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

Contents

2025.001S.Ac.v3.Avastrovirus_1nsp

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

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

Summary:
Taxonomic rank(s) affected:
Species

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

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

Justification:

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

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

TABLE 1 - *Avastrovirus*, 1 new taxon*

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

2025.002S.Ac.v3.Mamastrovirus_8nsp_1spren

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

Authors: Yulia Aleshina, Alexander N Lukashev, Torsten Seuberlich

Summary:
Taxonomic rank(s) affected: species

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

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

Proposed taxonomic change(s):

To establish 8 new species:

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

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

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

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TABLE 2 - *Mamastrovirus*, 8 new taxa*

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

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

TABLE 3 - *Mamastrovirus*, 1 rename taxon*

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

2025.003S.A.v2.Paslahepevirus_1nsp

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

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

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

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

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

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

Submitted: 20/06/2025; *Revised:* —

TABLE 4 - *Paslahepevirus*, 1 new taxon*

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

2025.004S.A.v2.Sinaivirus_2spren

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

Authors: Jens H Kuhn

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

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

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

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

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

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

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TABLE 5 - *Sinaivirus*, 2 rename taxa*

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

2025.005S..v1.Pestivirus_8spren

Title: Renaming species of pestiviruses

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

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

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

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

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

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TABLE 6 - *Pestivirus*, 8 rename taxa*

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

2025.006S.Ac.v2.Amarillovirales_3reorgfam

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

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

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

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

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

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

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

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

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

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

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

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

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

TABLE 9 - *Amarillovirales*, 23 new taxa*

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

2025.007S.A.v3.Orthoflavivirus_2nsp_1spren

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

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

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

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

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

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

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

TABLE 10 - *Orthoflavivirus*, 2 new taxa*

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

TABLE 11 - *Orthoflavivirus*, 1 rename taxon*

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