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

Contents

2025.001P.Ac.v3.Aspiviridae_splitgen_1ng_14nsp

Title: Split one genus, and create one genus and 14 species in the family *Aspiviridae*

Authors: Nicolas Bejerman, Humberto Debat, Selma Gago-Zachert, John Hammond, Laura Miozzi, Tomohide Natsuaki, Yutaro Neriya , Vicente Pallás, Carina A Reyes, Mark PS Rivarez, Takahide Sasaya , Ioannis Tzanetakis, Anna Maria Vaira, Martin Verbeek

Summary:
Taxonomic rank(s) affected:
Genus *Ophiovirus, family Aspiviridae*

Description of current taxonomy:
The family *Aspiviridae* comprises the single genus *Ophiovirus.* Eight virus species are currently classified in the genus *Ophiovirus,* six of which infect dicotyledonous plants of widely different taxonomy, and the other two have monocot species as their plant host. The assignment of viruses to this genus is based on the placement of viruses in a Maximum Likelihood tree inferred from complete RdRp or CP protein sequences.

Proposed taxonomic change(s):
Split the genus *Ophiovirus,* creating one new genus *("Miraophiovirus")* and assigning the current *Ophiovirus* species to the appropriate genus; create 14 new species in the family *Aspiviridae.*

Justification:
Recently, 14 new putative ophioviruses were discovered, which we propose to classify into 14 new species. The phylogenetic relationships of the now significantly expanded number of known ophiovirus species provide support for splitting the genus *Ophiovirus* to establish two genera *(Ophiovirus* and *"Miraophiovirus")* that represent distinct evolutionary lineages.

Submitted: 16/05/2025; *Revised:* 08/12/2025

TABLE 1 - *Aspiviridae*, 15 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Ophiovirus allii*	Allium ophiovirus	BK062657; BK062658; BK062659
New taxon	Species	*Ophiovirus arctotis*	Arctotis ophiovirus	BK062660; BK062661; BK062662
New taxon	Species	*Ophiovirus chrysanthemi*	Chrysanthemum ophiovirus	BK062669; BK062670; BK062671
New taxon	Species	*Ophiovirus citrulli*	Citrullus ophiovirus	BK062675; BK062676; BK062677
New taxon	Species	*Ophiovirus daturae*	Datura ophiovirus	BK062682; BK062683; BK062684
New taxon	Species	*Ophiovirus gentianae*	Gentiana ophiovirus	BK062690; BK062691; BK062692
New taxon	Species	*Ophiovirus osteospermi*	Osteospermum ophiovirus	BK062711; BK062712; BK062713
New taxon	Genus	*Miraophiovirus*		
New taxon	Species	*Miraophiovirus caladeniae*	Caladenia ophiovirus	BK062666; BK062667; BK062668
New taxon	Species	*Miraophiovirus carotae*	carrot ophiovirus 1	OM419178; OM419179; OM419180; OM419181
New taxon	Species	*Miraophiovirus cyrtomii*	Cyrtomium ophiovirus	BK062679; BK062680; BK062681
New taxon	Species	*Miraophiovirus erythranthis*	Erythranthe ophiovirus	BK062687; BK062688; BK062689
New taxon	Species	*Miraophiovirus lepidoziae*	Lepidozia ophiovirus	BK062699; BK062700; BK062701
New taxon	Species	*Miraophiovirus violae*	Viola ophiovirus	BK062735; BK062736; BK062737

New taxon	Species	*Miraophiovirus xerochrysi*	Xerochrysum ophiovirus	BK062740; BK062741; BK062742

TABLE 2 - *Aspiviridae*, 6 move; rename taxa*

Operation	**Rank**	**New taxon name**	**Old taxon name**	**New parent taxon**	**Old parent taxon**
Move; rename taxon	Species	*Miraophiovirus capsici*	*Ophiovirus capsici*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus freesiae*	*Ophiovirus freesiae*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus lactucae*	*Ophiovirus lactucae*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus mirafioriense*	*Ophiovirus mirafioriense*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus ranunculi*	*Ophiovirus ranunculi*	*Riboviria*	*Riboviria*
Move; rename taxon	Species	*Miraophiovirus tulipae*	*Ophiovirus tulipae*	*Riboviria*	*Riboviria*

2025.002P.Ac.v3.Alphaflexiviridae_Allexivirus_1nsp

Title: Create one (1) new species in the family *Alphaflexiviridae*

Authors: Peter Abrahamian, Miguel A. Aranda, Thierry Candresse, Livia Donaire, John Hammond, Beata Hasiów-Jaroszewska, Luisa Rubino, Anna Maria Vaira

Summary:
Taxonomic rank(s) affected:
Genus *Allexivirus* in the family *Alphaflexiviridae*

Description of current taxonomy:
The *family Alphaflexiviridae* currently includes 72 virus species in genera *Allexivirus* (14), *Botrexvirus* (3), *Lolavirus* (1), *Platypuvirus* (1), *Potexvirus* (52) and *Sclerodarnavirus* (1).

Proposed taxonomic change(s):
This taxonomic proposal considers the creation of one (1) new species belonging to genus *Allexivirus* within the family *Alphaflexiviridae.*

Justification:
Throughout the family, isolates of different species should have less than 72% nucleotide identity (or 80% amino acid identity) between their respective coat protein or polymerase genes (or proteins). Viruses from different genera usually have less than about 45% nucleotide identity in these genes. The nucleotide and amino acid sequences of the virus belonging to the newly proposed species fit well within these demarcation criteria.

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

TABLE 3 - *Alphaflexiviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Allexivirus sauroandrogyni*	Sauropus androgynus virus	PQ177843

2025.003P.A.v3.Caulimoviridae_Badnavirus_1nsp

Title: Create one (1) new species in the genus *Badnavirus*

Authors: Marie Umber , Indranil Dasgupta , Andrew D.W. Geering , Anders Hafrén , Roger Hull , Jan Kreuze , Scott M. Leisner , Emmanuelle Muller , Hanu Pappu , Mikhail Pooggin , Katja Richert-Poeggeler , Susan Seal , Livia Stavolone , Pierre Yves Teycheney

Summary:
Taxonomic rank(s) affected:
Genus *Badnavirus* in the *family Caulimoviridae*

Description of current taxonomy:
The family *Caulimoviridae* [1] currently comprises 11 genera whose members share similar genome organization. The molecular species demarcation criterion is < 80% identity of nucleotide sequences in the reverse transcriptase (RT) / ribonuclease H (RNase H) region of the polymerase. Genus *Badnavirus* [2] currently includes 74 species and is the largest genus within the *family Caulimoviridae.*

Proposed taxonomic change(s):
We propose the creation of one new species in the genus *Badnavirus: "Badnavirus urticae"*

Justification:
The complete genomes of nettle badnavirus 1 (NBV1), was sequenced and published recently. Its organization is similar to that of other members of genus *Badnavirus.* Phylogenetic analyses place NBV1 in this genus as distinct representative of a novel species.

Submitted: 13/06/2025; *Revised:* 28/08/2025

TABLE 4 - *Caulimoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Badnavirus urticae*	nettle badnavirus 1	PP792697

2025.004P.Ac.v3.Kitaviridae_13nsp

Title: Create one (1) new species in the genus *Cilevirus,* and 12 novel species in the genus *Blunervirus,* family *Kitaviridae,* order *Martellivirales.*

Authors: Caixia Yang, Avijit Roy, Juliana Freitas-Astúa, Antonio Tiberini, Li Jun-Min, Kavi Sidharthan, Mónica Madariaga-Villarroel, Sergey Y. Morozov, Pedro L. Ramos-González

Summary:
Taxonomic rank(s) affected:
Genera *Cilevirus* and *Blunervirus* in the *family Kitaviridae*

Description of current taxonomy:
Kitaviruses comprise a group of plant-infecting viruses with single-stranded (ss), positive-sense (+), segmented RNA genomes. The family *Kitaviridae,* order *Martellivirales,* consists of three genera, currently including eight species in the genus *Cilevirus,* and three in each of the *genera Higrevirus* and

Blunervirus. Most members of the genera *Cilevirus* and *Higrevirus* are transmitted by tenuipalpid mites of the genus *Brevipalpus,* whereas at least two blunerviruses are shown to be transmitted by eriophyid mites.

Proposed taxonomic change(s):
Create one and 12 new species in the genera *Cilevirus and Blunervirus,* respectively, in the family *Kitaviridae,* order *Martellivirales.*

Justification:
Novel identified viruses possess relatively high nucleotide sequence identity, a compatible genomic organization, and/or a phylogenetic relationship with members of the known species within the family *Kitaviridae.* Biological and molecular characterization of a virus identified in large periwinkle *(Vinca major)* plants demonstrated that it should be classified into a novel species within the genus *Cilevirus.* Genomic analyses of other 12 novel viruses, obtained from either original high-throughput sequencing (HTS) data or publicly accessible sequence repositories, indicate they belong to new species in the genus *Blunervirus.* Deduced amino acid sequences of these novel viruses share less than 70% amino acid sequence identity with those of known and novel tentative blunerviruses. Phylogenetic analyses using the replication proteins place these novel viruses in the clade containing viruses of the known species of blunerviruses.

Submitted: 06/03/2025; *Revised:* 20/08/2025

TABLE 5 - *Kitaviridae*, 13 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Cilevirus chilense*	Vinca ringspot virus	RNA1: OQ116675; RNA2: OQ116676
New taxon	Species	*Blunervirus cinnamomi*	camphor tree blunervirus 1	RNA1: BK068192; RNA2: BK068193; RNA3: BK068194; RNA4: BK068195
New taxon	Species	*Blunervirus torreyae*	Chinese nutmeg tree blunervirus 1	RNA1: BK068220; RNA2: BK068221; RNA3: BK068222; RNA4: BK068223
New taxon	Species	*Blunervirus chrysanthemi*	Chrysanthemum blunervirus 1	RNA1: BK068200; RNA2: BK068201; RNA3: BK068202; RNA4: BK068203
New taxon	Species	*Blunervirus cupressus*	cypress blunervirus 1	RNA1: BK068188; RNA2: BK068189; RNA3: BK068190; RNA4: BK068191
New taxon	Species	*Blunervirus festucae*	Festuca sinensis blunervirus 1	RNA1: BK068204; RNA2: BK068205; RNA3: BK068206; RNA4: BK068207
New taxon	Species	*Blunervirus quercus*	oak blunervirus 1	RNA1: BK068208; RNA2: BK068209; RNA3: BK068210; RNA4: BK068211
New taxon	Species	*Blunervirus portulacae*	purslane blunervirus 1	RNA1: BK068216; RNA2: BK068217; RNA3: BK068218; RNA4: BK068219

New taxon	Species	*Blunervirus liquidambarum*	sweetgum blunervirus 1	RNA1: BK068212; RNA2: BK068213; RNA3: BK068214; RNA4: BK068215
New taxon	Species	*Blunervirus tritici*	wheat blunervirus 1	RNA1: BK068196; RNA2: BK068197; RNA3: BK068198; RNA4: BK068199
New taxon	Species	*Blunervirus paulowniae*	Paulownia tomentosa blunervirus	RNA1: GEFV01158142; RNA2: GEFV01018191; RNA3: GEFV01018861; RNA4: GEFV01018726
New taxon	Species	*Blunervirus ulmi*	elm blunervirus 1	RNA1: OL865294; RNA2: OL865295; RNA3: OL865296; RNA4: OL865297
New taxon	Species	*Blunervirus mali*	apple blunervirus 1	RNA1: OL344039; RNA2: OL344040; RNA3: OL344041; RNA4: OL344042; RNA5: OL344043

2025.005P.Benyviridae_Benyvirus_1nsp

Title: Create one new species in the *genus* Benyvirus *(Hepelivirales: Benyviridae)*

Authors: Juliana B. Valente, Fernando P. Sartori, Lucas A. Stempkowski, Monica Farias, Paulo R. Kuhnem, Douglas Lau, Thor V.M. Fajardo, Antonio Nhani Junior, Ricardo T. Casa, Amauri Bogo, Fábio N. Silva

Summary:
Taxonomic rank(s) affected:
Genus *Benyvirus* in the *family Benyviridae*

Description of current taxonomy:
Riboviria › Orthornavirae › Kitrinoviricota › Alsuviricetes › Hepelivirales › Benyviridae › *Benyvirus*
The genus *Benyvirus* consists of four species.

Proposed taxonomic change(s):
Create one species in *the genus Benyvirus: "Benyvirus tritici"*

Justification:
Based on the genomic organization of *P. graminis-associated* WhSMV-infected plant samples, as well as the nucleotide and amino acid sequences of the viral isolates characterized in this study, we propose that wheat stripe mosaic virus (WHSMV) is classified into a novel putative species within the family *Benyviridae,* for which the name *"Benyvirus tritici"* is *suggested.*

Submitted: 06/03/2025; *Revised:* 15/10/2025

TABLE 6 - *Benyviridae*, 1 new taxon*

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

New taxon	Species	*Benyvirus tritici*	wheat stripe mosaic virus	RNA1: MH151795; RNA 2: MH151801

2025.006P.Ac.v3.Konkoviridae_5nsp

Title: Create five (5) new species in the genus *Olpivirus (Hareavirales: Konkoviridae]*

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

Summary:Taxonomic rank(s) affected:
Genus *Olpivirus* in the *family Konkoviridae*

Description of current taxonomy:
The family *Konkoviridae* consists of the single genus *Olpivirus.* Two virus species are currently classified in the genus *Olpivirus,* Olpivirus *lactucae* and *Olpivirus tulipae.* The assignment of virus species to this genus is based on the placement of the corresponding viruses on a Neighbor-joining tree inferred from the complete RdRP protein sequences.

Proposed taxonomic change(s):
Create five new species in the genus *Olpivirus* to classify five newly *discovered konkoviruses.*

Justification:
Recently, five new putative konkoviruses were discovered. We propose the creation of five new species within the genus *Olpivirus* based on the species demarcation criterion of <90% identity in the amino acid sequence of the *RdRP.*

Submitted: 06/04/2025; *Revised:* 25/08/2025

TABLE 7 - *Konkoviridae*, 5 new taxa*

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

2025.007P.Ac.v3.Tospoviridae_8nsp

Title: Create eight [8] new species in the genus *Orthotospovirus (Elliovirales: Tospoviridae)*

Authors: Scott Adkins, Marleen Botermans, Jiahong Dong, Denis Kutnjak, David Read, Ronel Roberts, Zhongkai Zhang, Amalendu Ghosh, Holly R. Hughes, Naidu Rayapati, Massimo Turina, Anna Whitfield, Paolo Margaria

Summary:

Taxonomic rank(s) affected:
Genus *Orthotospovirus* in the family *Tospoviridae*

Description of current taxonomy:
Negarnaviricota, Polyploviricotina, Bunyaviricetes, Elliovirales, Tospoviridae, *Orthotospovirus.*
The genus *Orthotospovirus* is the only genus in the *family Tospoviridae.* It. currently includes 28 virus species.

Proposed taxonomic change(s):
Create eight (8) new species in the genus *Orthotospovirus* to classifyieight (8) novel orthotospoviruses on the basis of the species demarcation criterion in the % amino acid sequence identity (<90%) of the nucleocapsid protein (N).

Justification:
The identity value of the nucleocapsid (N) protein sequence of the eight novel orthotospoviruses to other established orthotospoviruses and across themselves, is below 90%, satisfying the criterion for novel species demarcation in the genus *Orthotospovirus* based on sequence identity of the amino acid sequence of the N protein.

Submitted: 15/06/2025; *Revised:* 23/08/2025

TABLE 8 - *Tospoviridae*, 8 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Orthotospovirus tomatonecroanuli*	tomato necrotic ringspot virus	L: MW256413; M: MW256414; S: MW256415
New taxon	Species	*Orthotospovirus limonii*	Limonium orthotospovirus 1	L: PQ587430; M: PQ587431; S: PQ587432
New taxon	Species	*Orthotospovirus barlerichlorosis*	Barleria chlorosis-associated virus	L: MW251496; M: MW251497; S: MW251498
New taxon	Species	*Orthotospovirus scadoxiflavianuli*	Scadoxus chlorotic ringspot virus	L: MW080808; M: MW080809; S: MW080810
New taxon	Species	*Orthotospovirus macadamianuli*	Macadamia ringspot-associated virus	L: OP604037; M: OP604038; S: OP604039
New taxon	Species	*Orthotospovirus mercurialis*	Mercurialis orthotospovirus 1	L: OL471964; M: OL471965; S: OL471966

New taxon	Species	*Orthotospovirus capsiciflavianuli*	chilli yellow ringspot virus isolate	L: MH779497; M: MH779496; S: MH779495
New taxon	Species	*Orthotospovirus tomatonecromaculae*	tomato necrotic spot-associated virus	L: KT984754; M: KT984753; S: KM355773

2025.008P.Ac.v3.Betaflexiviridae_9nsp_2abolishsp

Title: Create nine (9) new species and abolish two (2) species in the family *Betaflexiviridae*

Authors: Tatsuya Nagata, Arnaud G Blouin, Thierry Candresse, Mengji Cao, Won K Cho, Fiona Constable, Massimiliano Morelli, Sead Sabanadzovic, Ioannis E Tzanetakis, Dan EV Villamor

Summary:Taxonomic rank(s) affected:
Genera *Banmivirus, Carlavirus, Robigovirus, Capillovirus, Chordovirus, Citrivirus, Vitivirus* in the *family Betaflexiviridae*

Description of current taxonomy:
The family *Betaflexiviridae* is divided into two subfamilies, *Quinvirinae* (5 genera) and *Trivirinae* (10 genera). Species in the family *Betaflexiviridae* are classified into the following genera: *Banmivirus* (2 species), *Carlavirus* (73), *Foveavirus* (12), *Robigovirus (5),* Sustrivirus *(1),* Capillovirus *(8), Chordovirus* (4), *Citrivirus* (2), *Divavirus (3), Prunevirus* (4), *Ravavirus* (1), *Tepovirus* (5), *Trichovirus* (10), *Vitivirus* (19), *Wamavirus* (1). The currently approved species demarcation criteria based on sequence identity are <72% nucleotide identity in the replication-associated protein (Rep) or <80% amino acid identity in the capsid protein (CP).

Proposed taxonomic change(s):
We propose that the primary species demarcation criterion for the family *Betaflexiviridae* should be <80% aa identity of the Rep. If the aa identity is in the borderline range (78–82%), the CP aa identity (<85%) can be used as a secondary criterion [1].
Based on these new demarcation criteria, we propose to create nine (9) new species in seven genera of the family *Betaflexiviridae*: *Banmivirus* (1 new species), *Carlavirus* (1), *Robigovirus* (1), *Capillovirus* (1), *Chordovirus* (1), *Citrivirus* (1) and *Vitivirus* (3). Species *Carlavirus cacti* and *Carlavirus cornutum* will be abolished. The exemplar accessions of seven carlaviruses, one foveavirus and one vitivirus will be changed to other ones which have complete or coding-complete genomes.

Justification:
Recent analyses using all complete genomes available in GenBank and published as the study case by the *Beta-, Delta-* and *Gammaflexiviridae* study group established a more adequate threshold of Rep amino acid sequence identity for species demarcation.
The addition of nine new species is proposed in the family *Betaflexiviridae* since their Rep amino acid sequences identities are below 80%, according to the new species demarcation criteria described above.
Carlavirus cacti and *Carlavirus cornutum* will be abolished due to the lack of sufficient sequence information.

Submitted: 30/05/2025; *Revised:* 14/08/2025

TABLE 9 - *Betaflexiviridae*, 9 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Banmivirus miscanthi*	Miscanthus virus M	ON986335

New taxon	Species	*Carlavirus menthae*	mint virus C	PQ562895
New taxon	Species	*Robigovirus menthae*	Mentha arvensis robigovirus 1	OR397129
New taxon	Species	*Capillovirus paris*	Paris polyphylla severe chlorotic mottle virus	MW822017
New taxon	Species	*Chordovirus angelicae*	Angelica chordovirus	OR656535
New taxon	Species	*Citrivirus rudbeckiae*	Rudbeckia citrivirus A	ON216317
New taxon	Species	*Vitivirus muviti*	grapevine virus M	MK492703
New taxon	Species	*Vitivirus rhoviti*	grapevine virus P	LC746753
New taxon	Species	*Vitivirus gammactinidiae*	Actinidia virus C	MN022352

TABLE 10 - *Betaflexiviridae*, 2 abolish taxa*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Carlavirus cacti*
Abolish taxon	Species	*Carlavirus cornutum*

2025.009P.Ac.v3.Potyviridae_5nsp

Title: Create one (1) new species in genus *Arepavirus,* one (1) new species in genus *Macluravirus,* one (1) new species in genus *Poacevirus* and two (2) new species in genus *Potyvirus (Patatavirales: Potyviridae)*

Authors: Alice K Inoue-Nagata, Ramon Jordan, Jan F Kreuze, Fan Li, Juan J López-Moya, Kristiina Mäkinen, Kazusato Ohshima, Stephen J Wylie

Summary:

Taxonomic rank(s) affected:

Genera *Arepavirus, Macluravirus, Poacevirus, Potyvirus* in the family *Potyviridae*

Description of current taxonomy:

The family *Potyviridae* includes 13 genera and 259 species. Genus *Arepavirus* consists of 2 species, *Macluravirus* of 12 species, *Poacevirus* of 3 species and *Potyvirus* of 214 species. For the remaining 9 genera no recommendation for changes is proposed.

Proposed taxonomic change(s):

Creation of 5 new species: 1 species in the genus *Arepavirus (“Arepavirus karnatakense”),* 1 species in the genus *Macluravirus (“Macluravirus amomi”),* 1 species in the genus *Poacevirus (“Poacevirus avenae”)* and 2 species in the genus *Potyvirus (“Potyvirus* heraclei”, “Potyvirus shilinense”).

Justification:

According to the ICTV Report chapter on *Potyviridae,* the 13 genera are distinguished based on biological criteria - primarily transmission by specific vectors - and molecular data, with members of different genera sharing less than 46% nucleotide sequence identity. Viruses from different species typically have complete ORF sequences that share less than 76% nucleotide identity and less than 82% amino acid identity. The genome sequences of the five proposed new viruses analyzed showed nucleotide and amino acid identities below the species demarcation thresholds. Additionally, biological data were available to support their classification as members of new species.

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

TABLE 11 - *Potyviridae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Arepavirus karnatakense*	areca palm necrotic ringspot virus 2	PQ197196
New taxon	Species	*Macluravirus amomi*	tsaoko stripe mosaic virus	PQ068101
New taxon	Species	*Poacevirus avenae*	wild oat poacevirus 1	PQ561517
New taxon	Species	*Potyvirus heraclei*	hogweed virus Y	OR537212
New taxon	Species	*Potyvirus shilinense*	Paris potyvirus 5	OR608917

2025.010P.Ac.v4.Geminiviridae_Begomovirus_3nsp

Title: Create three (3) new species in the genus *Begomovirus* (family *Geminiviridae)*

Authors: F Murilo Zerbini, José T Ascencio- Ibáñez, Cica Urbino, Jean-Michel Lett, Paola López-Lambertini, Jesús Navas-Castillo, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Arvind Varsani

Summary:
Taxonomic rank affected:
Genus *Begomovirus* in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria -> *Shotokuvirae* -> *Cressdnaviricota* -> *Repensiviricetes* -> *Geplafuvirales* -> *Geminiviridae* -> *Begomovirus*
Begomovirus is one of the largest genera in the virosphere, with 464 species. Within the genus *Begomovirus,* viruses are classified into species based on a 91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity threshold [1].

Proposed taxonomic changes:
Creation of 3 new species to classify new begomoviruses that have been identified and described in the literature over the past two years.

Justification:
Members of all 3 proposed new species share <91% genome-wide (or DNA-A in the case of bipartite viruses) pairwise identity with sequences of members of currently established begomovirus species.

Submitted: 06/05/2025; *Revised:* 28/08/2025

TABLE 12 - *Geminiviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Begomovirus clitoriae*	butterfly pea yellow mosaic virus	DNA-A: PQ298353; DNA-B: PQ298354
New taxon	Species	*Begomovirus melochiasecundi*	Melochia associated virus	DNA-A: PP897773
New taxon	Species	*Begomovirus citharexyli*	Citharexylum leaf curl virus	DNA-A: OR437368

2025.011P.Ac.v3.Geminiviridae_Capulavirus_1nsp

Title: Create one (1) new species in the *genus* Capulavirus *(Geplafuvirales: Geminiviridae)*

Authors: Philippe Roumagnac, Jose T Ascencio- Ibáñez, Jean-Michel Lett, Paola M. López-Lambertini, Darren P. Martin, Jesús Navas-Castillo, Simone Ribeiro, Cica Urbino, Arvind Varsani, F. Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Genus Capulavirus in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria / Shotokuvirae / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae / Capulavirus*

Proposed taxonomic change(s):
We proposed to create one new species in the *genus Capulavirus: "Capulavirus betae"*

Justification:
Similar to members of the *Capulavirus* genus, members of the proposed new species *"Capulavirus betae"* have the virion-strand origin of replication nonanucleotide motif 'TAATATTAC' and show a typical capulavirus organization, with putative multiple overlapping short ORFs (V3 and V4) upstream of the CP gene that encode putative movement proteins. In addition, genome-wide pairwise analysis of the representative genomes of capulaviruses showed that beet capulavirus 1 sequence genome shared less than 78% identity with all representative genomes of capulaviruses. Since 78% nucleotide identity is the genome-wide species demarcation threshold for capulaviruses, we conclude that beet capulavirus 1 can be classified into the species *"Capulavirus betae",* a new species in the genus *Capulavirus.*

Submitted: 06/10/2025; *Revised:* 22/08/2025

TABLE 13 - *Geminiviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Capulavirus betae*	beet capulavirus 1	PQ682516

2025.012P.Ac.v3.Geminiviridae_Mastrevirus_5nsp

Title: Create five new species in the genus *Mastrevirus* (family *Geminiviridae)*

Authors: Arvind Varsani, Jean-Michel Lett, José T Ascencio- Ibáñez , Cica Urbino, Jesús Navas-Castillo, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, F Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Genus *Mastrevirus* in the *family Geminiviridae*

Description of current taxonomy:
Monodnaviria; Shotokuvirae; Cressdnaviricota; Repensiviricetes; Geplafuvirales; Geminiviridae; Mastrevirus

There are currently 50 established species in the genus *Mastrevirus.* New species in the genus *Mastrevirus* are determined based on a 78% pairwise identity threshold coupled with phylogenetic support.

Proposed taxonomic change(s):
Create five new species in the *genus Mastrevirus*

Justification:
In the last year, eight genomes of mastreviruses have been identified that cannot be classified at the species level within the current taxonomy framework. These can be classified into five new species sharing <78% pairwise identity with all classified mastreviruses.

Submitted: 06/06/2025; *Revised:* 22/08/2025

TABLE 14 - *Geminiviridae*, 5 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Mastrevirus cenchri*	Cenchrus echinatus associated virus	PQ434710
New taxon	Species	*Mastrevirus croci*	Mastrevirus sp. croci	PQ392009
New taxon	Species	*Mastrevirus mexicoense*	Mastrevirus sp. UHMV-1.PC-W	MN203180
New taxon	Species	*Mastrevirus purpurei*	Cenchrus purpureus mild streak virus	PQ434729
New taxon	Species	*Mastrevirus tripterygii*	Tripterygium mastrevirus A	MT159331

2025.013P.Ac.v3.Alphasatellitidae_2ng_8nsp

Title: Create two (2) new genera and 8 new species in the family *Alphasatellitidae*

Authors: F Murilo Zerbini, José T Ascencio- Ibáñez, Cica Urbino, Jean-Michel Lett, Jesús Navas-Castillo, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Arvind Varsani

Summary:Taxonomic rank affected:
Family *Alphasatellitidae*

Description of current taxonomy:
The family *Alphasatellitidae* is divided into three subfamilies: *Geminialphasatellitinae, Nanoalphasatellitinae,* and *Petromoalphasatellitinae,* consisting of 7, 6 and 5 genera, respectively.

Proposed taxonomic changes:
We propose the creation of 2 new genera (1 in subfamily *Geminialphasatellitinae* and 1 in subfamily *Nanoalphasatellitinae)* and 8 new species (4 in the 2 new genera, 4 in previously existing genera) to classify new alphasatellites that have been identified and described in the literature over the last two years.

Justification:
The exemplar members of the 3 proposed new species in the proposed new genus *"Banaphisatellite"* (subfamily *Nanoalphasatellitinae)* have <67% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily. The exemplar member of the 1 proposed new species in the proposed new genus *"Whedwasatellite"* (subfamily *Geminialphasatellitinae)* has <70% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily. The exemplar members of the 4 proposed new species in the genera *Clecrusatellite, Colecusatellite* and *Gosmusatellite* (subfamily *Geminialphasatellitinae)* have <88% genome-wide pairwise sequence identity with members of currently established alphasatellite species in this subfamily.

Submitted: 13/06/2025; *Revised:* 22/08/2025

TABLE 15 - *Alphasatellitidae*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Banaphisatellite*		
New taxon	Species	*Banaphisatellite alphamusae*	banana bunchy top alphasatellite 4	OK546212
New taxon	Species	*Banaphisatellite betamusae*	banana bunchy top alphasatellite 5	ON960014
New taxon	Species	*Banaphisatellite gammamusae*	banana bunchy top alphasatellite 6	ON960025
New taxon	Genus	*Whedwasatellite*		
New taxon	Species	*Whedwasatellite triticiparvi*	wheat dwarf virus-associated alphasatellite	PP445014
New taxon	Species	*Colecusatellite asystasiae*	Asystasia yellow mosaic alphasatellite 1	LC724062
New taxon	Species	*Gosmusatellite asystasiae*	Asystasia yellow mosaic alphasatellite 2	LC724021
New taxon	Species	*Gosmusatellite lactucae*	pepper leaf curl Yunnan alphasatellite	PQ352199
New taxon	Species	*Clecrusatellite solanumbrasiliense*	tomato golden vein alphasatellite	MT214093

2025.014P.Ac.v3.Betasatellite_1nsp

Title: Create one new species in the genus *Betasatellite* (family *Tolecusatellitidae)*

Authors: Jesús Navas-Castillo, José T Ascencio-Ibáñez, Cica Urbino, Jean-Michel Lett, Paola López-Lambertini, Darren P Martin, Simone G Ribeiro, Philippe Roumagnac, Cica Urbino, Arvind Varsani, F Murilo Zerbini

Summary:Taxonomic rank affected:
Genus *Betasatellite* in the family *Tolecusatellitidae*

Description of current taxonomy:
Tolecusatellitidae -> *Betasatellite*
To date, the genus *Betasatellite* consists of 119 species.
Within the genus *Betasatellite,* DNA satellites are classified into species based on a 91% genome-wide pairwise identity threshold [1].

Proposed taxonomic changes:
Creation of one (1) new species to classify a new betasatellite that has been identified and described in the literature over the past four years.

Justification:
The member of the proposed new species shares <91% genome-wide pairwise identity with sequences of members of currently established betasatellite species.

Submitted: 13/06/2025; *Revised:* 22/08/2025

TABLE 16 - *Betasatellite*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Betasatellite trigonellae*	fenugreek leaf curl betasatellite	MZ648030

2025.015P.Ac.v3.Deltasatellite_1nsp

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

Authors: Jesús Navas-Castillo, Philippe Roumagnac, Jose T Ascencio-Ibáñez, Jean-Michel Lett, Paola M. López-Lambertini, Darren P. Martin, Simone Ribeiro, Cica Urbino, Arvind Varsani, F. Murilo Zerbini

Summary:Taxonomic rank affected:
Genus Deltasatellite in the *family* Tolecusatellitidae

Description of current taxonomy:
Tolecusatellitidae / Deltasatellite
The genus *Deltasatellite* consists of 12 species.

Proposed taxonomic change:
We proposed to create one new species in the *genus Deltasatellite: "Deltasatellite brassicae".*

Justification:
Similar to members of the *genus Deltasatellite,* members of the proposed new species *"Deltasatellite brassicae"* have all conserved features of deltasatellites, including an A-rich region, a stem-loop with the TAATATTAC nonanucleotide motif, and a region with identity to betasatellites. The isolates share 100% nucleotide identity among themselves, and ≤73.9% identity with known deltasatellites, below the 91% species demarcation threshold. Phylogenetic analysis shows the group forms a distinct clade within New World deltasatellites. We conclude that *"Deltasatellite brassicae"* represents a new species in the genus *Deltasatellite.*

Submitted: 06/05/2025; *Revised:* 22/08/2025

TABLE 17 - *Deltasatellite*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Deltasatellite brassicae*	cabbage leaf curl deltasatellite	OK073969

2025.016P.Ac.v3.Geminiviridae_3ng_3nsp

Title: Create three new species and three new genera in the *family Geminiviridae* (order *Geplafuvirales).*

Authors: Philippe Roumagnac, Jose T Ascencio- Ibáñez, Jean-Michel Lett, Paola M López-Lambertini, Darren P Martin, Jesús Navas-Castillo, Simone G Ribeiro, Cica Urbino, Arvind Varsani, F Murilo Zerbini

Summary:
Taxonomic rank(s) affected:
Family *Geminiviridae* in the *order Geplafuvirales*

Description of current taxonomy:
Monodnaviria / *Shotokuvirae* / *Cressdnaviricota* / *Repensiviricetes* / *Geplafuvirales* / *Geminiviridae*
The family *Geminiviridae* consists of 15 genera

Proposed taxonomic change(s):

We proposed to create three new genera into the *Geminiviridae* family: *"Cobecusvirus", "Oleurovirus"* and *"Pylecuvirus".* We also propose to create one new species *("Cobecusvirus phaseoli")* in the new *"Cobecusvirus"* genus, one new species *("Oleurovirus oleae")* in the new *"Oleurovirus"* genus and one new species *("Pylecuvirus petroselini")* in the new *"Pylecuvirus" genus*

Justification:
We propose to classify new geminiviruses into 3 new species based on species demarcation guidelines already established for the family *Geminiviridae.* Based on the inferred genome organizations of these viruses coupled with phylogenetic analysis, we propose to create 3 new genera in the family *Geminiviridae* to accommodate these 3 new species.

Submitted: 06/10/2025; *Revised:* 22/08/2025

TABLE 18 - *Geminiviridae*, 6 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Cobecusvirus*		
New taxon	Species	*Cobecusvirus phaseoli*	common bean curly stunt virus	MK673513
New taxon	Genus	*Oleurovirus*		
New taxon	Species	*Oleurovirus oleae*	Olea europaea geminivirus	MW316657
New taxon	Genus	*Pylecuvirus*		
New taxon	Species	*Pylecuvirus petroselini*	parsley yellow leaf curl virus	MN243534

2025.017P.Ac.v3.Secoviridae_53nsp_3abolishsp

Title: Create 53 new species and abolish three previously recognized species in the family *Secoviridae (Picornavirales)*

Authors: Marc Fuchs, Jean-Michel Hily, Hélène Sanfaçon, Lucy Stewart, Jeremy Thompson, Rene Van der Vlugt, Thierry Wetzel

Summary:
Taxonomic rank(s) affected:
Genera *Comovirus, Cheravirus, Fabavirus, Nepovirus, Sadwavirus, Stralarivirus, Torradovirus, Sequivirus, Waikavirus* in the *family Secoviridae*

Description of current taxonomy:
The recognition of new virus species is based on demarcation criteria in the family *Secoviridae* of less than 75% amino acid sequence identity in the coat protein (CP)(s) and/or less than 80% amino acid sequence identity in the conserved Protease (Pro)-Polymerase (Pol) region (from the protease CG motif to the polymerase GDD motif), *and/or* distinct plant hosts and biological properties.

Proposed taxonomic change(s):
Create two new species in the genus *Comovirus: "Comovirus caricae", "Comovirus cardaminis"*
Create three new species in the genus *Cheravirus: "Cheravirus lagerstroemiae", "Cheravirus corymbii", "Cheravirus pternopetali"*
Create five new species in the genus *Fabavirus: "Fabavirus phipiperis", "Fabavirus camphorae", "Fabavirus reaumuriae", "Fabavirus multiflorum", "Fabavirus squamellariae"*
Create 25 new species in the genus *Nepovirus: "Nepovirus alphacucumis", "Nepovirus thymi", "Nepovirus paeoniae", "Nepovirus chrysanthemi", "Nepovirus pinnatifolium", "Nepovirus glycyrrhizae", "Nepovirus pholismae", "Nepovirus berberidopsis", "Nepovirus silenis", "Nepovirus galax", "Nepovirus saururi", "Nepovirus musae", "Nepovirus cenchri", "Nepovirus hypolepsis", "Nepovirus pogonati", "Nepovirus begoniae", "Nepovirus caladeniae", "Nepovirus astragali", "Nepovirus gentianae", "Nepovirus leucadendri", "Nepovirus yunnanense", "Nepovirus rhododendri", "Nepovirus hanseniae",*

“Nepovirus beldersayense”, “Nepovirus jasmini”
Create two new species in the *genus* Sadwavirus: *“Sadwavirus kappananas”, “Sadwavirus morifolii”*
Create two new species in the genus *Stralarivirus: “Stralarivirus beldersayense”, “Stralarivirus scaevolae”*
Create four new species in the *genus* Torradovirus: *“Torradovirus rorippae”, “Torradovirus ophistopappi”, “Torradovirus lophophyti”, “Torradovirus sesami”*
Create one new species in the genus *Sequivirus: “Sequivirus primulae”*
Create nine new species in the genus *Waikavirus: “Waikavirus convallariae”, “Waikavirus euphorbiae”, “Waikavirus swalleniae”, “Waikavirus gentianae”, “Waikavirus lycopi”, “Waikavirus pagodae”, “Waikavirus heveae”, “Waikavirus artemisiae”, “Waikavirus duoplantae”*
Abolish two previously recognized species in the genus *Nepovirus:* Nepovirus americaense, Nepovirus *australiense*
Abolish one previously recognized species in the genus *Waikavirus:* Waikavirus anthrisci

Justification:
The creation of the proposed new 53 species is justified based on less than 75% amino acid sequence identity in the CP(s) and/or less than 80% amino acid sequence identity in the conserved Pro-Pol region (from the protease CG motif to the polymerase GDD motif) compared with classified species of the family *Secoviridae.*
The abolishment of three previous recognized species *(Nepovirus* americaense, Nepovirus australiense, Waikavirus *anthrisci)* is justified based on a lack of sequence information.

Submitted: 06/04/2025; *Revised:* 18/08/2025

TABLE 19 - *Secoviridae*, 53 new taxa*. Table too large, see supplementary information sheet supp_info_tab_19

TABLE 20 - *Secoviridae*, 3 abolish taxa*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Nepovirus americaense*
Abolish taxon	Species	*Nepovirus australiaense*
Abolish taxon	Species	*Waikavirus anthrisci*

2025.018P.Ac.v3.Tombusviridae_1ng_9nsp

Title: Create one (1) new genus containing nine (9) new species in the family *Tombusviridae*

Authors: W. Allen Miller, Zachary Lozier, , , , , ,

Summary:
Taxonomic rank(s) affected:
Subfamily *Procedovirinae* in the *family Tombusviridae*

Description of current taxonomy:
Currently there are 19 genera and 93 species in the family *Tombusviridae.* Genera are grouped based on genome organization and sequence similarities of RNA-dependent RNA polymerase (RdRp).

Proposed taxonomic change(s):
Create one new genus in the subfamily *Procedovirinae,* called *“Rimosavirus”,* and classify nine new viruses (maize-associated rimosavirus 1 (MaRV1), *Plasmopara viticola* lesion-associated rimosavirus 1 (PVLaRV1), Taian Tombu tick-associated virus 1 (TTTaV1), Nanning Tombu tick-associated virus 1 (NTTaV1), Hubei rimosavirus 2 (HubRV2), *Brassica caulorapa-associated* rimosavirus 1 (BCaRV1), *Zizania latifolia-associated* rimosavirus 1 (ZLaRV1), Hubei rimosavirus 1 (HubRV1), tuatara cloaca-

associated rimosavirus 1 (TCaRV1) into nine new species in the *genus "Rimosavirus".*

Justification:
All members of the proposed genus have RdRp sequences more similar to those of other tombusvirids than to viruses in other families, but they diverge from those of other tombusvirid genera by as much as the RdRps in different established genera diverge from each other. Secondly, the *"Rimosavirus"* genome organizations feature tombusvirid-like characteristics such as probable translation of the RdRp (ORF2) by readthrough of a leaky stop codon (placing rimosaviruses in the *Procedovirinae)* and an intergenic region between ORF2 and the coat protein (CP)-encoding ORF (ORF3). Genomes in the proposed genus differ from other tombusvirids by having (i) a predicted 5' untranslated region (UTR) over 400 nt long and containing AUGs, (ii) a possible ORF (ORF4) overlapping with ORF3 starting upstream of ORF3. This would be the first genus to combine translation of the RdRp by translational readthrough (which defines members of the *Procedovirinae* subfamily), with a luteovirus-like readthrough of the ORF3 stop codon.

Submitted: 06/05/2025; *Revised:* 28/08/2025

TABLE 21 - *Tombusviridae*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Rimosavirus*		
New taxon	Species	*Rimosavirus zeae*	maize-associated rimosavirus 1	OK018181
New taxon	Species	*Rimosavirus plasmoparae*	Plasmopara viticola lesion-associated rimosavirus 1	MT311687
New taxon	Species	*Rimosavirus haemaphysalis*	Taian Tombu tick-associated virus 1	ON746540
New taxon	Species	*Rimosavirus rhipicephali*	Nanning Tombu tick-associated virus 1	ON746539
New taxon	Species	*Rimosavirus unhubeiense*	Hubei rimosavirus 1	KX883244
New taxon	Species	*Rimosavirus duohubeiense*	Hubei rimosavirus 2	KX883240
New taxon	Species	*Rimosavirus brassicae*	Brassica caulorapa-associated rimosavirus 1	MN728812
New taxon	Species	*Rimosavirus zizaniae*	Zizania latifolia-associated rimosavirus 1	MN728813
New taxon	Species	*Rimosavirus sphenodonis*	tuatara cloaca-associated rimosavirus 1	OP080581

2025.019P.Ac.v3.Closteroviridae_31nsp_abolish_1sp

Title: Create 31 new species in the genera *Ampelovirus,* Closterovirus, *Crinivirus, Olivavirus* and *Velarivirus* and abolish one species in the genus *Closterovirus*

Authors: Nina Aboughanem-Sabanadzovic, Moshe Bar-Joseph, Thierry Candresse, Hano J Maree, Michael Melzer, Wulf Menzel, Angelantonio Minafra, Dimitre Mollov, Ioannis E Tzanetakis, Luisa Rubino, Sead Sabanadzovic

Summary:
Taxonomic rank(s) affected:
Genera *Ampelovirus,* Closterovirus, *Crinivirus, Olivavirus* and *Velarivirus* in the *family Closteroviridae*

Description of current taxonomy:
Family *Closteroviridae* is currently composed of seven genera that accommodate 58 species, most of

which are classified in one of the four "traditional" genera: *Closterovirus* (17), *Crinivirus* (14), *Ampelovirus* (13) and *Velarivirus* (9). Two of three recently established genera *(Bluvavirus* and *Menthavirus)* are monospecific, while the genus *Olivavirus* includes 3 species.

Proposed taxonomic change(s):
We propose creation of 31 new species in the family based on recently published data on characterization of viruses with affinities with currently recognized members of the family *Closteroviridae.*

Justification:
During the search of GenBank, 31 viral genomes with required quality and completeness along with availability of a valid publication were selected as exemplar isolates for typifying proposed new species. All these viruses meet the molecular criteria for species demarcation in the genera as they differ in amino acid content of all 3 relevant virus-encoded proteins (HSP70h, RdRP and CP) with counterparts of 58 already recognized members of the family.

Submitted: 25/06/2025; *Revised:* 28/08/2025

TABLE 22 - *Closteroviridae*, 31 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Ampelovirus allamandae*	Allamanda chlorotic virus A	PP212980
New taxon	Species	*Ampelovirus alpiniae*	Alpinia vein clearing virus	OQ550018
New taxon	Species	*Ampelovirus unesculentae*	Manihot esculenta associated ampelovirus 1	MT773586
New taxon	Species	*Ampelovirus duesculentae*	Manihot esculenta associated ampelovirus 2	MT773592
New taxon	Species	*Ampelovirus unocitri*	citrus associated ampelovirus 1	MW365401
New taxon	Species	*Ampelovirus duocitri*	citrus associated ampelovirus 2	MW365402
New taxon	Species	*Ampelovirus odontonemae*	firespike leafroll-associated virus	MW147758
New taxon	Species	*Ampelovirus pentananas*	pineapple mealybug wilt-associated virus 5	OQ850040
New taxon	Species	*Ampelovirus hexananas*	pineapple mealybug wilt-associated virus 6	OP860296
New taxon	Species	*Ampelovirus septananas*	pineapple mealybug wilt-associated virus 7	OQ850042
New taxon	Species	*Ampelovirus sacchari*	sugarcane mild mosaic virus	MN116751
New taxon	Species	*Ampelovirus croton*	croton golden spot associated virus A	OR041673
New taxon	Species	*Ampelovirus alphaolivae*	olive virus A	OQ863254
New taxon	Species	*Ampelovirus kaki*	persimmon ampelovirus	LC488185
New taxon	Species	*Ampelovirus perseae*	lingue ampelovirus 1	OQ805851
New taxon	Species	*Closterovirus alphafici*	fig virus A	MN817232
New taxon	Species	*Closterovirus betafici*	fig virus B	MN817233
New taxon	Species	*Closterovirus cnidi*	Cnidium closterovirus 1	OL804208
New taxon	Species	*Closterovirus duocarotae*	carrot closterovirus 2	OP886455
New taxon	Species	*Closterovirus thesii*	Thesium chinense closterovirus 1	OM801605
New taxon	Species	*Closterovirus stellariae*	Stellaria aquatica virus C	PP280820
New taxon	Species	*Closterovirus tritici*	wheat closterovirus 1	LC735716
New taxon	Species	*Closterovirus dregeae*	Dregea volubilis virus 1	MZ779122

New taxon	Species	*Crinivirus kurdistanfragariae*	strawberry Kurdistan virus	RNA1: OR387513; RNA2: OR387514
New taxon	Species	*Crinivirus dioscoreae*	yam virus 1	RNA1: PP378481; RNA2: PP378483
New taxon	Species	*Crinivirus mori*	mulberry crinivirus	RNA1: ON931610; RNA2: ON931611
New taxon	Species	*Crinivirus papyriferae*	paper mulberry crinivirus 1	RNA1: OL344036; RNA2: OL344037
New taxon	Species	*Crinivirus arracaciae*	arracacha latent virus C	RNA1: KY451034; RNA2: KY451035
New taxon	Species	*Olivavirus oleae*	olive leaf mottling virus	PP869314
New taxon	Species	*Velarivirus agapanthi*	Agapanthus velarivirus	MT533601
New taxon	Species	*Velarivirus oleae*	olive virus V	OQ863266

TABLE 23 - *Closteroviridae*, 1 abolish taxon*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Species	*Closterovirus flavarctii*

2025.020P.Solemoviridae_Enamovirus_10nsp

Title: Create ten species in the *genus* Enamovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:

Taxonomic rank(s) affected:
Genus *Enamovirus* in the *family Solemoviridae*

Description of current taxonomy:
Sobelivirales: Solemoviridae: Enamovirus
Currently, the genus *Enamovirus* consists of 15 species.

Proposed taxonomic change(s):
Create ten new species in the *genus Enamovirus*

Justification:
High-throughput sequencing (HTS) of raspberry samples collected in 2021 from Czechia and Norway has revealed 14 isolates of a novel *Enamovirus* candidate, raspberry enamovirus 1 (RaEV1). Carrot enamovirus 1 (CaEV1) was discovered in wild carrot populations in Southwestern France. In addition, the analyses of publicly available plant transcriptome data have enabled the assembly of 16 additional full or partial genome sequences characteristic of enamoviruses: Brunioides conebush enamovirus, Bunge's buttercup enamovirus, cassava enamovirus, common thyme enamovirus, Coriandrum sativum enamovirus, decurrent goldenrod enamovirus, Fukien tea tree enamovirus, oriental arborvitae enamovirus, rubber tree enamovirus, Rugel's plantain enamovirus, sea-buckthorn enamo-like virus, showy sunflower enamovirus, silver birch enamovirus, spruce enamovirus, Western salsify enamovirus, and Yunnan pine enamovirus. Eight of these 16 candidates have genome sequences covering all coding regions, while they also cluster with accepted members in the phylogenetic RdRP tree. In total, ten out of 18 candidate species are proposed as the new members of genus *Enamovirus,* fulfilling the species demarcation criteria and having complete or coding-complete genomes sequences.

Submitted: 16/06/2025; *Revised:* 28/10/2025

TABLE 24 - *Solemoviridae*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Enamovirus BUBEV*	Bunge's buttercup enamovirus	BK068694
New taxon	Species	*Enamovirus CAEV*	carrot enamovirus	OP886449
New taxon	Species	*Enamovirus CTEV*	common thyme enamovirus	BK068696
New taxon	Species	*Enamovirus CSEV*	Coriandrum sativum enamovirus	BK063225
New taxon	Species	*Enamovirus DEGEV*	decurrent goldenrod enamovirus	BK068695
New taxon	Species	*Enamovirus FTEV*	Fukien tea tree enamovirus	BK068686
New taxon	Species	*Enamovirus ORAEV*	oriental arborvitae enamovirus	BK068685
New taxon	Species	*Enamovirus RAEV*	raspberry enamovirus	OR683427
New taxon	Species	*Enamovirus WSEV*	western salsify enamovirus	BK068692
New taxon	Species	*Enamovirus YPEV*	Yunnan pine enamovirus	BK068688

2025.021P.Solemoviridae_Sobemovirus_1nsp

Title: Create one species in the *genus* Sobemovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:
Taxonomic rank(s) affected:
Genus *Sobemovirus* in the *family Solemoviridae*

Description of current taxonomy:
Currently, the genus *Sobemovirus* consists of 26 members infecting plants from different taxa.

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

Justification:
The presence of olive virus S (OlVS), a putative novel member of the family *Solemoviridae,* was determined by HTS in 10 samples of olive leaf petioles collected in the commercial orchards in Stellenbosch, South Africa. The assembled genome of OlVS shared sequence similarity with sobemoviruses, being closest to southern bean mosaic virus (SBMV) with an average identity of 52.5%. The terminal genomic sequences were determined by Sanger sequencing of RACE cDNA clones. The genome length and organization of OlVS was characteristic of sobemoviruses. The phylogenetic analysis confirmed clustering within the genus *Sobemovirus.*

Submitted: 16/06/2025; *Revised:* 28/10/2025

TABLE 25 - *Solemoviridae*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Sobemovirus OLVS*	olive virus S	OR252867

2025.022P.Solemoviridae_Polerovirus_17nsp

Title: Create seventeen [17] new species in the *genus* Polerovirus *(Sobelivirales:Solemoviridae)*

Authors: Denis Fargette, Fiona Filardo, Mahan Ghafari, Eugenie Hebrard, Cecilia Sarmiento, Merike Sõmera, John Thomas

Summary:
Taxonomic rank(s) affected:
Genus *Polerovirus* in the family *Solemoviridae*

Description of current taxonomy:
Currently, the genus *Polerovirus* consists of 77 species.

Proposed taxonomic change(s):
Create 17 new species in the *genus Polerovirus*

Justification: Recent high-throughput sequencing projects have revealed 23 putative novel poleroviruses that have not yet been assigned to species. The assembled genomes share the highest sequence identities with poleroviruses. Phylogenetic analysis of their genome nucleotide sequences and the amino acid sequences of their RdRPs confirmed clustering within the genus *Polerovirus.* The putative novel candidate viruses are: *Actinidia* polerovirus, *Ageratum* virus 3, arachis mottle-associated virus, bitter apple aphid-borne yellows virus, bitter gourd yellowing crumple virus, cacao leafroll virus, carrot polerovirus 1, carrot polerovirus 2, Chrysanthemum virus D, *Cynanchum* yellow mottle-associated virus, Ficus esquiroliana polerovirus, gladiolus polerovirus, Ixeridium yellow mottle virus, Musa polerovirus, noble dendrobium polerovirus, parsley polerovirus, pepper vein yellows virus 10, rice dwarf polerovirus, spruce polerovirus, sweet leaf bush polerovirus, tomato necrotic yellowing virus, Viola philippica polerovirus, and wild carrot red leaf virus. We propose that 17 out of these 23 viruses could be recognized as members of species in the genus *Polerovirus.*

Submitted: 16/06/2025; *Revised:* 29/10/2025

TABLE 26 - *Solemoviridae*, 17 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Polerovirus AGV*	Agratum virus 3	PQ675349
New taxon	Species	*Polerovirus ARMOV*	Arachis mottle-associated virus	LC818997
New taxon	Species	*Polerovirus CALRV*	cacao leafroll virus	OR423049
New taxon	Species	*Polerovirus CAPV*	carrot polerovirus 2	OP886451
New taxon	Species	*Polerovirus CHDV*	Chrysanthemum virus D	OR453957
New taxon	Species	*Polerovirus CYMAV*	Cynanchum yellow mottle-associated virus	LC699794
New taxon	Species	*Polerovirus IXYMAV*	Ixeridium yellow mottle virus 1	KT868949
New taxon	Species	*Polerovirus PEVYV10*	pepper vein yellows virus 10	OR225495
New taxon	Species	*Polerovirus RDPV*	rice polerovirus	PP925870
New taxon	Species	*Polerovirus VPPV*	Viola philippica polerovirus	PP770488
New taxon	Species	*Polerovirus ACTPV*	Actinidia polerovirus	BK069690
New taxon	Species	*Polerovirus FEQPV*	Ficus esquiroliana polerovirus	BK068690
New taxon	Species	*Polerovirus GLPV*	Gladiolus polerovirus	BK068697
New taxon	Species	*Polerovirus MUSPV*	Musa polerovirus	BK068683
New taxon	Species	*Polerovirus NBPV*	noble dendrobium polerovirus	BK068693
New taxon	Species	*Polerovirus SPRPV*	spruce polerovirus	BK068705
New taxon	Species	*Polerovirus SLBPV*	sweet leaf bush polerovirus	BK068689

2025.023P.Ac.v3.Rhabdoviridae_Trirhavirus_1nsp

Title: Create one new species in the genus *Trirhavirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Trirhavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae*

Description of current taxonomy:
Five virus species are currently classified in the recently created genus *Trirhavirus,* whose main feature is the tri-segmented genomic organization of their members. The assignment of viruses to this genus is based on their genome composition, and the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create one new species in the genus *Trirhavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* This species is proposed to be named *"Trirhavirus rubi".*

Justification:
A novel tri-segmented rhabdovirus was identified in Rubus [1]**.** The characterization of the genome sequence showed that it should be assigned to a novel species within the genus *Trirhavirus* [1] based on the nucleotide sequence divergence from previously reported trirhaviruses and phylogenetic placement.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 27 - *Rhabdoviridae*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Trirhavirus rubi*	Rubus trirhavirus 1	RNA1: PQ317245; RNA2: PQ317246; RNA3: PQ317247

2025.024P.Ac.v3.Rhabdoviridae_Betanucleorhabdovirus_7nsp

Title: Create seven new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Betanucleorhabdovirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genus *Betanucleorhabdovirus* belongs to the subfamily *Betarhabdovirinae,* family *Rhabdoviridae* and consists of 19 species. Viruses classified into species in the genus *Betanucleorhabdovirus* infect a wide range of plants, and the assignment of viruses to this genus is based on the placement of the viruses

on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create seven new species in the genus *Betanucleorhabdovirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named as *"Betanucleorhabdovirus* alpiniae", "Betanucleorhabdovirus betae", "Betanucleorhabdovirus alphasambuci", "Betanucleorhabdovirus betasambuc"i, "Betanucleorhabdovirus gammasambuci", "Betanucleorhabdovirus *deltasambuci" and* "Betanucleorhabdovirus *epsilonsambuci".*

Justification:
Seven novel rhabdoviruses were identified in *Alpinia purpurata* [1], beet [Mehrvar and Abkho, unpublished (OR227650)] and elderberry [2]. The characterization of these seven viruses showed that they should be classified into novel species within the genus *Betanucleorhabdovirus.*

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 28 - *Rhabdoviridae*, 7 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Betanucleorhabdovirus alpiniae*	Alpinia vein streaking virus	OQ538192
New taxon	Species	*Betanucleorhabdovirus betae*	beet betanucleorhabdovirus 1	OR227650
New taxon	Species	*Betanucleorhabdovirus alphasambuci*	Sambucus betanucleorhabdovirus 1	PP711309
New taxon	Species	*Betanucleorhabdovirus betasambuci*	Sambucus betanucleorhabdovirus 2	PP711310
New taxon	Species	*Betanucleorhabdovirus gammasambuci*	Sambucus betanucleorhabdovirus 3	PP711317
New taxon	Species	*Betanucleorhabdovirus deltasambuci*	Sambucus betanucleorhabdovirus 4	PP711315
New taxon	Species	*Betanucleorhabdovirus epsilonsambuci*	Sambucus betanucleorhabdovirus 5	PP711313

2025.025P.Ac.v3.Rhabdoviridae_Alpha_and_Betacytorhabdovirus_3nsp

Title: Create three (3) new species, one in the genus *Alphacytorhabdovirus,* and the other two in the genus *Betacytorhabdovirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas-A Astúa, Hideki Kondo, Pedro Luis Ramos- González , Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* belong to the subfamily *Betarhabdovirinae,* family *Rhabdoviridae* and consist of 18 and 19 species, respectively. Viruses classified into species in the genera *Alphacytorhabdovirus* and *Betacytorhabdovirus* infect a wide range of plants, and the assignment of viruses to these genera is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences

Proposed taxonomic change(s):
Create one new species in the genus *Alphacytorhabdovirus,* and two new species in the genus

Betacytorhabdovirus, subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named *"Alphacytorhabdovirus* lonicerae", "Betacytorhabdovirus dioscoreae" *and* "Betacytorhabdovirus *pyri".*

Justification:
Three novel rhabdoviruses were identified in honeysuckle [1], *Dioscorea rotundata* [Silva et al., unpublished (ON924784)] and pear [2]. The characterization of these viruses showed that the honeysuckle-associated virus should be classified into a novel species within the genus *Alphacytorhabdovirus* [1]; while the *Dioscorea rotundata-associated* and pear-associated viruses should be assigned to novel species within the genus *Betacytorhabdovirus* [Silva et al., unpublished (ON924784) and 2, respectively].

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 29 - *Rhabdoviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Alphacytorhabdovirus lonicerae*	honeysuckle-associated cytorhabdovirus 1	PQ587056
New taxon	Species	*Betacytorhabdovirus dioscoreae*	Dioscorea rotundata virus 1	ON924784
New taxon	Species	*Betacytorhabdovirus pyri*	pear rhabdovirus 1	PP512586

2025.026P.Ac.v3.Rhabdoviridae_Varicosavirus_3nsp

Title: Create three (3) new species in the genus *Varicosavirus,* subfamily *Betarhabdovirinae (Mononegavirales: Rhabdoviridae)*

Authors: Nicolas Bejerman, Humberto Debat, Ralf G Dietzgen , Juliana Freitas- Astúa, Hideki Kondo, Pedro Luis Ramos- González, Anna E Whitfield , Peter J Walker

Summary:Taxonomic rank(s) affected:
Genus *Varicosavirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Viruses classified into species in the genus *Varicosavirus* are bi-segmented and infect a wide range of plants. The assignment of viruses to this genus is based on the placement of the viruses on Maximum Likelihood trees inferred from complete L protein sequences.

Proposed taxonomic change(s):
Create three new species in the genus *Varicosavirus,* subfamily *Betarhabdovirinae,* family *Rhabdoviridae.* These species are proposed to be named *"Varicosavirus* agastachi", "Varicosavirus orychophragmi" *and* "Varicosavirus *rubi".*

Justification:
Three novel rhabdoviruses were identified in *Agastache rugosa* [1], *Orychophragmus violaceus* [2] and *Rubus* spp. [3]. The characterization of these three viruses showed that they should be classified into novel species within the genus *Varicosavirus* based on the nucleotide sequence divergence from previously reported varicosaviruses and phylogenetic placement.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 30 - *Rhabdoviridae*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Varicosavirus agastachi*	Agastache rugosa associated varicosavirus	RNA1: PP987314;RNA2: PP987315
New taxon	Species	*Varicosavirus orychophragmi*	Orychophragmus violaceus varicosavirus	RNA1: PP770489; RNA2: PP777177
New taxon	Species	*Varicosavirus rubi*	Rubus varicosavirus 1	RNA1: PQ317243; RNA2: PQ317244

2025.027P.Ac.v3.Rhabdoviridae_Dichorhavirus_2nsp

Title: Create two (2) new species in the genus *Dichorhavirus (Mononegavirales: Rhabdoviridae)*

Authors: Peter J Walker, Nicolas Bejerman, Kim R Blasdell, Humberto Debat, Ralf G Dietzgen, Anthony R Fooks, Juliana Freitas-Astúa, Kyle Garver, Pedro Luis Ramos-González, Hideki Kondo, Mang Shi, Robert B Tesh, Noël Tordo, Nikos Vasilakis, Anna E Whitfield, Monica Madariaga-Villarroel

Summary:Taxonomic rank(s) affected:
Genus *Dichorhavirus* in the *family Rhabdoviridae*

Description of current taxonomy:
Genus *Dichorhavirus,* family *Rhabdoviridae,* encompasses viruses assigned to six species. They are plant-infecting viruses transmitted by mites of the genus *Brevipalpus* . The genome of dichorhaviruses includes bi-segmented, negative-sense, single-stranded RNA molecules, in which genes *N, P, P3(ORF3), M,* and *G* are located in RNA1, whereas the gene *L* is in RNA2. In nature, dichorhaviruses cause non-systemic diseases, mostly producing chlorotic and necrotic spots; however, sometimes orchid fleck virus (OFV) can induce systemic infection in orchids. Dichorhaviruses also replicate in their vectors .

Proposed taxonomic change(s):
Create two new species in the genus *Dichorhavirus, subfamily Betarhabdovirinae, family Rhabdoviridae.* The two new taxa are proposed to be named *“Dichorhavirus* chilense” *and* “Dichorhavirus *piracicabense”, respectively.*

Justification: Two novel viruses were identified in bleeding-heart vine *(Clerodendrum thomsoniae)* and large periwinkle *(Vinca major)* plants, respectively (Ramos-González et al., unpublished results). Biological and molecular characterization of these viruses demonstrated that they should be classified as novel species within the genus *Dichorhavirus.* The complete sequences of RNA1 and *L* ORF in the RNA2 of both viruses share less than 80% of nucleotide sequence identity with known dichorhaviruses. Phylogenetic analyses using the L proteins place both viruses in a subclade with viruses of the known species of the genus.

Submitted: 21/05/2025; *Revised:* 19/08/2025

TABLE 31 - *Rhabdoviridae*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Dichorhavirus chilense*	Vinca chlorotic spot virus	RNA1: OR372158; RNA2: OR372159
New taxon	Species	*Dichorhavirus piracicabense*	Clerodendrum leaf spot virus	RNA1: PV555428; RNA2: PV555429