

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

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2024.001D.A.v1.Alphabaculovirus-1nsp

Title: Create the new species *Alphabaculovirus alterhycuneeae* 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* nucleopolyhedrovirus 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 alterhycuneeae*”, 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	<i>Alphabaculovirus alterhycuneeae</i>	<i>Hypantria cuneae</i> 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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.001D.A.v1.Alphabaculovirus-1nsp.xlsx](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* (*Cirivirales: 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	<i>Circovirus dever</i>	bream circovirus 1	KF358279
New taxon	species	<i>Circovirus razbora</i>	Pseudorasbora circovirus 1	MN837844
New taxon	species	<i>Circovirus baizhenhe</i>	white-naped crane circovirus 1	MN928908
New taxon	species	<i>Circovirus patkany</i>	brown rat circovirus 1	OR553090
New taxon	species	<i>Circovirus python</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.002D.A.v2.Circoviridae_5ns.xlsx](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 LTA_g 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	<i>Alphapolyomavirus castoris</i>	Castor fiber polyomavirus 1	OR735477
New taxon	species	<i>Alphapolyomavirus epserotini</i>	Eptesicus serotinus polyomavirus 1	OK428546
New taxon	species	<i>Alphapolyomavirus myodaubentonii</i>	Myotis daubentonii polyomavirus 2	OK300052
New taxon	species	<i>Betapolyomavirus hipposideri</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.003D.A.v1.Polyomaviridae_4ns.xlsx](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	<i>Mastadenovirus marmotae</i>	marmot adenovirus 1	PP098964
New taxon	species	<i>Mastadenovirus capreoli</i>	roe deer adenovirus 1, adenovirus capreolus32301	BK066828
New taxon	species	<i>Mastadenovirus vespertilionis</i>	bat adenovirus 33390	BK066631
New taxon	species	<i>Mastadenovirus desmodi</i>	vampire bat adenovirus, adenovirus desmodus35011	BK066905
New taxon	species	<i>Mastadenovirus cardiodermatis</i>	heart-nosed bat adenovirus	PP711818
New taxon	species	<i>Mastadenovirus fructus</i>	Leschenault's rousette adenovirus	OR998962
New taxon	species	<i>Mastadenovirus arvicolinae</i>	vole adenovirus 1, myodes38640	BK066403
New taxon	species	<i>Aviadenovirus phalacrocoracidae</i>	great cormorant adenovirus 1	OR529407
New taxon	species	<i>Aviadenovirus oti</i>	Eurasian scops owl adenovirus 1, Otus scops adenovirus	ON843719
New taxon	species	<i>Aviadenovirus orioli</i>	black-naped oriole adenovirus, Oriolus adenovirus	MZ819701
New taxon	species	<i>Aviadenovirus roseae</i>	psittacine adenovirus 12	OR871655
New taxon	species	<i>Aviadenovirus cerasi</i>	duck adenovirus 6	MK757473
New taxon	species	<i>Barthadenovirus gerygonae</i>	grey warbler adenovirus 1	OQ986611
New taxon	species	<i>Barthadenovirus zootherae</i>	scaly thrush (<i>Zoothera dauma</i>) adenovirus 1	OR233592
New taxon	species	<i>Barthadenovirus varani</i>	varanus adenovirus 37597	BK066675
New taxon	species	<i>Barthadenovirus zootocae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.004D.A.v1.Adenoviridae_16ns.xlsx](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	<i>Alphabaculovirus pastagnalis</i>	Parapoynx stagnalis nucleopolyhedrovirus	ON704650
New taxon	species	<i>Alphabaculovirus pavitrealis</i>	Palpita vitrealis nucleopolyhedrovirus	OL685370
New taxon	species	<i>Alphabaculovirus spocosmioidis</i>	Spodoptera cosmioides nucleopolyhedrovirus	MK419955
New taxon	species	<i>Betabaculovirus psincretae</i>	Psilogramma increta granulovirus	ON803509

TABLE 6 - Baculoviridae, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	species	<i>Alphabaculovirus altermaconfiguratae</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.005D.A.v1.Baculoviridae_4nsp_1absp.xlsx](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	<i>Filamentoviridae</i>		
New taxon	genus	<i>Alphafilamentovirus</i>		
New taxon	species	<i>Alphafilamentovirus leboulardi</i>	<i>Leptopilina boulardi</i> filamentous virus	KY009685
New taxon	genus	<i>Betafilamentovirus</i>		
New taxon	species	<i>Betafilamentovirus cocongregatae</i>	<i>Cotesia congregata</i> filamentous virus 1	OY734801
New taxon	species	<i>Betafilamentovirus altercocongregatae</i>	<i>Cotesia congregata</i> 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.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](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: Péntzes 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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.008D.A.v2.Parvoviridae_55nsp.xlsx](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	<i>Upsilononorquevirus ursid6</i>	<i>Dalettorquevirus</i>	<i>Upsilononorquevirus</i>	<i>Dalettorquevirus ursid6</i>
Move; rename taxon	species	<i>Sadetorquevirus hominid8</i>	<i>Hetorquevirus</i>	<i>Sadetorquevirus</i>	<i>Hetorquevirus hominid8</i>
Move; rename taxon	species	<i>Sadetorquevirus hominid7</i>	<i>Hetorquevirus</i>	<i>Sadetorquevirus</i>	<i>Hetorquevirus hominid7</i>
Move; rename taxon	species	<i>Petorquevirus ixodi1</i>	<i>Thetorquevirus</i>	<i>Petorquevirus</i>	<i>Thetorquevirus ixodi1</i>
Move; rename taxon	species	<i>Petorquevirus canid1</i>	<i>Thetorquevirus</i>	<i>Petorquevirus</i>	<i>Thetorquevirus canid1</i>

Move; rename taxon	species	<i>Petorquevirus viver4</i>	<i>Thetatorquevirus</i>	<i>Petorquevirus</i>	<i>Thetatorquevirus viver4</i>
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TABLE 11 - *Anelloviridae*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	genus	<i>Dalettorquevirus</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.009D.A.v2.Anelloviridae_4ngen_70nsp.xlsx](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	<i>Singelaviria</i>		
New taxon	kingdom	<i>Abadenavirae</i>		
New taxon	phylum	<i>Produgelaviricota</i>		
New taxon	class	<i>Belvinaviricetes</i>		
New taxon	subphylum	<i>Prepoliviricotina</i>		
New taxon	subphylum	<i>Polisuviricotina</i>		
New taxon	class	<i>Pharingeaviricetes</i>		
New taxon	class	<i>Aquintoviricetes</i>		
New taxon	order	<i>Archintovirales</i>		
New taxon	family	<i>Phypoliviridae</i>		
New taxon	genus	<i>Tetrivirus</i>		
New taxon	species	<i>Tetrivirus crimaeaeense</i>	Tetraselmis viridis virus S1	HQ332143
New taxon	class	<i>Mriyaviricetes</i>		

TABLE 13 - *Varidnaviria*, 11 move taxa*

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

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	<i>Virophaviricetes</i>	<i>Preplasmiviricota</i>	<i>Polisuviricotina</i>	<i>Maveriviricetes</i>
Move; rename taxon	family	<i>Eupolintoviridae</i>	<i>Preplasmiviricota</i>	<i>Polisuviricotina</i>	<i>Adintoviridae</i>
Move; rename taxon	order	<i>Amphintovirales</i>	<i>Preplasmiviricota</i>	<i>Polisuviricotina</i>	<i>Orthopolintovirales</i>

TABLE 15 - *Varidnaviria*, 1 rename taxon*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	species	<i>Asfivirus haemorrhagiae</i>	<i>African swine fever virus</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.010D.A.v2.Varidnaviria_reorg.xlsx](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 *Cressdnviricota* 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	<i>Commensaviricota</i>
New taxon	class	<i>Cardeaviricetes</i>
New taxon	order	<i>Sanitavirales</i>

TABLE 17 - *Shotokuvirae*, 1 move taxon*

Operation	Rank	Taxon name	Old parent taxon	New parent taxon
Move taxon	family	<i>Anelloviridae</i>		<i>Monodnaviria</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Animal%20DNA%20viruses%20and%20Retroviruses%20\(D\)%20proposals/2024.012D.A.v2.Shotokuvirae_newphylum.xlsx](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	<i>Semotivirus mooseanophelae</i>	<i>Anopheles gambiae</i> <i>Moose virus</i>
Rename taxon	species	<i>Semotivirus tamyantheraeae</i>	<i>Antheraea semotivirus</i> <i>Tamy</i>
Rename taxon	species	<i>Semotivirus tasascaridis</i>	<i>Ascaris lumbricoides</i> <i>Tas virus</i>
Rename taxon	species	<i>Semotivirus paobombycis</i>	<i>Bombyx mori</i> <i>Pao virus</i>
Rename taxon	species	<i>Semotivirus certredicum</i>	<i>Caenorhabditis elegans</i> <i>Cer13 virus</i>
Rename taxon	species	<i>Semotivirus beldrosophilae</i>	<i>Drosophila melanogaster</i> <i>Bel virus</i>
Rename taxon	species	<i>Semotivirus roodrosophilae</i>	<i>Drosophila melanogaster</i> <i>Roo virus</i>
Rename taxon	species	<i>Semotivirus maxdrosophilae</i>	<i>Drosophila semotivirus</i> <i>Max</i>
Rename taxon	species	<i>Semotivirus ninjadrosophilae</i>	<i>Drosophila simulans</i> <i>Ninja virus</i>

Rename taxon	species	<i>Semotivirus sinbadschistosomae</i>	<i>Schistosoma semotivirus Sinbad</i>
Rename taxon	species	<i>Semotivirus suzutakifugu</i>	<i>Takifugu rubripes Suzu virus</i>

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