

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

Main Text

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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, Digiario M (digiario@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	<i>Emaravirus clematis</i>	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.docx)
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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	<i>Allexivirus rehmanniae</i>	Rehmannia allexivirus	PP097219
New taxon	species	<i>Botrexvirus unosclerotinae</i>	Sclerotinia sclerotiorum alphaflexivirus 1	ON993219
New taxon	species	<i>Botrexvirus duosclerotinae</i>	Sclerotinia sclerotiorum alphaflexivirus 2	OQ865609
New taxon	species	<i>Potexvirus ecsadenii</i>	Adenium obesum virus X; desert rose mottle virus	OR039325; OR240084
New taxon	species	<i>Potexvirus chaenostomae</i>	Chaenostoma potexvirus	OL979628
New taxon	species	<i>Potexvirus ecshibisci</i>	Hibiscus virus X	PP115950
New taxon	species	<i>Potexvirus ecscaricae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.002P.A.v1.Alphaflexiviridae_7nsp.xlsx](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	<i>Orthotospovirus eustomae</i>	lisianthus necrotic ringspot virus	MF469045; MF469046; MF469047
New taxon	species	<i>Orthotospovirus fatsiae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.003P.A.v1.Tospoviridae_2nsp.xlsx](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, Schravessande 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	<i>Olpivirus lactucae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.004P.A.v2.Konkoviridae_1nsp.xlsx](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, Stabolone 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	<i>Badnavirus fatsiae</i>	Fatsia badnavirus 1	OM540428
New taxon	species	<i>Badnavirus tetainflatheobromae</i>	cacao swollen shoot GhanaT virus	MN179342
New taxon	species	<i>Badnavirus ziziphi</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.005P.A.v1.Caulimoviridae_3nsp.xlsx](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	<i>Higrevirus amurense</i>	Phellodendron-associated higre-like virus	RNA1: OP324809; RNA2: OP324810; RNA3: OP324811
New taxon	species	<i>Higrevirus pistaciae</i>	Pistachio virus X	RNA1: MT334620; RNA2: MT334619; RNA3: MT334618
New taxon	species	<i>Cilevirus pistaciae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.006P.A.v1.Kitaviridae_3nsp.xlsx](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	<i>Capulavirus trifolii</i>	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.docx)

[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.007P.A.v1.Geminiviridae_Capulavirus_1nsp.xlsx](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 myrica*.

Justification:

Similar to members of the *Citlodavirus* genus, members of the proposed new species *Citlodavirus apijamaicaense* and *Citlodavirus myrica* 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	<i>Citlodavirus apijamaicaense</i>	apiscitlodal virus	PP467584
New taxon	species	<i>Citlodavirus myricae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.008P.A.v1.Geminiviridae_Citlodavirus_2nsp.xlsx](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
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New taxon	species	<i>Mastrevirus urochloareunionense</i>	Urochloa decumbens associated virus	OQ451139
New taxon	species	<i>Mastrevirus nomiae</i>	Nomiamastrel virus	PP467585
New taxon	species	<i>Mastrevirus brachypodiumprimi</i>	Brachypodium phoenicoides associated virus 1	OR596402
New taxon	species	<i>Mastrevirus bothriochloae</i>	Bothriochloa barbinodis associated virus	OR596403
New taxon	species	<i>Mastrevirus brachypodiumsecundi</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.009P.A.v1.Geminiviridae_Mastrevirus_5nsp.xlsx](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	<i>Begomovirus chuxiongense</i>	tomato leaf curl Chuxiong virus	OR543988
New taxon	species	<i>Begomovirus solanumaureusreti</i>	tomato golden net virus	MT214095
New taxon	species	<i>Begomovirus solanumflavusreti</i>	tomato yellow net viurs	MT214096
New taxon	species	<i>Begomovirus whitaniae</i>	Withania leaf curl virus	OP617239
New taxon	species	<i>Begomovirus sidaflavusfolii</i>	sida chlorotic leaf vrius	MN013784; MN013785
New taxon	species	<i>Begomovirus cajani</i>	Cajanus scarabaeoides yellow mosaic virus	OM397101; OM397102
New taxon	species	<i>Begomovirus hortuscrotoni</i>	garden croton enation leaf curl virus	MW816855; MW816857
New taxon	species	<i>Begomovirus jatrophauntureense</i>	Jatropha leaf curl Guntur virus	MZ217773

New taxon	species	<i>Begomovirus hyptidis</i>	Hyptis golden mosaic virus	ON073795; ON073796
New taxon	species	<i>Begomovirus galii</i>	Galium leaf distortion virus	OL689630
New taxon	species	<i>Begomovirus myanmarensis</i>	tobacco curly shoot Myanmar virus	MK920410
New taxon	species	<i>Begomovirus caboniensis</i>	Cnidoscolus mild mosaic virus	MZ465527; MZ465585
New taxon	species	<i>Begomovirus pyrenacanthae</i>	Pyrenacantha yellow mosaic virus	MZ390982; MZ390984
New taxon	species	<i>Begomovirus puerense</i>	tobacco leaf curl Puer virus	MZ465370
New taxon	species	<i>Begomovirus solanumdistorsionis</i>	tomato mottle leaf distortion virus	MW561191; MW650837
New taxon	species	<i>Begomovirus alceacrispi</i>	hollyhock vein yellowing virus	LK028571
New taxon	species	<i>Begomovirus muntiflavi</i>	Muntingia yellow spot virus	MW032664; MW032665
New taxon	species	<i>Begomovirus flavintervenae</i>	tomato interveinal yellowing virus	MW057360
New taxon	species	<i>Begomovirus sidaflavitessellati</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.010P.A.v1.Geminiviridae_Begomovirus_19nsp.xlsx](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	<i>Ilarvirus ApNMV</i>	apple necrotic mosaic virus	LC108993; LC108994; LC108995
New taxon	species	<i>Ilarvirus BabIV1</i>	babaco ilarvirus 1	OQ256238; OQ256239; OQ256240
New taxon	species	<i>Ilarvirus TIV1</i>	tomato ilarvirus 1	OL472057; OL472058; OL472059
New taxon	species	<i>Ilarvirus ToNSV</i>	tomato necrotic spot virus	MH780154; MH780155; MH780156

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[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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.011P.A.v2.Bromoviridae_4nsp.xlsx](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 parisflavitesellati
Potyvirus catharanthiflavitesellati
Potyvirus polygonatimaculae
Potyvirus crocitesellati
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: 11/06/2024; Revised: 21/09/2024

TABLE 12 - *Potyviridae*, 11 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	<i>Potyvirus aconiti</i>	Aconitum virus 2	MZ389235
New taxon	species	<i>Potyvirus puerariae</i>	Kudzu chlorotic ring blotch virus	OQ148665
New taxon	species	<i>Potyvirus alilii</i>	Lily virus A	OR879085
New taxon	species	<i>Potyvirus parisflavitesellati</i>	Paris yunnanensis mosaic chlorotic virus	ON871824
New taxon	species	<i>Potyvirus catharanthiflavitesellati</i>	Periwinkle mild yellow mosaic virus	PP382205
New taxon	species	<i>Potyvirus polygonatimaculae</i>	Polygonatum kingianum mottle virus	ON428226
New taxon	species	<i>Potyvirus crocitesellati</i>	Saffron yellow mosaic virus	OK632024
New taxon	species	<i>Potyvirus galanthi</i>	Snowdrop virus Y	OP871788

New taxon	genus	<i>Phragmivirus</i>		
New taxon	species	<i>Phragmivirus phragmii</i>	Common reed chlorotic stripe virus	KY612317
New taxon	species	<i>Phragmivirus spartinae</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.012P.Uc.v2.Potyviridae_1ng_10nsp.xlsx](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, Wetzell 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: *Mersevivirus*

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 *Mersevivirus*: *Mersevivirus mercurialis*, *Mersevivirus paris*, *Mersevivirus boehmeriae*, *Mersevivirus jujubae*

Create two new species in the genus *Nepovirus*: *Nepovirus betaparis*, *Nepovirus mirae*

Create three new species in the genus *Sadwavirus*: *Sadwavirus cattleyae*, *Sadwavirus gymnaeae*, *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 trifocoidentale*, *Waikavirus thapsiae*, *Waikavirus violae*, *Waikavirus carotae*, *Waikavirus celtis*, *Waikavirus pittospori*

Justification:

The creation of the proposed new genus *Mersevivirus* is justified based on the distinct genome organization of *Mersevivirus mercurialis*, *Mersevivirus paris*, *Mersevivirus boehmeriae*, and *Mersevivirus 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	<i>Mersevirus</i>		
New taxon	species	<i>Mersevirus boehmeriae</i>	Boehmeria nivea secovirus	BK061322; BK061323
New taxon	species	<i>Mersevirus jujubae</i>	jujube-associated virus 1	MT375548; MT375547
New taxon	species	<i>Mersevirus mercurialis</i>	Mercurialis secovirus 1	OR544055; OR544056
New taxon	species	<i>Mersevirus paris</i>	Paris polyphylla secovirus 2	BK061330; BK061331
New taxon	subgenus	<i>Actinidivirus</i>		
New taxon	species	<i>Waikavirus betacamelliae</i>	Camellia virus B	BK062984
New taxon	species	<i>Waikavirus carotae</i>	carrot psyllid-borne associated virus	OM801008
New taxon	species	<i>Waikavirus celtis</i>	hackberry virus A	OP533794
New taxon	species	<i>Waikavirus hirtae</i>	Ficus hirta waikavirus	BK062987
New taxon	species	<i>Waikavirus juglandis</i>	Juglans nigra waikavirus	BK062989
New taxon	species	<i>Waikavirus pittospori</i>	Pittosporum tobira virus	OR659471
New taxon	species	<i>Waikavirus populi</i>	Populus alba waikavirus	BK062992
New taxon	species	<i>Waikavirus querci</i>	Quercus robur waikavirus	BK062996
New taxon	species	<i>Waikavirus trifocoidentale</i>	Trifolium occidentale waikavirus	BK063000
New taxon	subgenus	<i>Ritunrivirus</i>		
New taxon	species	<i>Waikavirus ajugae</i>	Ajuga Reptans waikavirus	BK062980
New taxon	species	<i>Waikavirus anacycli</i>	Anacyclus depressus waikavirus	BK062979
New taxon	species	<i>Waikavirus eleocharis</i>	Eleocharis dulcis waikavirus	BK062986
New taxon	species	<i>Waikavirus ligustici</i>	Ligusticum chuanxiong waikavirus	BK062990
New taxon	species	<i>Waikavirus mertensiae</i>	Mertensia paniculata waikavirus	BK062991
New taxon	species	<i>Waikavirus pedicularis</i>	Pedicularis rex waikavirus	BK062993
New taxon	species	<i>Waikavirus primulae</i>	Primula vulgaris waikavirus	BK062995
New taxon	species	<i>Waikavirus ranunculi</i>	Ranunculus cantoniensis waikavirus	BK062997
New taxon	species	<i>Waikavirus thapsiae</i>	Thapsia villosa waikavirus	BK063001
New taxon	species	<i>Waikavirus thymi</i>	Thymus vulgaris waikavirus	BK062999
New taxon	species	<i>Waikavirus violae</i>	Viola inconspicua waikavirus	BK063002
New taxon	species	<i>Fabavirus betavitis</i>	grapevine secovirus	OR947508; OR947509
New taxon	species	<i>Fabavirus cirsii</i>	cirsium virus A	OP794357; OP794358
New taxon	species	<i>Nepovirus betaparis</i>	Paris polyphylla secovirus 1	BK061328; BK061329
New taxon	species	<i>Nepovirus mirae</i>	Prunus mira virus A	BK064709; BK064710
New taxon	species	<i>Sadwavivirus cattleyae</i>	Cattleya purple ringspot virus	OR439368; OR439369

New taxon	species	<i>Sadwavirus gymnemae</i>	Gymnema sylvestre virus 1	BK062888; BK062889
New taxon	species	<i>Sadwavirus chysanthemi</i>	chrysanthemum sadwavirus	OR413567; OR413568
New taxon	species	<i>Torradovirus arctii</i>	burdock mosaic virus	OQ087134; OQ087135
New taxon	species	<i>Torradovirus nanorugosum</i>	potato rugose stunting virus	ON871623; ON871624
New taxon	species	<i>Torradovirus physalis</i>	Physalis torrado virus	MZ357183; MZ357184

TABLE 14 - *Secoviridae*, 13 move taxa*

Operation	Rank	Taxon name	Old parent taxon	New parent taxon
Move taxon	species	<i>Waikavirus actinidiae</i>	<i>Waikavirus</i>	<i>Actinidivirus</i>
Move taxon	species	<i>Waikavirus camelliae</i>	<i>Waikavirus</i>	<i>Actinidivirus</i>
Move taxon	species	<i>Waikavirus diospyri</i>	<i>Waikavirus</i>	<i>Actinidivirus</i>
Move taxon	species	<i>Waikavirus liegense</i>	<i>Waikavirus</i>	<i>Actinidivirus</i>
Move taxon	species	<i>Waikavirus rhododendri</i>	<i>Waikavirus</i>	<i>Actinidivirus</i>
Move taxon	species	<i>Waikavirus brassicae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus campanulae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus lactucae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus oryzae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus ribesnigri</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus rosae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus trifolii</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>
Move taxon	species	<i>Waikavirus zeae</i>	<i>Waikavirus</i>	<i>Ritunrivirus</i>

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[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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.013P.Uc.v2.Secoviridae_1ng_2nsg_34nsp.xlsx](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.xlsx

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 - *Rhabdoviridae*, 2 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	species	<i>Alphanucleorhabdovirus babaci</i>	babaco nucleorhabdovirus 1	OQ256237
New taxon	species	<i>Betanucleorhabdovirus paridis</i>	Paris yunnanensis rhabdovirus 1	OL439478

*Source / full text:

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[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.014P.A.v1.Rhabdoviridae_2nsp.xlsx](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.gov.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	<i>Cytorhabdovirus brassicae</i>
Abolish taxon	species	<i>Cytorhabdovirus festucae</i>
Abolish taxon	species	<i>Cytorhabdovirus sonchi</i>
Abolish taxon	species	<i>Cytorhabdovirus tritici</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.015P.A.v2.Rhabdoviridae_Cytorhabdovirus_splitgen.xlsx](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	<i>Trirhavirus</i>		
New taxon	species	<i>Trirhavirus alni</i>	<i>Alnus trirhavirus</i> 1	BK064247; BK064248; BK064249
New taxon	species	<i>Trirhavirus chrysanthemi</i>	<i>Chrysanthemum trirhavirus</i> 1	BK064250; BK064251; BK064252

New taxon	species	<i>Trirhavirus erysimi</i>	Erysimum trirhavirus 1	BK064253; BK064254; BK064255
New taxon	species	<i>Trirhavirus medicagonis</i>	Medicago trirhavirus	BK064256; BK064257; BK064258
New taxon	species	<i>Trirhavirus picridis</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.016P.A.v1.Rhabdoviridae_1ngen_5nsp.xlsx](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	<i>Ahlum waterborne virus</i>
Abolish taxon	species	<i>Bean mild mosaic virus</i>
Abolish taxon	species	<i>Chenopodium necrosis virus</i>
Abolish taxon	species	<i>Cucumber soil-borne virus</i>
Abolish taxon	species	<i>Weddel waterborne virus</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.017P.A.v1.Tombusviridae_abolishsp.xlsx](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 zae*, 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	<i>Machlomovirus liegense</i>	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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.018P.A.v1.Tombusviridae_1nsp.xlsx](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	<i>Velarivirus gembloutense</i>	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.docx)

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	<i>Papanivirus panici</i>	<i>Panicum papanivirus 1</i>
Rename taxon	species	<i>Virtovirus tabaci</i>	<i>Tobacco virtovirus 1</i>
Rename taxon	species	<i>Albetovirus alphatabaci</i>	<i>Tobacco albetovirus 1</i>
Rename taxon	species	<i>Albetovirus betatabaci</i>	<i>Tobacco albetovirus 2</i>
Rename taxon	species	<i>Albetovirus gammatabaci</i>	<i>Tobacco albetovirus 3</i>
Rename taxon	species	<i>Aumaivirus maidis</i>	<i>Maize aumaivirus 1</i>

TABLE 24 - *Riboviria*, 5 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	family	<i>Sarthroviridae</i>	<i>Tombendovirales</i>
Move taxon	genus	<i>Papanivirus</i>	<i>Tombendovirales</i>
Move taxon	genus	<i>Virtovirus</i>	<i>Tombendovirales</i>
Move taxon	genus	<i>Albetovirus</i>	<i>Tonesaviridae</i>
Move taxon	genus	<i>Aumaivirus</i>	<i>Tonesaviridae</i>

TABLE 25 - *Riboviria*, 4 new taxa*

Operation	Rank	New taxon name
New taxon	order	<i>Tombendovirales</i>
New taxon	family	<i>Pamosaviridae</i>
New taxon	family	<i>Tomosaviridae</i>
New taxon	family	<i>Tonesaviridae</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.021P.A.v1.Riboviria_1nord.xlsx](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	<i>Banana virus X</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.022P.A.v1.Betaflexiviridae_abolishsp.xlsx](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: Sömera 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	<i>Sobemovirus CFMV</i>	<i>Cocksfoot mottle virus</i>
Rename taxon	species	<i>Sobemovirus SMAMV</i>	<i>Sobemovirus smamv</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.023P.A.v2.Solemoviridae_rename_sp.xlsx](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	<i>Bombyx mori latent virus</i>
Abolish taxon	species	<i>Poinsettia mosaic virus</i>

*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.docx)
[https://ictv.global/system/files/proposals/pending/Plant%20virus%20\(P\)%20proposals/2024.024P.A.v1.Tymoviridae_abolish_sp.xlsx](https://ictv.global/system/files/proposals/pending/Plant%20virus%20(P)%20proposals/2024.024P.A.v1.Tymoviridae_abolish_sp.xlsx)