Waikavirus* defined by the amino acid sequence of the combined three CPs and conserved Pro-Pol region.

The creation of the proposed new 34 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.*

Submitted: 10/06/2024; *Revised:* 11/10/2024

TABLE 13 - *Secoviridae*, 37 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	genus	*Mersevirus*		
New taxon	species	*Mersevirus boehmeriae*	Boehmeria nivea secovirus	BK061322; BK061323
New taxon	species	*Mersevirus jujubae*	jujube-associated virus 1	MT375548; MT375547
New taxon	species	*Mersevirus merculiaris*	Merculiaris secovirus 1	OR544055; OR544056
New taxon	species	*Mersevirus paris*	Paris polyphylla secovirus 2	BK061330; BK061331
New taxon	subgenus	*Actinidivirus*		
New taxon	species	*Waikavirus betacamelliae*	Camellia virus B	BK062984
New taxon	species	*Waikavirus carotae*	carrot psyllid-borne assocaited virus	OM801008
New taxon	species	*Waikavirus celtis*	hackberry virus A	OP533794
New taxon	species	*Waikavirus hirtae*	Ficus hirta waikavirus	BK062987
New taxon	species	*Waikavirus juglandis*	Juglans nigra waikavirus	BK062989
New taxon	species	*Waikavirus pittospori*	Pittosporum tobira virus	OR659471
New taxon	species	*Waikavirus populi*	Populus alba waikavirus	BK062992
New taxon	species	*Waikavirus querci*	Quercus robur waikavirus	BK062996
New taxon	species	*Waikavirus trifoccidentale*	Trifolium occidentale waikavirus	BK063000
New taxon	subgenus	*Ritunrivirus*		
New taxon	species	*Waikavirus ajugae*	Ajuga Reptans waikavirus	BK062980
New taxon	species	*Waikavirus anacycli*	Anacyclus depressus waikavirus	BK062979
New taxon	species	*Waikavirus eleocharis*	Eleocharis dulcis waikavirus	BK062986
New taxon	species	*Waikavirus ligustici*	Ligusticum chuanxiong waikavirus	BK062990
New taxon	species	*Waikavirus mertensiae*	Mertensia paniculata waikavirus	BK062991
New taxon	species	*Waikavirus pedicularis*	Pedicularis rex waikavirus	BK062993
New taxon	species	*Waikavirus primulae*	Primula vulgaris waikavirus	BK062995
New taxon	species	*Waikavirus ranunculi*	Ranunculus cantoniensis waikavirus	BK062997
New taxon	species	*Waikavirus thapsiae*	Thapsia villosa waikavirus	BK063001
New taxon	species	*Waikavirus thymi*	Thymus vulgaris waikavirus	BK062999
New taxon	species	*Waikavirus violae*	Viola inconspicua waikavirus	BK063002
New taxon	species	*Fabavirus betavitis*	grapevine secovirus	OR947508; OR947509
New taxon	species	*Fabavirus cirsii*	cirsium virus A	OP794357; OP794358
New taxon	species	*Nepovirus betaparis*	Paris polyphylla secovirus 1	BK061328; BK061329
New taxon	species	*Nepovirus mirae*	Prunus mira virus A	BK064709; BK064710
New taxon	species	*Sadwavirus cattleyae*	Cattleya purple ringspot virus	OR439368; OR439369

New taxon	species	*Sadwavirus gymnemae*	Gymnema sylvestre virus 1	BK062888; BK062889
New taxon	species	*Sadwavirus chysanthemi*	chrysanthemum sadwavirus	OR413567; OR413568
New taxon	species	*Torradovirus arctii*	burdock mosaic virus	OQ087134; OQ087135
New taxon	species	*Torradovirus nanorugosum*	potato rugose stunting virus	ON871623; ON871624
New taxon	species	*Torradovirus physalis*	Physalis torrado virus	MZ357183; MZ357184

TABLE 14 - *Secoviridae*, 13 move taxa*

Operation	Rank	Taxon name	Old parent taxon	New parent taxon
Move taxon	species	*Waikavirus actinidiae*	*Waikavirus*	*Actinidivirus*
Move taxon	species	*Waikavirus camelliae*	*Waikavirus*	*Actinidivirus*
Move taxon	species	*Waikavirus diospyri*	*Waikavirus*	*Actinidivirus*
Move taxon	species	*Waikavirus liegense*	*Waikavirus*	*Actinidivirus*
Move taxon	species	*Waikavirus rhododendri*	*Waikavirus*	*Actinidivirus*
Move taxon	species	*Waikavirus brassicae*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus campanulae*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus lactucae*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus oryzae*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus ribesnigri*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus rosae*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus trifolii*	*Waikavirus*	*Ritunrivirus*
Move taxon	species	*Waikavirus zeae*	*Waikavirus*	*Ritunrivirus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.013P.Uc.v2.Secoviridae_1ng_2nsg_34nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.013P.Uc.v2.Secoviridae_1ng_2nsg_34nsp.xlsx

2024.014P.A.v1.Rhabdoviridae_2nsp.xslx

Title: Create one new species in the genus *Alphanucleorhabdovirus,* and one species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae (Mononegavirales*: *Rhabdoviridae)*

Authors: Bejerman M (bejerman.nicolas@inta.gob.ar), Debat H, Dietzgen R, Freitas-Astua J, Kondo H, Ramos-Gonzalez P, Whitfield A, Walker P

Summary:
Taxonomic rank(s) affected: Species

Description of current taxonomy: Viruses classified in the genera *Alphanucleorhabdovirus* and *Betanucleorhabdovirus* 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 *Alphanucleorhabdovirus* and one new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named *Alphanucleorhabdovirus babaci* and *Betanucleorhabdovirus paridis,* respectively.

Justification: Two novel rhabdoviruses were identified in babaco [1] and *Paris polyphylla* [2]. The characterization of both viruses showed that the babaco-associated virus should be classified as a novel species within the genus *Alphanucleorhabdovirus* [1] while the *Paris polyphylla-associated* virus should be classified as a novel species within the genus *Betanucleorhabdovirus* [2].

Submitted: 10/06/2024; *Revised:* -

TABLE 15 - *Rhabdviridae*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	*Alphanucleorhabdovirus babaci*	babaco nucleorhabdovirus 1	OQ256237
New taxon	species	*Betanucleorhabdovirus paridis*	Paris yunnanensis rhabdovirus 1	OL439478

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.014P.A.v1.Rhabdoviridae_2nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.014P.A.v1.Rhabdoviridae_2nsp.xlsx

2024.015P.A.v1.Rhabdoviridae_Cytorhabdovirus_splitgen

Title: Abolish one genus and create three new genera to include 98 new species in the subfamily *Betarhabdovirinae (Mononegavirales*: *Rhabdoviridae)*

Authors: Bejerman M (bejerman.nicolas@inta.gob.ar), Debat H, Dietzgen R, Freitas-Astua J, Kondo H, Ramos-Gonzalez P, Whitfield A, Walker P

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

Description of current taxonomy: Viruses classified in the genus *Cytorhabdovirus* 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 tree inferred from complete L protein sequences.

Proposed taxonomic change(s): Split and abolish the genus *Cytorhabdovirus,* creating three new genera *(Alphacytorhabdovirus, Betacytorhabdovirus,* and *Gammacytorhabdovirus)* including 98 new species in the subfamily *Betarhabdovirinae (Mononegavirales*: *Rhabdoviridae),* and reassign current *Cytorhabdovirus* species to the new genera. Also, we propose to abolish four cytorhabdovirus species.

Justification: Recently, 98 new putative cytorhabdoviruses were discovered. The phylogenetic relationships of the now significantly expanded number of known cytorhabdoviruses provide support for splitting the genus *Cytorhabdovirus* to establish three genera that represent distinct evolutionary lineages, which we propose to name *Alphacytorhabdovirus, Betacytorhabdovirus* and *Gammacytorhabdovirus.* Also, we propose to abolish four cytorhabdovirus species due to the lack of sequence data for the four viruses.

Submitted: 10/06/2024; *Revised:* 03/10/2024

TABLE 16 - *Rhabdoviridae*, 101 new taxa*. Table too large, see supplementary information sheet supp_info_tab_16

TABLE 17 - *Rhabdoviridae*, 51 move; rename taxa*. Table too large, see supplementary information sheet supp_info_tab_17

TABLE 18 - *Rhabdoviridae*, 4 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	species	*Cytorhabdovirus brassicae*
Abolish taxon	species	*Cytorhabdovirus festucae*
Abolish taxon	species	*Cytorhabdovirus sonchi*
Abolish taxon	species	*Cytorhabdovirus tritici*

*Source / full text
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.015P.A.v2.Rhabdoviridae_Cytorhabdovirus_splitgen.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.015P.A.v2.Rhabdoviridae_Cytorhabdovirus_splitgen.xlsx

2024.016P.A.v1.Rhabdoviridae_1ngen_5nsp

Title: Create one new genus to include five new species in the subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Bejerman M (bejerman.nicolas@inta.gob.ar), Debat H, Dietzgen R, Freitas-Astua J, Kondo H, Ramos-Gonzalez P, Whitfield A, Walker P

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

Description of current taxonomy: Almost all viruses classified in the subfamily *Betarhabdovirinae,* family *Rhabdoviridae* are unsegmented, but plant-associated rhabdoviruses with bi-segmented genomes have also been identified and included in the genera *Varicosavirus* and *Dichorhavirus* within the subfamily *Betarhabdovirinae.* 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 genus to include five new species in the subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These five new species named as *Trirhavirus alni, Trirhavirus chrysanthemi, Trirhavirus erysimi, Trirhavirus medicagonis,* and *Trirhavirus picridis* are proposed to be classified in a new genus named *Trirhavirus.*

Justification: Five novel rhabdoviruses were identified in *Alnus rubra, Chrysanthemum morifolium, Erysimum nevadense, Medicago sativa,* and *Picris echioides* [1]. Unexpectedly, these five viruses have tri-segmented genomes, which represent the first tri-segmented genomes among rhabdoviruses. The characterization of these five viruses showed they should be classified as novel species within a novel genus within the subfamily *Betarhabdovirinae,* family *Rhabdoviridae,* for which we propose the name *"Trirhavirus"* [1].

Submitted: 10/06/2024; *Revised:* -

TABLE 19 - *Rhabdoviridae*, 6 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	genus	*Trirhavirus*		
New taxon	species	*Trirhavirus alni*	Alnus trirhavirus 1	BK064247; BK064248; BK064249
New taxon	species	*Trirhavirus chrysanthemi*	Chrysanthemum trirhavirus 1	BK064250; BK064251; BK064252

New taxon	species	*Trirhavirus erysimi*	Erysimum trirhavirus 1	BK064253; BK064254; BK064255
New taxon	species	*Trirhavirus medicagonis*	Medicago trirhavirus	BK064256; BK064257; BK064258
New taxon	species	*Trirhavirus picridis*	Picris trirhavirus 1	BK064259; BK064260; BK064261

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.016P.A.v1.Rhabdoviridae_1ngen_5nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.016P.A.v1.Rhabdoviridae_1ngen_5nsp.xlsx

2024.017P.A.v1.Tombusviridae_abolishsp

Title: Abolish five unassigned species in the family *Tombusviridae*

Authors: Scheets K (kay.scheets@okstate.edu), Hernandez C, Jordan R, Miller WA, Prigigallo MI, Rubino L,

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

Description of current taxonomy: *Ahlum waterborne virus*, *Bean mild mosaic virus*, *Chenopodium necrosis virus*, *Cucumber soil-borne virus*, *Weddel waterborne virus* are currently classified as unassigned species in the family *Tombusviridae.*

Proposed taxonomic change(s): We propose these species to be abolished.

Justification: We propose to abolish these five tombusvirid species due to the lack of sequence data for the five viruses.

Submitted: 21/06/2024; *Revised:* -

TABLE 20 - *Tombusviridae*, 5 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	species	*Ahlum waterborne virus*
Abolish taxon	species	*Bean mild mosaic virus*
Abolish taxon	species	*Chenopodium necrosis virus*
Abolish taxon	species	*Cucumber soil-borne virus*
Abolish taxon	species	*Weddel waterborne virus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.017P.A.v1.Tombusviridae_abolishsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.017P.A.v1.Tombusviridae_abolishsp.xlsx

2024.018P.A.v1.Tombusviridae_1nsp

Title: Create one new species in the genus *Machlomovirus (Tolivirales*: *Tombusviridae)*

Authors: Maclot F, Massart S (sebastien.massart@uliege.be)

Summary:Taxonomic rank(s) affected:
Genus *Machlomovirus (Tolivirales*: *Tombusviridae)*

Description of current taxonomy:

One virus species, *Machlomovirus zeae,* is currently described within the genus *Machlomovirus.*

Proposed taxonomic change(s):
We propose to create a second species (*Machlomovirus liegense*) in the genus *Machlomovirus* to accommodate a recently identified virus in the wild grass common bent (*Agrostis capillaris*), tentatively named Poaceae Liege machlomovirus - PoLMV.

Justification:
Analysis of PoLMV genomic structure and phylogenetic analyses of its full sequence and specific genes (polymerase and coat protein) placed PoLMV as a novel species in the genus *Machlomovirus.*

Submitted: 21/06/2024; *Revised:* -

TABLE 21 - *Tombusviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Machlomovirus liegense*	Poaceae Liege machlomovirus	ON137711

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.018P.A.v1.Tombusviridae_1nsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.018P.A.v1.Tombusviridae_1nsp.xlsx

2024.019P.A.v1.Closteroviridae_1nsp.xslx

Title: Create one new species in the genus *Velarivirus* (order *Martellivirales,* family *Closteroviridae*)

Authors: Fontdevila N, Massart S (sebastien.massart@uliege.be)

Summary:
Taxonomic rank(s) affected:
Genus *Velarivirus* (order *Martellivirales,* family *Closteroviridae*)

Description of current taxonomy:
The family *Closteroviridae* comprises plant viruses with long, filamentous particles (650-2,200 nm in length) and large positive-sense RNA genomes (mono-, bi-, or tripartite). There are 57 recognized species in the family, classified in one of the seven existing genera *(Ampelovirus, Bluvavirus*, *Closterovirus*, *Crinivirus*, *Menthavirus*, *Olivavirus,* and *Velarivirus).* Within the genus *Velarivirus,* there are currently eight recognized species.

Proposed taxonomic change(s):
The authors propose adding a ninth species in the genus *Velarivirus,* named *Velarivirus gembloutense,* to classify recently identified virus Pyrus virus A (PyVA) in pear trees *(Pyrus communis* L.).

Justification:
Analysis of the genomic structure of this novel virus (PyVA) and subsequent phylogenetic analyses of the specific HSP70h gene placed PyVA as a novel member of the genus *Velarivirus* within the family *Closteroviridae.*

Submitted: 21/06/2024; *Revised:* 07/10/2024

TABLE 22 - *Closteroviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	species	*Velarivirus gembloutense*	Pyrus virus A	OR887735

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.019P.A.v2.Closteroviridae_1nsp.docx

https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.019P.A.v2.Closteroviridae_1nsp.xlsx

2024.021P.A.v1.Riboviria_1nord

Title: Create one new unassigned order in realm *Riboviria,* including four new families for four currently unassigned genera of plant satellite viruses

Authors: Krupovic M (mart.krupovic@pasteur.fr), Fischer MG, Kuhn JH

Summary:
Taxonomic rank(s) affected: Species, genus, family

Description of current taxonomy: *Riboviria:* unassigned family *Sarthroviridae* and genera *Albetovirus, Aumaivirus, Papanivirus,* and *Virtovirus*

Proposed taxonomic change(s): *Riboviria: Tombendovirales* to include family *Sarthroviridae* and two new families, *Pamosaviridae* (*Papanivirus*), and *Tomosaviridae* (*Virtovirus*); and *Riboviria*: *Tonesaviridae* (*Albetovirus, Aumaivirus*); renaming of all species in the four genera to fulfill the ICTV's binomial naming mandate.

Justification: Structural comparison of the satellite virus capsid proteins indicates that these viruses are not monophyletic and form two distinct assemblages.

Submitted: 21/06/2024; *Revised:* -

TABLE 23 - *Riboviria*, 6 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Papanivirus panici*	*Panicum papanivirus 1*
Rename taxon	species	*Virtovirus tabaci*	*Tobacco virtovirus 1*
Rename taxon	species	*Albetovirus alphatabaci*	*Tobacco albetovirus 1*
Rename taxon	species	*Albetovirus betatabaci*	*Tobacco albetovirus 2*
Rename taxon	species	*Albetovirus gammatabaci*	*Tobacco albetovirus 3*
Rename taxon	species	*Aumaivirus maidis*	*Maize aumaivirus 1*

TABLE 24 - *Riboviria*, 5 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	family	*Sarthroviridae*	*Tombendovirales*
Move taxon	genus	*Papanivirus*	*Tombendovirales*
Move taxon	genus	*Virtovirus*	*Tombendovirales*
Move taxon	genus	*Albetovirus*	*Tonesaviridae*
Move taxon	genus	*Aumaivirus*	*Tonesaviridae*

TABLE 25 - *Riboviria*, 4 new taxa*

Operation	Rank	New taxon name
New taxon	order	*Tombendovirales*
New taxon	family	*Pamosaviridae*
New taxon	family	*Tomosaviridae*
New taxon	family	*Tonesaviridae*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.021P.A.v1.Riboviria_1nord.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.021P.A.v1.Riboviria_1nord.xlsx

2024.022P.A.v1.Betaflexiviridae_abolishsp

Title: Abolish five unassigned species in the family *Betaflexiviridae*

Authors: Nagata, Tatsuya (tastuya@unb.br), Blouin, Arnaud, Candresse, Thierry, Cao, Mengji, Cho, Won Kyong, Constable, Fiona, Sabanadzovic, Sead, Saldarelli, Pasquale, Tzanetakis, Ioannis, Villamor, Dan

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

Description of current taxonomy: *Banana* virus *X* is currently classified as unassigned species in the family *Betaflexiviridae.*

Proposed taxonomic change(s): We propose this species to be abolished.

Justification: We propose to abolish this betaflexivirid species due to the lack of Rep sequence data.

Submitted: 30/06/2024; *Revised:* -

TABLE 26 - *Betaflexiviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	species	*Banana virus X*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.022P.A.v1.Betaflexiviridae_abolishsp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.022P.A.v1.Betaflexiviridae_abolishsp.xlsx

2024.023P.Solemoviridae_rename_sp

Title: Rename two species in the genus *Solemovirus* (family *Solemoviridae)*

Authors: Sõmera M (merike.somera@taltech.ee), Fargette D, Filardo F, Ghafari M, Hebrard E, Sarmiento C, Thomas JE,

Summary:
Taxonomic rank(s) affected: species

Description of current taxonomy:
Riboviria;Orthornavirae;Pisuviricota;Pisoniviricetes;Sobelivirales;Solemoviridae;Sobemovirus;Cocksfoot mottle virus
Riboviria;Orthornavirae;Pisuviricota;Pisoniviricetes;Sobelivirales;Solemoviridae;Sobemovirus;Sobemovirus smamv

Proposed taxonomic change(s): Renaming of *Cocksfoot* mottle *virus* and of *Sobemovirus smamv*.

Justification: Renaming of *Cocksfoot* mottle *virus* to fulfill the ICTV's binomial naming mandate. Renaming of *Sobemovirus smamv* for consistency with other species in the family *Solemoviridae.*

Submitted: 28/06/2024; *Revised:* 07/10/2024

TABLE 27 - *Solemoviridae*, 2 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	*Sobemovirus CFMV*	*Cocksfoot mottle virus*
Rename taxon	species	*Sobemovirus SMAMV*	*Sobemovirus smamv*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.023P.A.v2.Solemoviridae_rename_sp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.023P.A.v2.Solemoviridae_rename_sp.xlsx

2024.024P.A.v1.Tymoviridae_abolish_sp

Title: Abolish two unassigned species in the family *Tymoviridae*

Authors: Hammond R (rose.hammond@usda.gov), Abrahamian P, Bejerman N, Mollov D, Nagata T, Sabanadzovic S

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

Description of current taxonomy: *Bombyx mori latent virus* and *Poinsettia mosaic virus* are currently classified as unassigned species in the family *Tymoviridae.*

Proposed taxonomic change(s): We propose these species to be abolished.

Justification: *Bombyx mori latent virus* and *Poinsettia mosaic virus* are unassigned species in the family *Tymoviridae,* therefore it is not possible to comply with the ICTV mandate of a binomial format for virus species. We propose to abolish these tymovirid species.

Submitted: 14/07/2024; *Revised:* -

TABLE 28 - *Tymoviridae*, 2 abolish taxa*

Operation	Rank	Abolished taxon name
Abolish taxon	species	*Bombyx mori latent virus*
Abolish taxon	species	*Poinsettia mosaic virus*

*Source / full text:
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.024P.A.v1.Tymoviridae_abolish_sp.docx
https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.024P.A.v1.Tymoviridae_abolish_sp.xlsx

Summary of taxonomy changes ratified by the International Committee on Taxonomy of Viruses (ICTV) - General Taxonomy Proposals, 2024

Main Text

Contents

2024.001G.Name_format_of_-Taxonomy_Proposal_Corrections

Title: Name format for expedited corrections of taxonomy proposals

Authors: Simmonds P (Peter.Simmonds@ndm.ox.ac.uk), Zerbini M, Lefkowitz EJ

Summary:
Brief description of current situation: The ratified taxonomy proposal (TP) 2020.002G.R.Expedited_error_correction describes how errors in the proposal spreadsheet may be corrected with approval from the ICTV President, Data Secretary and Proposals Secretary without need to re-submit a corrected TP in the next ICTV cycle. However, it was not specified how the name used for the correction TP should be formatted.

Proposed changes: We propose that the TP code will be suffixed with an X, and the name suffixed with the term "_Error_Correction"

Justification: It is useful to use a standard format that unambiguously links the original and the correction TPs together.

*Source
https://ictv.global/system/files/proposals/pending/General%20%28G%29%20proposals/2024.001G.A.v1.Name_format_of_-Taxonomy_Proposal_Corrections.docx

2024.002G.ICVCN-and-Statutes-harmonization

Title: Revise the ICTV Statutes and the ICVCN

Authors: Zerbini M (zerbini@ufv.br), Lefkowitz EJ (elliotl@uab.edu), Crane A, Kuhn J (kuhnjens@mail.nih.gov)

Summary:
Brief description of current situation: In recent years, numerous individual and several bulk changes were made to the ICTV's International Code of Virus Classification and Nomenclature (ICVCN) and the ICTV's Statutes. These changes left both documents somewhat in disarray, including problems associated with terminology consistency, orthography and grammar, clarity, and application examples.

Proposed changes: We propose several changes to both documents to improve their qualities.

*Source
https://ictv.global/system/files/proposals/pending/General%20%28G%29%20proposals/2024.002G.Uc.v2.ICVCN-and-Statutes-harmonization.docx

2024.003G.Nomination-Stuart-Siddell-as-Life-Member

Title: Nomination of Stuart Siddell as a Life Member of the ICTV

Authors: Lefkowitz EJ (elliotl@uab.edu), Zerbini M

Summary:

Given Dr. Stuart Siddell's long service as a member of ICTV Study Groups, Subcommittees, and the Executive Committee, given his key role in helping to define and modernize the guiding principles used to create the virus taxonomy, and given his calm demeanor, comforting presence, and unwavering friendship to members of the EC over many years, we hereby nominate Stuart Siddell as a Life Member of the ICTV.

*Source
https://ictv.global/system/files/proposals/pending/General%20%28G%29%20proposals/2024.003G.U.v1.Nomination-Stuart-Siddell-as-Life-Member.doc