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

Contents

2024.035B.Uc.v3.Tubulavirales_34ng_49ns

Title: Create new genera and species in order *Tubulavirales* – 34 genera and 48 species in the family *Inoviridae* and 1 species in the family *Paulinoviridae*

Authors: Petar Knezevic, Damir Gavric, , Rob Lavigne , Andrew M Kropinski , Dann Turner

Summary:Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The order *Tubulavirales* currently comprise families *Inoviridae* with 26 genera; *Plectroviridae* with four genera and *Paulinoviridae* with two genera

Proposed taxonomic change(s):
Create 38 new genera and 48 new species in the family *Inoviridae.*
Create one new species in the *family Paulinoviridae*

Justification:

Based on the indicated demarcation criteria, all new genera and species fulfil criteria for proposed classification, as shown in supplementary tables and figures. These classifications are supported by data from BLASTn, BLASTp, VIRIDIC, CoreGenes3.5 and by phylogenetic analysis of the Zot and CoaB proteins.

Submitted: 18/07/2024; *Revised:* 26/08/2025

TABLE 1 - *Tubulavirales*, 83 new taxa*. Table too large, see supplementary information sheet supp_info_tab_1

2025.001B.Ac.v3.Alphabravovirinae_1nsf_2ng_2ns

Title: Create a new subfamily *Alphabravovirinae* containing two new genera, *Siouxcentervirus and Merionvirus* and the existing genus *Mapvirus (Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

Summary:

Taxonomic rank(s) affected:
Subfamily, genus, species

Description of current taxonomy:
The genus *Mapvirus* was originally established under the name Ff47virus in 2015 (proposal) and renamed in 2018 (proposal 2018.007B.A.v4.rename137gen6sp). The genus is currently comprised of two species. The other viruses described in this proposal are unclassified lytic siphoviruses which are related to phages of the *genus Mapvirus*

Proposed taxonomic change(s):
Create two new genera *(Siouxcentervirus, Merionvirus)* and assign these genera and *Mapvirus* to a new *subfamily, Alphabravovirinae.*

Justification: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses this proposal is in accord with the demarcation of a subfamily [8].

Submitted: —; *Revised:* 19/08/2025

TABLE 2 - *Alphabravovirinae*, 5 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Alphabravovirinae*		
New taxon	Genus	*Siouxcentervirus*		
New taxon	Species	*Siouxcentervirus jacoren57*	Mycobacterium phage JacoRen57	MK279840
New taxon	Genus	*Merionvirus*		
New taxon	Species	*Merionvirus boshow*	Mycobacterium phage NoShow	ON108645

TABLE 3 - *Alphabravovirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Mapvirus*	*Alphabravovirinae*

2025.002B.Ac.v3.Alvaradovirinae_1nsf_3ng_10ns

Title: Create a new subfamily, *Alvaradovirinae,* with three genera in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru, Anca M. Segall, Johannes Wittmann

Summary:
Taxonomic rank(s) affected:
Subfamily, genus and species

Description of current taxonomy:
Achromobacter phage JWX belongs to the genus *Steinhofvirus* which was created via Taxonomy Proposals 2018.007B.A.v4.rename137gen6sp and 2016.020a-dB.A.v1.Jwxvirus. This genus currently contains two species: *Steinhofvirus JWX* and *Steinhofvirus sv8324*

Proposed taxonomic change(s):
To create a new subfamily *"Alvaradovirinae"* with three genera *"Steinhofvirus", "Amaduovirus" and "Nyaakvirus";* and move *Steinhofvirus sv8324* to the *genus "Amaduovirus"*

Justification: In keeping with the criteria established [3] and supported by VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses we have sufficient evidence to support the creation of this new subfamily, genera and associated species

Submitted: 15/06/2025; *Revised:* 28/08/2025

TABLE 4 - *Alvaradovirinae*, 14 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Alvaradovirinae*		
New taxon	Species	*Steinhofvirus SE2*	Achromobacter phage SE2	OQ817844
New taxon	Genus	*Amaduovirus*		
New taxon	Species	*Amaduovirus AMA2*	Achromobacter phage AMA2	MT241607
New taxon	Genus	*Nyaakvirus*		
New taxon	Species	*Nyaakvirus tuull*	Achromobacter phage tuull	OR396896
New taxon	Species	*Nyaakvirus Axy06*	Achromobacter phage vB_AxyS_19-32_Axy06	MK962627
New taxon	Species	*Nyaakvirus ehaak*	Achromobacter phage ehaak_LB5	OQ817833
New taxon	Species	*Nyaakvirus emuu*	Achromobacter phage emuu_LB7	OQ817834
New taxon	Species	*Nyaakvirus ama1*	Achromobacter phage AMA1	MT241605
New taxon	Species	*Nyaakvirus maay*	Achromobacter phage maay_LB1	OQ817838
New taxon	Species	*Nyaakvirus Axy14*	Achromobacter phage vB_AxyS_19-32_Axy14	MK962633
New taxon	Species	*Nyaakvirus nyaak*	Achromobacter phage nyaak_TL1	OQ817839
New taxon	Species	*Nyaakvirus ART*	Achromobacter phage vB_Ade_ART	MH746817

TABLE 5 - *Alvaradovirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Steinhofvirus*	*Alvaradovirinae*

TABLE 6 - *Alvaradovirinae*, 1 move; rename taxon*

Operation	Rank	New taxon name	New parent taxon	Old taxon name

Move; rename taxon	Species	*Amaduovirus sv8324*	*Alvaradovirinae*	*Steinhofvirus sv8324*

2025.004B.Ac.v3.Shangdongvirus_3ns

Title: To create three new species, in the genus *Shangdongvirus* (class *Caudoviricetes)*

Authors: Sezin Ünlü, Aylin Üsküdar Güçlü

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The virus classified in this proposal does not have a current taxonomic assignment. The *genus Shangdongvirus was* created in 2023 and currently includes a single species (

Proposed taxonomic change(s):
We propose three new species in the genus *Shandongvirus*

Justification:
Phylogenetic, VIRIDIC, and vConTACT2 analysis of a newly isolated phage Baskent_P4_1 infecting *Pseudomonas aeruginosa* suggests that this phage is related to three other bacterial viruses; *Pseudomonas* phage PSASB_03, *Stenotrophomonas* phage vB_SM_ytsc_ply2008005c and *Stenotrophomonas* vB_SmaS_Bhz54. Analysis of genome similarity, TBLASTX distances and phylogeny of the major capsid protein supports its inclusion as new species in the genus *Shangdongvirus.*

Submitted: 14/04/2025; *Revised:* 18/08/2025

TABLE 7 - *Shangdongvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Shangdongvirus baskent*	Pseudomonas phage Baskent_P4_1	PP992516
New taxon	Species	*Shangdongvirus kolkata*	Pseudomonas phage PSASB_03	PQ621116
New taxon	Species	*Shangdongvirus braunschweig*	Stenotrophomonas phage vB_SmaS_Bhz54	OR797041

2025.005B.Ac.v3.Aussievirus_1ng_2ns

Title: Create one new genus *Aussievirus* with two species (class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

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

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

Proposed taxonomic change(s):
To create a new genus, *"Aussievirus"*, with two new species

Justification:
On the basis of VIRIDIC and ViPTree analysis and in keeping with the demarcation criteria described below we have created a new genus for two temperate phages of *Sinorhizobium meliloti.*

Submitted: —; *Revised:* 19/08/2025

TABLE 8 - *Aussievirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Aussievirus*		
New taxon	Species	*Aussievirus aussie*	Sinorhizobium phage Aussie	OR786373
New taxon	Species	*Aussievirus stopsmel*	Sinorhizobium phage StopSmel	OR786374

2025.006B.Uc.v3.Buchnerviridae_1nf_6ng_1mg_1mrs_13ns

Title: Create a new family *(Buchnerviridae)* with seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus)* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

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

Description of current taxonomy:
According to the current taxonomy, the genus *Vieuvirus* has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Vieuvirus* genus includes two species: *Vieuvirus R3177* and *Vieuvirus B1251.*

Proposed taxonomic change(s):
Create new family *(Buchnerviridae)* with seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus)* for a group of *Acinetobacter-specific* phages (realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Vieuvirus.* Based on our analysis, we propose the creation of a family for these phages along with seven distinct genera.

To create a new family, *Buchnerviridae,* with seven genera.
To create a new single species genus, *Slezavirus.*
To create a new genus *Olaviavirus,* with six species.
To create a new single species genus, *Valdenburkvirus.*
To create a new genus *Svidnicavirus,* with two species.
To create a new single species genus, *Lubinvirus.*
To move the genus *Vieuvirus* to new family, *Buchnerviridae.*
To move *Vieuvirus R3177* from *Vieuvirus* genus and rename to new *Jauervirus* genus with one species

(Jauervirus R3177).
To create one new species in *genus Vieuvirus.*

Justification:
After examination of 20 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Buchnerviridae,* to accommodate seven genera *(Slezavirus, Olaviavirus, Valdenburkvirus, Svidnicavirus, Lubinvirus, Jauervirus, Vieuvirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 24/03/2025; *Revised:* 22/10/2025

TABLE 9 - *Buchnerviridae*, 19 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Buchnerviridae*		
New taxon	Genus	*Slezavirus*		
New taxon	Species	*Slezavirus Ab1052phi*	Acinetobacter phage Ab105-2phi	KT588075
New taxon	Genus	*Olaviavirus*		
New taxon	Species	*Olaviavirus phi5013M1*	Acinetobacter phage phi5013-M1	PQ432284
New taxon	Species	*Olaviavirus phi4197*	Acinetobacter phage phi4197	PQ432283
New taxon	Species	*Olaviavirus phi5013M2*	Acinetobacter phage phi5013-M2	PQ432285
New taxon	Species	*Olaviavirus Ab11510phi*	Acinetobacter phage Ab11510-phi	MT361972
New taxon	Species	*Olaviavirus phi503811536*	Acinetobacter phage phi5038-11536	PQ432286
New taxon	Species	*Olaviavirus phi503811551*	Acinetobacter phage phi5038-11551	PQ432288
New taxon	Genus	*Valdenburkvirus*		
New taxon	Species	*Valdenburkvirus Acba23*	Acinetobacter phage Acba_23	PV067694
New taxon	Genus	*Svidnicavirus*		
New taxon	Species	*Svidnicavirus Ftm*	Acinetobacter phage vB_AbaS_Ftm	PP236950
New taxon	Species	*Svidnicavirus Eva*	Acinetobacter phage vB_AbaS_Eva	PP236951
New taxon	Genus	*Lubinvirus*		
New taxon	Species	*Lubinvirus Ab16562*	Acinetobacter phage Ab1656-2	MZ675741
New taxon	Species	*Vieuvirus A24903*	Acinetobacter phage A2490.3	OR180313
New taxon	Genus	*Jauervirus*		

TABLE 10 - *Buchnerviridae*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Vieuvirus*	*Buchnerviridae*

TABLE 11 - *Buchnerviridae*, 1 move; rename taxon*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old taxon name**
Move; rename taxon	Species	*Jauervirus R3177*	*Buchnerviridae*	*Vieuvirus R3177*

2025.007B.Ac.v3.Cardingvirinae_1nsf_2ng_18ns

Title: Create a new subfamily *(Cardingvirinae)* with two genera and 18 species *(Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Nina Chanisvili

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

Description of current taxonomy:
There is no current taxonomy for these lytic phages isolated against *Bacteroides fragilis*

Proposed taxonomic change(s):
Add two new genera, *"Kherlenvirus"* and *"Gotuavirus",* and 18 new species to a new *subfamily "Cardingvirinae"*

Justification: On the basis of VIRIDIC, CoreGenes and phylogenetic analyses and in keeping with the criteria which we have established for creation of new species, genera and subfamilies these previously unclassified Bacteroides lytic siphoviruses belong to two genera in a new subfamily [8].

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 12 - *Cardingvirinae*, 21 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Cardingvirinae*		
New taxon	Genus	*Kherlenvirus*		
New taxon	Species	*Kherlenvirus BF486P1*	Bacteroides phage BF486P1	OP172666
New taxon	Species	*Kherlenvirus BK649P1*	Bacteroides phage BK649P1	OP172680
New taxon	Species	*Kherlenvirus BF695P2*	Bacteroides phage BF695P2	OP172673
New taxon	Species	*Kherlenvirus BF698P1*	Bacteroides phage BF698P1	OP172675
New taxon	Species	*Kherlenvirus BF698P3*	Bacteroides phage BF698P3	OP172676
New taxon	Genus	*Gotuavirus*		
New taxon	Species	*Gotuavirus B408*	Bacteroides phage B40-8	FJ008913
New taxon	Species	*Gotuavirus BF10P2*	Bacteroides phage BF10P2	OP172663
New taxon	Species	*Gotuavirus BF10P3*	Bacteroides phage BF10P3	OP172664
New taxon	Species	*Gotuavirus BF766P1*	Bacteroides phage BF766P1	OP172678
New taxon	Species	*Gotuavirus VA7*	Bacteroides phage GEC_vB_Bfr_VA7	MW916539
New taxon	Species	*Gotuavirus Barc2635*	Bacteroides phage Barc2635	MN078104
New taxon	Species	*Gotuavirus NCTC*	Bacteroides phage vB_BfraS_NCTC	MW314138
New taxon	Species	*Gotuavirus BF344P1*	Bacteroides phage BF344P1	OP172665
New taxon	Species	*Gotuavirus BF766P4*	Bacteroides phage BF766P4	OP172679
New taxon	Species	*Gotuavirus BF702P1*	Bacteroides phage BF702P1	OP172677
New taxon	Species	*Gotuavirus B12414*	Bacteroides phage B124-14	HE608841
New taxon	Species	*Gotuavirus gv23*	Bacteroides phage vB_BfrS_23	MT630433
New taxon	Species	*Gotuavirus UZM3*	Bacteroides phage vB_BfrS_UZM3	OQ116603

2025.008B.Ac.v2.Caudoviricetes_11ns

Title: To create eleven new species in the Class *Caudoviricetes*

Authors: Andrew D. Millard, Andrew M. Kropinski, , , , , ,

Summary:Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
Add one new species to the genus *Maaswegvirus*
Add one new species to the genus *Efquatrovirus*
Add one new species to the genus *Kuravirus*
Add one new species to the genus *Gilesvirus*
Add one new species to the genus *Karamvirus*
Add one new species to the genus Nanditavirus
Add one new species to the genus Corndogvirus
Add one new species to the genus Birdsnestvirus
Add one new species to the genus Przondovirus
Add one new species to the genus Rosenblumvirus
Add one new species to the genus Tequatrovirus

Justification:
These new taxa were identified using taxMyPhage which shows 96.7% accuracy at the genus level and 97.9% accuracy at the species level. The system also detects inconsistencies in current ICTV classifications, identifying cases where genera did not adhere to ICTV's 70% inter-genomic similarity threshold for genus classification or 95% similarity for species. Each of the bacteriophages detailed in this proposal fall within the demarcation criteria for inclusion as new species in existing genera within the class *Caudoviricetes.*

Submitted: 05/06/2025; *Revised:* 26/08/2025

TABLE 13 - *Caudoviricetes*, 11 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Maaswegvirus centimanus*	Klebsiella phage vB_KpM_Centimanus	OZ240615
New taxon	Species	*Efquatrovirus MFDL*	Enterococcus phage vB_EfaS_MF-DL	PQ799575
New taxon	Species	*Kuravirus PE006*	Escherichia phage vB_EcoM_PE006	PQ812250
New taxon	Species	*Gilesvirus ZM2*	Mycobacterium phage ZM2	PQ821648
New taxon	Species	*Karamvirus id4496*	Enterobacter phage vB_Ecl_id4496	PQ824230
New taxon	Species	*Nanditavirus quinnavery*	Arthrobacter phage QuinnAvery	PQ844483
New taxon	Species	*Corndogvirus vagabond*	Mycobacterium phage Vagabond	PQ844484
New taxon	Species	*Birdsnestvirus hashim76*	Mycobacterium phage Hashim76	PQ844485
New taxon	Species	*Przondovirus HJK2*	Klebsiella phage HJK2	PQ858442
New taxon	Species	*Rosenblumvirus cap046*	Staphylococcus phage CapO46	PV007823
New taxon	Species	*Tequatrovirus BMB16*	Escherichia phage vB_EcoM_BMB16	PV102577

2025.009B.Ac.v3.Ceeteevirinae_1nsf_1ng_15ns

Title: Create one new genus, *Margaretvirus,* with seven species in a new subfamily, *Ceeteevirinae* (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

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

Description of current taxonomy: These are unclassified lytic siphoviruses which are related to *Aziravirus, Ponsvirus and Emalynvirus*

Proposed taxonomic change(s): Create a new genus *(Margaretvirus)* and cluster it with *Aziravirus,* Ponsvirus *and Emalynvirus* in a new *subfamily, Ceeteevirinae.*

Justification: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in accord with the criteria for the establishment of new species, genera and subfamilies this group of viruses belong to a new subfamily which we have chosen to call *Ceeteevirinae* after Cluster CT in the Actinobacteriophage Database[8].

Submitted: —; *Revised:* 19/08/2025

TABLE 14 - *Ceeteevirinae*, 17 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Ceeteevirinae*		
New taxon	Species	*Aziravirus fribs8*	Gordonia phage Fribs8	OR553910
New taxon	Species	*Aziravirus nibbles*	Gordonia phage Nibbles	OR253918
New taxon	Species	*Ponsvirus manor*	Gordonia phage MAnor	PQ184784
New taxon	Species	*Ponsvirus summitacademy*	Gordonia phage SummitAcademy	OP297531
New taxon	Species	*Ponsvirus elinal*	Gordonia phage Elinal	OR553897
New taxon	Species	*Emalynvirus swatntears*	Gordonia phage SweatNTears	MK967383
New taxon	Species	*Emalynvirus billdoor*	Gordonia phage BillDoor	PP208920
New taxon	Species	*Emalynvirus tolls*	Gordonia phage Tolls	MW862988
New taxon	Genus	*Margaretvirus*		
New taxon	Species	*Margaretvirus orla*	Gordonia phage Orla	MT889367
New taxon	Species	*Margaretvirus yakult*	Gordonia phage Yakult	MK875791
New taxon	Species	*Margaretvirus margaret*	Gordonia phage Margaret	MH271302
New taxon	Species	*Margaretvirus ranchparmcat*	Gordonia phage RanchParmCat	PQ868985
New taxon	Species	*Margaretvirus GiKK*	Gordonia phage GiKK	OL455888
New taxon	Species	*Margaretvirus button*	Gordonia phage Button	ON970621
New taxon	Species	*Margaretvirus jamzy*	Gordonia phage Jamzy	OR159649

TABLE 15 - *Ceeteevirinae*, 3 move taxa*

Operation	**Rank**	**Taxon name**	**New parent taxon**
Move taxon	Genus	*Aziravirus*	*Ceeteevirinae*
Move taxon	Genus	*Ponsvirus*	*Ceeteevirinae*

Move taxon	Genus	*Emalynvirus*	*Ceeteevirinae*

2025.011B.Ac.v3.Chaseviridae_1ng_12ns

Title: Add species to existing genera in the family *Chaseviridae* and create one new genus, *Qiaoyingvirus* (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Hany Anany

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The family *Chaseviridae* was created through Taxonomy Proposal 2019.047B. The family currently consists of two subfamilies *(Cleopatravirinae* and *Nefertitivirinae)* and 13 genera.

Proposed taxonomic change(s):
Add new species to the genera *Fifivirus,* Loessnervirus, Carltongylesvirus *Longwangvirus* and *Shantouvirus;* and create a new genus *"Qiaoyingvirus"*

Justification:
Species included in the family *Chaseviridae* are myoviruses which infect members of the genera *Escherichia,* Erwinia, Pectobacterium, *Shewanella* and *Aeromonas.* Common proteins include a RNA polymerase, DNA polymerase, primase and exonuclease. This proposal adds new species to several existing genera and creates one new genus. These genomes satisfy the existing demarcation criteria for the creation of new species and genera.

Submitted: 15/05/2025; *Revised:* 25/08/2025

TABLE 16 - *Chaseviridae*, 13 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Fifivirus EaPF7*	Erwinia phage EaPF7	PQ431420
New taxon	Species	*Fifivirus aioli*	Erwinia phage Aioli	OQ818694
New taxon	Species	*Fifivirus SNUABM27*	Erwinia phage pEa_SNUABM_27	MW349138
New taxon	Species	*Loessnervirus papaline*	Erwinia phage Papaline	OQ818704
New taxon	Species	*Loessnervirus fougasse*	Erwinia phage Fougasse	OQ818698
New taxon	Species	*Carltongylesvirus YSF*	Escherichia phage Ecp_YSF	OR327751
New taxon	Species	*Carltongylesvirus FXie2024a*	Escherichia phage FXie-2024a	PP107930
New taxon	Species	*Carltongylesvirus JL1*	Escherichia phage vB_EcoM_JL1	OR791690
New taxon	Species	*Carltongylesvirus EcoM1*	Escherichia phage EcoM1	PQ818760
New taxon	Genus	*Qiaoyingvirus*		
New taxon	Species	*Qiaoyingvirus A050*	Aeromonas phage phiA050	PP763568
New taxon	Species	*Longwangvirus h1*	Aeromonas phage vB_AhydM-H1	OR795024
New taxon	Species	*Shantouvirus LA93P1*	Aeromonas phage LA93P1	PV258714

2025.012B.Ac.v3.Comeauvirus_1ng_2ns

Title: Create one new genus *Comeauvirus* with two new species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
Create a new genus *"Comeauvirus"* and two new species

Justification:
The majority of the *Vibrio cholerae* phages that we have classified are siphoviruses, while the ones belonging to the proposed genus, "Comeauvirus" are small lytic myoviruses. VIRIDIC and ViPTree analyses reveal that this forms a genus in a cluster of phages including *Yokohamavirus PEi21, Yokohamavirus MSW3* and *Iodovirus PLPE*

Submitted: —; *Revised:* —

TABLE 17 - *Comeauvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Comeauvirus*		
New taxon	Species	*Comeauvirus cv138*	Vibrio phage vB_VchM-138	JQ177064
New taxon	Species	*Comeauvirus CPT1*	Vibrio phage CP-T1	JQ177061

2025.013B.Uc.v4.Crassvirales_reorganisation

Title: Reclassifying the order *Crassvirales* to establish two sister orders and one sister family, with the creation of six new families, 38 new genera, and 99 new species

Authors: Fabian TS Bastiaanssen, Rémi Denise, George S Bouras, Steven R Stockdale, Robert A Edwards, Colin Hil, Andrey N Shkoporov,

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

Description of current taxonomy:
Crassvirales was established under taxonomic proposal 2021.022B

Proposed taxonomic change(s):
We propose:
The establishment of demarcation criteria for the order *Crassvirales*
The establishment of the order *Paracrassvirales* containing one novel family
The establishment of the order *Metacrassvirales* containing one novel family
The adjustment of demarcation criteria for families within *Crassvirales*
The creation of one new family within *Crassvirales*
The moving and renaming of one genus within *Crassvirales*
The adjustment of demarcation criteria for subfamilies within *Crassvirales*

The adjustment of demarcation criteria for genera within *Crassvirales* to reflect ICTV guidelines
The creation of 38 new genera
The adjustment of demarcation criteria for species within *Crassvirales* to reflect ICTV guidelines
The creation of 99 new species

Justification:
Currently, *Crassvirales* lacks demarcation criteria. The existing criteria within *Crassvirales* are ambiguous, unintuitive and based on outdated methods and results. Phylogenetic trees utilizing structural and maximum likelihood approaches based on marker genes reveal the formation of unique clades that align with the proposed orders and support the proposed changes to family, genus and species demarcation criteria.

Submitted: 22/06/2025; *Revised:* 29/10/2025

TABLE 18 - *Crassvirales*, 108 new taxa*. Table too large, see supplementary information sheet supp_info_tab_18

TABLE 19 - *Crassvirales*, 26 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old parent taxon	Old taxon name
Move; rename taxon	Species	*Smehivirus intestinihominis*	*Darmviridae*	*Suoliviridae*	*Burzaovirus intestinihominis*
Move; rename taxon	Species	*Scendivirus animalis*	*Darmviridae*	*Suoliviridae*	*Buhlduvirus animalis*
Move; rename taxon	Species	*Arseivirus communis*		*Coarsevirinae*	*Junduvirus communis*
Move; rename taxon	Species	*Flerehovirus oralis*		*Asinivirinae*	*Kahnovirus oralis*
Move; rename taxon	Species	*Sdahravirus coli*	*Darmviridae*	*Suoliviridae*	*Burzaovirus coli*
Move; rename taxon	Species	*Cervivirus coli*		*Bearivirinae*	*Afonbuvirus coli*
Move; rename taxon	Species	*Ponsivirus faecalis*		*Loutivirinae*	*Buchavirus faecalis*
Move; rename taxon	Species	*Ildiruevirus splanchnicus*		*Loutivirinae*	*Buchavirus splanchnicus*
Move; rename taxon	Species	*Ildiruevirus oralis*		*Loutivirinae*	*Buchavirus oralis*
Move; rename taxon	Species	*Ildiruevirus coli*		*Loutivirinae*	*Buchavirus coli*
Move; rename taxon	Species	*Snepbuvirus splanchnicus*		*Asinivirinae*	*Kehishuvirus splanchnicus*

Move; rename taxon	Species	*Burzaovirus faecalis*	*Darmviridae*	*Suoliviridae*	*Burzaovirus faecalis*
Move; rename taxon	Species	*Ibumevirus hominis*		*Uncouvirinae*	*Birpovirus hominis*
Move; rename taxon	Species	*Buhlduvirus porcinus*	*Darmviridae*	*Suoliviridae*	*Buhlduvirus porcinus*
Move; rename taxon	Species	*Cacepaovirus simiae*	*Darmviridae*	*Suoliviridae*	*Cacepaovirus simiae*
Move; rename taxon	Species	*Snuvovirus hominis*		*Uncouvirinae*	*Aurodevirus hominis*
Move; rename taxon	Species	*Wiibonovirus intestinalis*		*Churivirinae*	*Jahgtovirus intestinalis*
Move; rename taxon	Species	*Sulruvirus americanus*		*Loutivirinae*	*Blohavirus americanus*
Move; rename taxon	Species	*Trofluuvirus faecalis*		*Boorivirinae*	*Canhaevirus faecalis*
Move; rename taxon	Species	*Chuhaivirus simiae*	*Darmviridae*	*Suoliviridae*	*Chuhaivirus simiae*
Move; rename taxon	Species	*Taduhovirus hiberniae*		*Uncouvirinae*	*Aurodevirus hiberniae*
Move; rename taxon	Species	*Shuolduvirus copri*		*Loutivirinae*	*Buchavirus copri*
Move; rename taxon	Species	*Horekuvirus hominis*		*Loutivirinae*	*Buchavirus hominis*
Move; rename taxon	Species	*Horekuvirus hiberniae*		*Loutivirinae*	*Buchavirus hiberniae*
Move; rename taxon	Species	*Shelovirus americanus*		*Boorivirinae*	*Culoivirus americanus*
Move; rename taxon	Species	*Shelovirus intestinalis*		*Boorivirinae*	*Culoivirus intestinalis*

TABLE 20 - *Crassvirales*, 1 move taxon*

Operation	**Rank**	**Taxon name**	**New parent taxon**	**Old parent taxon**
Move taxon	Subfamily	*Oafivirinae*	*Darmviridae*	*Suoliviridae*

2025.014B.Ac.v3.Dravavirinae_1nsf_3ng_5ns

Title: Create a new subfamily *Dravavirinae* with three new genera *(Hualiencityvirus, Rodicavirus* and *Tongtianvirus)* and five species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Maja Rupnik, Tomaž Accetto

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

Description of current taxonomy:
The lytic siphophages isolated against *Bacteroides,* Parabacteroides, *Elizabethkingia* and *Alistipes (Order Bacteroidales)* described in this proposal are currently unclassified.

Proposed taxonomic change(s):
Create three new genera, *"Hualiencityvirus", "Tongtianvirus"* and *"Rodicavirus"* consisting of five new species and assign them to a new *subfamily, "Dravavirinae"*

Justification:
These five viruses are lytic, possess a siphophage morphology and have ca. 44.5 kb genomes. On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in keeping with our definitions for what constitute a subfamily, we propose to create *"Dravavirinae"* with three genera *"Hualiencityvirus", "Tongtianvirus"* and *"Rodicavirus"*

Submitted: 15/06/2025; *Revised:* —

TABLE 21 - *Dravavirinae*, 9 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Dravavirinae*		
New taxon	Genus	*Hualiencityvirus*		
New taxon	Species	*Hualiencityvirus TCUEAP2*	Elizabethkingia phage TCUEAP2	OK632025
New taxon	Genus	*Tongtianvirus*		
New taxon	Species	*Tongtianvirus AS73P1*	Alistipes phage AS73P1	OP172640
New taxon	Genus	*Rodicavirus*		
New taxon	Species	*Rodicavirus PD491P1*	Parabacteroides phage PD491P1	OP172815
New taxon	Species	*Rodicavirus PDS1*	Parabacteroides phage PDS1	MN929097
New taxon	Species	*Rodicavirus C185S2P*	Bacteroides phage C1_85S2P	OR296437

2025.015B.Ac.v3.Drulisvirus_1ns

Title: Create one new species in the genus *Drulisvirus*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The genus *Drulisvirus* currently includes 19 species and is included in the subfamily Slopekvirinae,

family *Autoscriptoviridae, order Autographivirales*

Proposed taxonomic change(s):
Create one new species, *Drulisvirus workingina*

Justification:
Escherichia phage vB_VIPECOTPH05B was isolated from Tarlac Provincial Hospital, Tarlac, Philippines. Based on VIRIDIC analysis with other species in the genus *Drulisvirus,* we propose the creation of a new phage species, *Drulisvirus workingina* in honor of the working mothers and diverse individuals of the Virology and Vaccine Institute of the Philippines Program.

Submitted: 04/12/2025; *Revised:* —

TABLE 22 - *Drulisvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Drulisvirus workingina*	Escherichia phage vB_VIPECOTPH05B	PQ429080

2025.016B.Ac.v3.Durvirinae_1nsf_5ng_9ns

Title: Create a new subfamily, *Durvirinae,* with six genera (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke,

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

Description of current taxonomy:
The bacterial viruses described in this proposal are currently unclassified. These lytic siphoviruses are peripherally related to the genus *Sourvirus* (Taxonomy Protocol 2018.122B.A.v1.Sourvirus)

Proposed taxonomic change(s):
Create a new subfamily *("Durvirinae")* with *Sourvirus* and five new proposed genera, *"Mossrosevirus", "Ligmavirus"* , *"Nhagosvirus", "Anclarvirus"* and *Duluthvirus"* based upon The Actinobacteriophage Database Cluster DR phages.

Justification: On the basis of VIRIDIC, ViPTree and phylogenetic analyses we recognize that the lytic siphoviruses belonging to The Actinobacteriophages Database Cluster DR represent five new genera *("Mossrosevirus", "Ligmavirus", "Nhagosvirus", "Anclarvirus"* and *"Duluthvirus")* and propose to cluster these in a new subfamily *"Durvirinae"* with members of the *Sourvirus.*

Submitted: —; *Revised:* 20/08/2025

TABLE 23 - *Durvirinae*, 15 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Durvirinae*		
New taxon	Genus	*Ligmavirus*		
New taxon	Species	*Ligmavirus ligma*	Gordonia phage Ligma	OM105886
New taxon	Species	*Ligmavirus mariokart*	Gordonia phage Mariokart	MT657335
New taxon	Genus	*Mossrosevirus*		

New taxon	Species	*Mossrosevirus mossrose*	Gordonia phage MossRose	OR253912
New taxon	Species	*Mossrosevirus caib*	Gordonia phage CaiB	ON108644
New taxon	Species	*Mossrosevirus makomanhole*	Gordonia phage MakoManhole	PQ184807
New taxon	Genus	*Nhagosvirus*		
New taxon	Species	*Nhagosvirus nhagos*	Gordonia phage Nhagos	MN369758
New taxon	Genus	*Anclarvirus*		
New taxon	Species	*Anclarvirus anclar*	Gordonia phage AnClar	MN908693
New taxon	Species	*Anclarvirus biggitybass*	Gordonia phage BiggityBass	ON260813
New taxon	Genus	*Duluthvirus*		
New taxon	Species	*Duluthvirus littlemuchkin*	Gordonia phage LittleMunchkin	OP751153

TABLE 24 - *Durvirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Sourvirus*	*Durvirinae*

2025.017B.Ac.v3.Evaavirus_1ng_1ns

Title: Create one new genus, *Evaavirus,* with a single species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create one new genus, *"Evaavirus"* including one new species.

Justification: While the Actinobacteriophage Database groups lytic Gordonia phage Evaa in Cluster DR our BLASTN analysis reveals that it is sufficiently different from *Sourvirus* to deserve recognition as a separate genus. This is supported by VIRIDIC analysis which reveals that it only shares 44% overall DNA sequence identity with *Sourvirus sour.*
Submitted: —; *Revised:* 18/08/2025

TABLE 25 - *Evaavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Evaavirus*		
New taxon	Species	*Evaavirus evaa*	Gordonia phage Evaa	OP434461

2025.018B.Ac.v3.Felixounavirus_3ns

Title: Create three new species in the genus *Felixounavirus* (class *Caudoviricetes,* family *Andersonviridae,* subfamily *Ounavirinae)*

Authors: Emilia Andrea V. Sabban, Stephen Kyle C. Arcan, Adonis N. Eclipse, Dexter Bryan L. Esliza, Paul Jeremy C. Lanete, Lindley C. Susi, Gelito Joseph M. Sikat

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Felixounavirus* currently includes 97 species.

Proposed taxonomic change(s):
Add three new species, *Felixounavirus vipecomarii, Felixounavirus vipecomesa* and *Felixounavirus vipecohospii* to the *genus Felixounavirus.*

Justification:
Three new species within the genus *Felixounavirus* are proposed based on the species demarcation criteria of <95% intergenomic similarity. Escherichia phages vB_EcoM_D4, vB_EcoM_E9, and vB_EcoM_H12 are closely related to *Felixounavirus TP1* (GenBank NC_041979.1), exhibiting 92.2% intergenomic similarity.

Submitted: 29/08/2024; *Revised:* 26/08/2025

TABLE 26 - *Felixounavirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Felixounavirus vipecomarii*	Escherichia phage vB_EcoM_D4	PP886228
New taxon	Species	*Felixounavirus vipecomesa*	Escherichia phage vB_EcoM_E9	PP886229
New taxon	Species	*Felixounavirus vipecohospii*	Escherichia phage vB_EcoM_H12	PP952733

2025.019B.Ac.v3.Fenglinvirus_1ng_1ns

Title: Create one new genus *(Fenglinvirus)* with one species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
Create one new genus *"Fenglinvirus"* and one new species

Justification:
Bacillus alcalophilus CGMCC 1.3604 possesses two Mu-like transposable prophages now identified in GenBank as Bacillus phage BalMu-1 copy 1 (KP063902; 39873 bp; and NC_030945.1; Exemplar) and Bacillus phage BalMu-1 copy 2 (KP063903; 39861 bp). We have chosen the first mentioned as the exemplar.

Submitted: —; *Revised:* 19/08/2025

TABLE 27 - *Fenglinvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Fenglinvirus*		
New taxon	Species	*Fenglinvirus BalMu1*	Bacillus phage BalMu-1	KP063902

2025.020B.Ac.v3.Frobishervirinae_1nsf_1ng_1ns

Title: Create a new subfamily, *Frobishervirinae* with one existing *genus, Samwavirus,* and one new genus, *Branvirus* (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru

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

Description of current taxonomy:
The genus *Samwavirus* was created via Taxonomy Proposal 2019.027B and contains five species. *Corynebacterium* phage Bran is currently unclassified.

Proposed taxonomic change(s):
Create a new subfamily *"Frobishervirinae"* containing one new genus *"Branvirus"* with a single species. Move the existing genus *Samwavirus* into the *subfamily "Frobishervirinae"*

Justification: VIRIDIC and Clinker analyses reveal that there is sufficient evidence to create a subfamily for Branvirus and *Samwavirus* [8]

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 28 - *Frobishervirinae*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Frobishervirinae*		
New taxon	Genus	*Branvirus*		
New taxon	Species	*Branvirus bran*	Corynebacterium phage Bran	MK977714

TABLE 29 - *Frobishervirinae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Samwavirus*	*Frobishervirinae*

2025.021B.Uc.v3.Gelderlandvirus_1ns

Title: Create one new species in the genus *Gelderlandvirus* (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Iwona Gientka, Michał J. Wójcicki

Summary:
Taxonomic rank(s) affected:
Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:
Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Gelderlandvirus* genus includes five species: *Gelderlandvirus cgg41,* Gelderlandvirus melville, Gelderlandvirus s16, Gelderlandvirus stml198, *and Gelderlandvirus stp4a.*

Proposed taxonomic change(s):
Follwing a genomic analysis of phages deposited in the NCBI database we propose to create one new species in the *genus Gelderlandvirus.*

Justification:
Based on DNA and protein similarity, the one proposed new species is coherent and together with the five known species *(Gelderlandvirus cgg41,* Gelderlandvirus melville, Gelderlandvirus s16, Gelderlandvirus stml198, *and Gelderlandvirus stp4a)* can be classified in the genus *Gelderlandvirus.*

Submitted: 20/03/2025; *Revised:* 22/08/2025

TABLE 30 - *Gelderlandvirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Gelderlandvirus SEA1*	Salmonella phage SEA1	OQ927978

2025.023B.Ac.v4.Illiduovirus_1ng_3ns

Title: Create a new genus *(Illiduovirus)* with three species in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru, Andrew Millard

Summary:
Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
To create a new genus, Illiduovirus, with three species of *Pseudomonas phages*

Justification:
The bacterial viruses described in this proposal are lytic myoviruses with genomes of approximately 200 kb. Analysis with ViPTree and VIRIDIC indicate that these viruses form a distinct genus that includes three new species based on the current ICTV demarcation criteria for these ranks.

Submitted: 15/06/2025; *Revised:* 29/08/2025

TABLE 31 - *Illiduovirus*, 4 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Illiduovirus*		
New taxon	Species	*Illiduovirus peetri*	Pseudomonas phage vB_PpuM-Peetri	PP496444
New taxon	Species	*Illiduovirus voja6*	Pseudomonas phage vB_PpuM-Voja-6	PP496442
New taxon	Species	*Illiduovirus lauda*	Pseudomonas phage vB_PpuM-Lauda	PP496443

2025.024B.Ac.v3.Huairouvirus_1ng_1ns

Title: Create one new genus *(Huairouvirus)* with a single species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

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

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus, *Huairouvirus* with one new species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage P3.1 forms a single species in a new genus in accordance with the established demarcation criteria.

Submitted: —; *Revised:* 29/08/2025

TABLE 32 - *Huairouvirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Huairouvirus*		
New taxon	Species	*Huairouvirus P31*	Nocardia phage P3.1	MW582532

2025.025B.Ac.v2.Caudoviricetes_10ns_1rms

Title: Create 10 new species and abolish one species (Class: *Caudoviricetes)*

Authors: Ivan M. Pchelin, , , , , , ,

Summary:Taxonomic rank(s) affected:
Species

Proposed taxonomic change(s):
We propose to;
Abolish one species, *Pbunavirus pv141*
Create of 10 new species in existing genera

Justification:

The proposed species share ≤95% genome similarity with the existing ones. By genome similarity and clustering analysis, all these potential new species reside within existing genera. The species *Pbunavirus pv141* is proposed for removal since it shares >95% genome similarity with other existing species in that genus.

Submitted: 06/12/2025; *Revised:* 09/01/2025

TABLE 33 - *Caudoviricetes*, 10 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Pakpunavirus mediocris*	Pseudomonas phage vB_PaeM_37F	PQ758387
New taxon	Species	*Pakpunavirus js*	Pseudomonas phage JS	OQ210008
New taxon	Species	*Pakpunavirus hhbs181*	Pseudomonas phage HHBS18_1	PQ287651
New taxon	Species	*Pakpunavirus hhbs91*	Pseudomonas phage HHBS9_1	PQ287655
New taxon	Species	*Pbunavirus hhbs511*	Pseudomonas phage HHBS51_1	PQ287641
New taxon	Species	*Pbunavirus hhbs122*	Pseudomonas phage HHBS12_2	PQ287652
New taxon	Species	*Webervirus gbh029*	Klebsiella phage vB_Kpn_GBH029	OU342755
New taxon	Species	*Drulisvirus gbh038*	Klebsiella phage vB_Kpn_GBH038	OU509533
New taxon	Species	*Drulisvirus gbh001*	Klebsiella phage vB_Kpn_GBH001	OU509534
New taxon	Species	*Przondovirus gbh014*	Klebsiella phage vB_Kpn_GBH014	OU342754

TABLE 34 - *Caudoviricetes*, 1 abolish taxon*

Operation	Rank	Abolished taxon name
Abolish taxon	Species	*Pbunavirus PA8P1*

2025.027B.Ac.v3.Jianjiangvirinae_1nsf_2ng_22ns

Title: Create a new subfamily *(Jianjiangvirinae)* with two genera and 22 species (Class *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Juntao Shen

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

Description of current taxonomy:
There is no taxonomy for these lytic phages isolated against *Bacteroides caccae* and *Bacteroides ovatus* from sewage

Proposed taxonomic change(s):
Add two new genera *(Luojiangvirus* and *Caojiangvirus)* and 22 new species to a new subfamily

Justification:
In accord with the established demarcation criteria for delineating a new subfamily, genus and species [3] these *Bacteroides* phages, isolated in China, fall into two new genera *(Luojiangvirus* and *Caojiangvirus)* in a new subfamily which we have chosen to call *Pearlrivervirinae.*

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 35 - *Jianjiangvirinae*, 25 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Jianjiangvirinae*		
New taxon	Genus	*Luojiangvirus*		
New taxon	Species	*Luojiangvirus BC679P5*	Bacteroides phage BC679P5	OP172651
New taxon	Species	*Luojiangvirus BC669P1*	Bacteroides phage BC669P1	OP172644
New taxon	Species	*Luojiangvirus BC669P2*	Bacteroides phage BC669P2	OP172645
New taxon	Species	*Luojiangvirus BC679P1*	Bacteroides phage BC679P1	OP172647
New taxon	Species	*Luojiangvirus BC679P2*	Bacteroides phage BC679P2	OP172648
New taxon	Species	*Luojiangvirus BC669P3*	Bacteroides phage BC669P3	OP172646
New taxon	Species	*Luojiangvirus BC679P3*	Bacteroides phage BC679P3	OP172649
New taxon	Genus	*Caojiangvirus*		
New taxon	Species	*Caojiangvirus BO668P2*	Bacteroides phage BO668P2	OP172699
New taxon	Species	*Caojiangvirus BK687P4*	Bacteroides phage BK687P4	OP172684
New taxon	Species	*Caojiangvirus BK687P2*	Bacteroides phage BK687P2	OP172682
New taxon	Species	*Caojiangvirus BK687P3*	Bacteroides phage BK687P3	OP172683
New taxon	Species	*Caojiangvirus BK745P1*	Bacteroides phage BK745P1	OP172691
New taxon	Species	*Caojiangvirus BK745P4*	Bacteroides phage BK745P4	OP172693
New taxon	Species	*Caojiangvirus BC422P2*	Bacteroides phage BC422P2	OP172643
New taxon	Species	*Caojiangvirus BK687P1*	Bacteroides phage BK687P1	OP172681
New taxon	Species	*Caojiangvirus BK687P5*	Bacteroides phage BK687P5	OP172685
New taxon	Species	*Caojiangvirus BK745P3*	Bacteroides phage BK745P3	OP172692
New taxon	Species	*Caojiangvirus BK735P2*	Bacteroides phage BK735P2	OP172688
New taxon	Species	*Caojiangvirus BK735P3*	Bacteroides phage BK735P3	OP172689
New taxon	Species	*Caojiangvirus BO668P1*	Bacteroides phage BO668P1	OP172698
New taxon	Species	*Caojiangvirus BK735P1*	Bacteroides phage BK735P1	OP172687
New taxon	Species	*Caojiangvirus BK735P4*	Bacteroides phage BK735P4	OP172690

2025.029B.Ac.v3.Justusliebigvirus_1ns

Title: To create one species in the genus *Justusliebigvirus* (class *Caudoviricetes)*

Authors: Aaryan Harshith, Paul Bollyky, Jessica C. Sacher, Carlo Armijo

Summary:

Taxonomic rank(s) affected:

Species

Description of current taxonomy:

The genus *Justusliebigvirus* was established by the proposal 2021.080B. The genus currently contains six species.

Proposed taxonomic change(s):

This proposal adds one new species, *Escherichia* phage Cardinal, to the *genus Justusliebigvirus.*

Justification:

VIRIDIC analysis indicates that phage Cardinal satisfies the species similarity threshold proposed by the ICTV Bacterial Viruses Subcommittee. Proteomic and phylogenetic evidence further supports the placement of this phage in the genus *Justusliebigvirus.*

Submitted: 22/01/2025; *Revised:* —

TABLE 36 - *Justusliebigvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Justusliebigvirus cardinal*	Escherichia phage Cardinal	PQ567651

2025.030B.Ac.v3.Kagunavirus_3ns

Title: Create three new species in the genus *Kagunavirus* (Class *Caudoviricetes,* Family *Sarkviridae)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Kagunavirus* currently includes 12 species. The genus was originally established in 2015 and was included within the family *Sarkviridae* in 2024.

Proposed taxonomic change(s):
Create three new species in the genus *Kagunavirus; Kagunavirus ligaya, Kagunavirus* malou *and* Kagunavirus ohbeberoi

Justification:
Based on VIRIDIC analysis, we propose the creation of three new phage species in the genus *Kagunavirus. Kagunavirus ligaya* is named after the Filipino term "Ligaya" which explicitly means joy or happiness. *Kagunavirus malou* is derived from a nickname of one of co-authors parents. *Kagunavirus* ohbeberoi is derived from the Filipino slang term *"bebe" that* refers to friends and family.

Submitted: 04/12/2025; *Revised:* —

TABLE 37 - *Kagunavirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Kagunavirus ohbeberoi*	Escherichia phage vB_VIPECOMC04	PQ423993
New taxon	Species	*Kagunavirus ligaya*	Escherichia phage vB_ VIPECOTH07	PQ417132
New taxon	Species	*Kagunavirus malou*	Escherichia phage vB_ VIPECOTPH05A	PQ429079

2025.031B.Ac.v3.Kanagawavirus_4ns

Title: Create four new species in the genus *Kanagawavirus* (class *Caudoviricetes,* order

Pantevenvirales, family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:

Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:

Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Kanagawavirus* genus includes five species: *Kanagawavirus cipnine, Kanagawavirus eclm, Kanagawavirus mime, Kanagawavirus pei20,* and *Kanagawavirus threeohfive.*

Proposed taxonomic change(s):

We performed a genomic analysis of phages deposited in the NCBI database. We propose to create four new species in the *genus Kanagawavirus.*

Justification:

Based on DNA and protein similarity, the four proposed new species are coherent and together with the five known species *(Kanagawavirus cipnine, Kanagawavirus eclm, Kanagawavirus mime, Kanagawavirus pei20,* and *Kanagawavirus threeohfive)* can be classified in the genus *Kanagawavirus.*

Submitted: 17/03/2025; *Revised:* 28/09/2025

TABLE 38 - *Kanagawavirus*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Kanagawavirus KLB31*	Klebsiella phage vB_KM5a1-KLB31	PP582757
New taxon	Species	*Kanagawavirus ENC9*	MAG: Enterobacter phage ENC9	OL355124
New taxon	Species	*Kanagawavirus Entb45*	Enterobacter phage Entb_45	ON630910
New taxon	Species	*Kanagawavirus ZX14*	Enterobacter phage ZX14	PP236086

2025.032B.Ac.v3.Karamvirus_14ns

Title: Create 14 new species in the genus *Karamvirus* (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae,* subfamily *Tevenvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:

Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae, subfamily Tevenvirinae.*

Description of current taxonomy:

Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species. Currently, the *Karamvirus* genus includes four species: *Karamvirus cc31,* *Karamvirus mypsh1140, Karamvirus petcm34,* and *Karamvirus pg7.*

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create 14 new species in the *genus Karamvirus.*

Justification:
Based on DNA and protein similarity, the 14 proposed new species are coherent and together with the four known species *(Karamvirus cc31, Karamvirus mypsh1140, Karamvirus petcm34,* and *Karamvirus pg7)* can be classified in the genus *Karamvirus.*

Submitted: 16/03/2025; *Revised:* 29/08/2025

TABLE 39 - *Karamvirus*, 14 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Karamvirus KMB20*	Enterobacter phage vB-EclM_KMB20	OL828291
New taxon	Species	*Karamvirus KMB17*	Enterobacter phage vB-EclM_KMB17	OL849997
New taxon	Species	*Karamvirus EnC07*	Enterobacter phage EnC07	PQ096442
New taxon	Species	*Karamvirus PS49*	Aeromonas phage PS49	PP212877
New taxon	Species	*Karamvirus RZH*	Enterobacter phage vB_EluP_RZH	PQ140450
New taxon	Species	*Karamvirus CW742*	Enterobacter phage vB_ECC_CW742	PV019367
New taxon	Species	*Karamvirus EnC15*	Enterobacter phage EnC15	PQ096439
New taxon	Species	*Karamvirus Entb43*	Enterobacter phage Entb_43	ON585039
New taxon	Species	*Karamvirus VPA32*	Klebsiella phage vB_KpnM_VPA32	OP558005
New taxon	Species	*Karamvirus UFV01*	Enterobacter phage vB_EclM-UFV01	ON454249
New taxon	Species	*Karamvirus Ent31*	Enterobacter phage vB_Ent31	OR567511
New taxon	Species	*Karamvirus AS6*	Enterobacter phage vB_EclM_AS6	OR753410
New taxon	Species	*Karamvirus fGhEcl01*	Enterobacter phage fGh-Ecl01	ON212265
New taxon	Species	*Karamvirus EnA02*	Enterobacter phage EnA02	PQ096440

2025.033B.Ac.v3.Irusalimvirus_1ns

Title: Create one new species in the genus *Irusalimvirus* (class *Caudoviricetes)*

Authors: Jack S Canning, Kak-Ming Ling, Daniel R Laucirica, Joshua J Iszatt, Andrew Vaitekenas, Stephen M Stick, Anthony Kicic,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The current taxonomy for dsDNA bacterial viruses for the proposed change is as follows; *Duplodnaviria,* Heunggongvirae, Uroviricota, Caudoviricetes, Irusalimvirus

Proposed taxonomic change(s):
We propose to establish a new species in the *genus Irusalimvirus*

Justification:
Karil-mokiny-1 possesses 70.8% average nucleotide identity (ANI%) to *Irusalimvirus BCSR52,* meeting the requirements for a new species within the genus *Irusalimvirus.* Currently, the genus *Irusalimvirus* fall under the following ICTV taxonomy; *Duplodnaviria,* Heunggongvirae, Uroviricota, Caudoviricetes, *Irusalimvirus*

Submitted: —; *Revised:* 09/01/2025

TABLE 40 - *Irusalimvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Irusalimvirus karilmokiny1*	Burkholderia phage Karil-mokiny-1	PV388296

2025.034B.Ac.v3.Kayfunavirus_1ns

Title: Create one new species *Kayfunavirus rjtwin* (Class *Caudoviricetes,* Order *Autographivirales)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo,

Summary:Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Kayfunavirus* currently has 19 ICTV listed species.

Proposed taxonomic change(s):
Create one new species, *Kayfunavirus rjtwin*

Justification:
Enterobacter phage vB_VIPECLMCO6 was isolated from Masalasa Creek, Tarlac, Philippines.
The genome is complete with DTR based on checkV analysis and is publicly available in NCBI Genbank database. As a result of comparison of the genome of Enterobacter phage vB_VIPECLMO6 to existing members of the genus *Kayfunavirus* using VIRIDIC, we propose the addition of a new species, *Kayfunavirus rjtwin.*

Submitted: 04/12/2025; *Revised:* —

TABLE 41 - *Kayfunavirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Kayfunavirus rjtwin*	Enterobacter phage vB_ VIPECLMCO6	PQ411323

2025.035B.Ac.v3.Koserivirus_1ng_1ns

Title: Create a new genus *(Koserivirus)* with a single species to the *Tevenvirinae* subfamily (class *Caudoviricetes,* order *Pantevenvirales,* family *Straboviridae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik

Summary:
Taxonomic rank(s) affected:
Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class *Caudoviricetes,* order *Pantevenvirales, family Straboviridae.*

Description of current taxonomy:
Currently, the order *Pantevenvirales* includes three families: *Ackermannviridae, Kyanoviridae,* and *Straboviridae.* Within the *Straboviridae* family, three subfamilies have been distinguished: *Emmerichvirinae, Tevenvirinae,* and *Twarogvirinae.* The *Tevenvirinae* subfamily comprises 15 genera and 148 species.

Proposed taxonomic change(s):
We performed genomic analysis of Citrobacter phage CkP1. Genome and protein analyses suggest that this bacteriophage belongs to the *Tevenvirinae* subfamily. Still, the differences are too great to assign it to one of the 15 genera within this subfamily. Therefore, we propose to create a new genus, *"Koserivirus",* with one species – *"Koserivirus CkP1".*

Justification:
DNA and protein analysis to other species and genera in the family *Straboviridae* supports the establishment of a new genus.

Submitted: 20/03/2025; *Revised:* —

TABLE 42 - *Koserivirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Koserivirus*		
New taxon	Species	*Koserivirus CkP1*	Citrobacter phage CkP1	MW239124

2025.037B.Ac.v3.Lingdingyangvirus_1ng_22ns

Title: Create a new genus *(Lingdingyangvirus)* with 22 species (Caudoviricetes)

Authors: Andrew M. Kropinski, Cristina Moraru, Juntao Shen

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

Description of current taxonomy:
There is no taxonomy for these lytic phages isolated against *Bacteroides thetaiotaomicron* from sewage

Proposed taxonomic change(s): Add new genus and 22 new species

Justification:

In keeping with the demarcation criteria established for creation of a genus, these 22 phages are significantly different from one another to be considered separate species; and, significantly similar to each other to be considered part of the same genus for which the name *Lingdingyangvirus* is proposed

Submitted: 15/05/2025; *Revised:* 09/01/2025

TABLE 43 - *Lingdingyangvirus*, 23 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Lingdingyangvirus*		
New taxon	Species	*Lingdingyangvirus BT61P1*	Bacteroides phage BT61P1	OP172709
New taxon	Species	*Lingdingyangvirus HNL05*	Bacteroides phage HNL05	MT074143
New taxon	Species	*Lingdingyangvirus BT47P1*	Bacteroides phage BT47P1	OP172708
New taxon	Species	*Lingdingyangvirus BT638P5*	Bacteroides phage BT638P5	OP172723
New taxon	Species	*Lingdingyangvirus SJC22*	Bacteroides phage SJC22	MT074158
New taxon	Species	*Lingdingyangvirus SJC13*	Bacteroides phage SJC13	MT074151
New taxon	Species	*Lingdingyangvirus SJC12*	Bacteroides phage SJC12	MT074150
New taxon	Species	*Lingdingyangvirus ARB14*	Bacteroides phage ARB14	MT074134
New taxon	Species	*Lingdingyangvirus SJC10*	Bacteroides phage SJC10	MT074148
New taxon	Species	*Lingdingyangvirus SJC25*	Bacteroides phage SJC25	MT074160
New taxon	Species	*Lingdingyangvirus BT401P3*	Bacteroides phage BT401P3	OP172713
New taxon	Species	*Lingdingyangvirus BT709P1*	Bacteroides phage BT709P1	OP172730
New taxon	Species	*Lingdingyangvirus BT638P7*	Bacteroides phage BT638P7	OP172725
New taxon	Species	*Lingdingyangvirus BT638P1*	Bacteroides phage BT638P1	OP172719
New taxon	Species	*Lingdingyangvirus BT638P2*	Bacteroides phage BT638P2	OP172720
New taxon	Species	*Lingdingyangvirus BT638P8*	Bacteroides phage BT638P8	OP172726
New taxon	Species	*Lingdingyangvirus BT638P6*	Bacteroides phage BT638P6	OP172724
New taxon	Species	*Lingdingyangvirus BT638P3*	Bacteroides phage BT638P3	OP172721
New taxon	Species	*Lingdingyangvirus BT681P2*	Bacteroides phage BT681P2	OP172727
New taxon	Species	*Lingdingyangvirus BT681P4*	Bacteroides phage BT681P4	OP172729
New taxon	Species	*Lingdingyangvirus BT498P1*	Bacteroides phage BT498P1	OP172714
New taxon	Species	*Lingdingyangvirus BT566P2*	Bacteroides phage BT566P2	OP172718

2025.038B.Ac.v3.Lowersilesiavirus_1ng_6ns

Title: Create new genus, *"Lowersilesiavirus"* with six species (class: *Caudoviricetes)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

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

Description of current taxonomy:
Acinetobacter-specific temperate phages isolated and sequenced at the Bacteriophage Laboratory of the Hirszfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, have not been assigned to any family or genus of bacteriophages within the *class Caudoviricetes.*

Proposed taxonomic change(s):
We performed genomic analysis of our six *Acinetobacter-specific* temperate bacteriophages. We propose to create a new genus, *"Lowersilesiavirus",* with six species.

Justification:
Based on DNA and protein similarity, *"Lowersilesiavirus"* is a cohesive genus.

Submitted: 24/03/2025; *Revised:* —

TABLE 44 - *Lowersilesiavirus*, 7 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Lowersilesiavirus*		
New taxon	Species	*Lowersilesiavirus Acba3*	Acinetobacter phage Acba_3	OQ101248
New taxon	Species	*Lowersilesiavirus Acba4*	Acinetobacter phage Acba_4	OQ101249
New taxon	Species	*Lowersilesiavirus Acba11*	Acinetobacter phage Acba_11	OQ101254
New taxon	Species	*Lowersilesiavirus Acba13*	Acinetobacter phage Acba_13	OQ101255
New taxon	Species	*Lowersilesiavirus Acba14*	Acinetobacter phage Acba_14	OQ101256
New taxon	Species	*Lowersilesiavirus Acba15*	Acinetobacter phage Acba_15	OQ101257

2025.039B.Ac.v3.Luojiashanvirus_1ng_2ns

Title: Create one new genus *Luojiashanvirus,* with two species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
Create a new genus *"Luojiashanvirus"* and two new species

Justification:
Phages phiSHP3 and vB_SmaS_Bhz63 are both temperate siphoviruses of *Stenotrophomonas maltophilia.* These two phages exhibit 83% intergenomic nucleotide sequence similarity, satisfying the criteria for a new genus and two new species to be created.

Submitted: —; *Revised:* 09/01/2025

TABLE 45 - *Luojiashanvirus*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Luojiashanvirus*		
New taxon	Species	*Luojiashanvirus phiSHP3*	Stenotrophomonas phage phiSHP3	MT872956
New taxon	Species	*Luojiashanvirus Bhz63*	Stenotrophomonas phage vB_SmaS_Bhz63	OR797046

2025.040B.Ac.v3.Lutzviridae_1nf_1ng_1ns

Title: Create one (1) new family *(Lutzviridae),* including one (1) new genus *(Lutzvirus)* [Class: *Caudoviricetes]*

Authors: Adriele J C Santos, Bruna A L Ayupe, Roberto S Dias, Mirelly J F Silva, Carlos H M Da Silva, Andrew M Kropinski, Dann Turner, Sérgio O De Paula

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

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

Proposed taxonomic change(s):
We propose a new family, *Lutzviridae,* which includes a single genus, *Lutzvirus,* with a single species represented by Oceanotoga phage vB_OteS-UFV02.

Justification:
We propose the establishment of a new viral family, *Lutzviridae,* including one new genus genus, *Lutzvirus,* and a single species. Phylogenetic analysis based on whole-genome comparisons using VIPTree demonstrates that Oceanotoga phage vB_OteS-UFV02 (accession OR420712.1) forms an isolated clade, showing no close evolutionary relationship to any other known viruses within the class *Caudoviricetes.*
Furthermore, vB_OteS-UFV02 can be considered a genomic orphan, as it shares no significant nucleotide similarity with any previously classified viral genomes. BLASTn and VIRIDIC analyses reveal less than 4% nucleotide identity with its closest match, the unclassified *Clostridium* phage phiCTP1 (accession HM159959.1), which is far below the threshold recommended for family-level classification.
These lines of evidence strongly support the designation of *Lutzviridae* as a novel family within *Caudoviricetes,* encompassing bacteriophages that are highly divergent in both genomic content and evolutionary origin.

Submitted: —; *Revised:* 20/08/2025

TABLE 46 - *Lutzviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Lutzviridae*		
New taxon	Genus	*Lutzvirus*		
New taxon	Species	*Lutzvirus UFV02*	Oceanotoga phage vB_OteS-UFV02	OR420712

2025.041B.Ac.v3.Mariborvirus_1ng_1ns

Title: Create a new genus *Mariborvirus* with a single species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, Maja Rupnik, Tomaž Accetto

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial viruses described in this proposal, lytic siphoviruses isolates against *Bacteroides,* are currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Mariborvirus* with a single species.

Justification:
Analysis with VIRIDIC and ViPTree indicates that Bacteroides phage Bacuni_F1 forms a new genus and species that conforms to the established demarcation criteria. Bacteroides phage F2 (MT806186.1, MT806187.1) is probably a member of this genus but the sequence is incomplete

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 47 - *Mariborvirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Mariborvirus*		
New taxon	Species	*Mariborvirus bacuniF1*	Bacteroides phage Bacuni_F1	MT635598

2025.042B.Ac.v3.Mariniviridae_1nf

Title: Create a new family, *Mariniviridae,* including one new genus and species

Authors: Manuel Martinez-Garcia, Mart Krupovic

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

Description of current taxonomy:
The virus vSAG-37-F6 is not closely related to other known members of the *class Caudoviricetes.*

Proposed taxonomic change(s):
We propose classifying uncultured marine virus vSAG-37-F6 into a new species, *"Pelagimarinivirus ubique",* within a new genus, *"Pelagimarinivirus",* and a new family, *"Mariniviridae",* within the class *Caudoviricetes.*

Justification:
The virus vSAG-37-F6 encodes signature proteins conserved in tailed viruses of the class *Caudoviricetes,* but is not closely related to any classified member of this class. Thus, it is proposed to classify vSAG-37-F6 into a separate new family, *"Mariniviridae".*

Submitted: 20/06/2025; *Revised:* 25/08/2025

TABLE 48 - *Mariniviridae*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Mariniviridae*		
New taxon	Genus	*Pelagimarinivirus*		
New taxon	Species	*Pelagimarinivirus ubique*	Pelagibacter virus vSAG-37-F6	PQ625738

2025.043B.Ac.v4.Microviricetes_reorg

Title: Revision of the microvirus taxonomy

Authors: Cristina Moraru, Paul Kirchberger, Simon Roux, Arvind Varsani, Mart Krupovic, Eric Olo Ndela, Francois Enault

Summary:
Taxonomic rank(s) affected:
Monodnaviria; Sangervirae; Phixviricota

Description of current taxonomy:
Phylum Phixviricota currently includes a monotypic family *Microviridae* with two subfamilies *(Bullavirinae and Gokushovirinae).*

Proposed taxonomic change(s):
We propose to elevate *family Microviridae* to the level of a class, the *"Microviricetes",* within phylum *Sangervirae* (realm *Monodnaviria).* Inside this new class, we propose seven orders and 21 families.

Justification:
Metagenomic studies from the past decade have revealed many new microvirus genomes across ecosystems. Phylogenetic assessment confirmed that the established taxonomic structure of two existing subfamilies of *Microviridae* cannot adequately represent the diversity of this viral group. Thus, we propose a reorganization of the established taxonomy of microviruses by assessing the relationships between 21 previously classified and 137 new representative complete microvirus genome sequences obtained from either cultivated viruses or from metagenomic datasets. Orders and families were defined by their separation on the major capsid protein phylogeny.

Submitted: 20/06/2025; *Revised:* 29/08/2025

TABLE 49 - *Microviricetes*, 488 new taxa***.** Table too large, see supplementary information sheet supp_info_tab_49

TABLE 50 - *Microviricetes*, 46 move taxa***.** Table too large, see supplementary information sheet supp_info_tab_50

TABLE 51 - *Microviricetes*, 6 promote taxa*

Operation	New taxon name	Old taxon name	Old rank	New rank
Promote taxon	*Microviricetes*	*Malgrandaviricetes*	class	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class
Promote taxon	*Microviricetes*	*Malgrandaviricetes*	class	class
Promote taxon	*Microviricetes*	*Petitvirales*	order	class

Promote taxon	*Microviricetes*	*Petitvirales*	order	class

TABLE 52 - *Microviricetes*, 6 rename taxa*

Operation	**Rank**	**New taxon name**	**Previous taxon name**
Rename taxon	Species	*Chlamydiaduovirus Chp2*	*Chlamydiamicrovirus Chp2*
Rename taxon	Species	*Chlamydiaduovirus CPAR39*	*Chlamydiamicrovirus CPAR39*
Rename taxon	Species	*Chlamydiaduovirus CPG1*	*Chlamydiamicrovirus CPG1*
Rename taxon	Species	*Chlamydiaduovirus Chp2*	*Chlamydiamicrovirus Chp2*
Rename taxon	Species	*Chlamydiaduovirus CPAR39*	*Chlamydiamicrovirus CPAR39*
Rename taxon	Species	*Chlamydiaduovirus CPG1*	*Chlamydiamicrovirus CPG1*

TABLE 53 - *Microviricetes*, 6 abolish taxa*

Operation	**Rank**	**Abolished taxon name**
Abolish taxon	Order	*Petitvirales*
Abolish taxon	Class	*Malgrandaviricetes*
Abolish taxon	Species	*Bdellovibrio virus MAC1*
Abolish taxon	Order	*Petitvirales*
Abolish taxon	Class	*Malgrandaviricetes*
Abolish taxon	Species	*Bdellovibrio virus MAC1*

TABLE 54 - *Microviricetes*, 4 move; rename taxa*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old parent taxon**	**Old taxon name**
Move; rename taxon	Genus	*Chlamydiaduovirus*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus*
Move; rename taxon	Species	*Chlamydiaunovirus Chp1*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus Chp1*
Move; rename taxon	Genus	*Chlamydiaduovirus*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus*
Move; rename taxon	Species	*Chlamydiaunovirus Chp1*	*Microviricetes*	*Malgrandaviricetes*	*Chlamydiamicrovirus Chp1*

2025.044B.Ac.v3.Miyazakivirus_1ng_1ns

Title: Create one new genus *(Miyazakivirus)* with a single species *(Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus, *Miyazakivirus,* with one species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NS-I forms a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 55 - *Miyazakivirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Miyazakivirus*		
New taxon	Species	*Miyazakivirus NSI*	Nocardia phage NS-I	OP429095

2025.045B.Ac.v3.Mosigvirus_1ns

Title: Create one new species *Mosigvirus lindsay* (Class *Caudoviricetes,* Order *Pantevenvirales,* Family *Straboviridae)*

Authors: Aubrey Joy P. Tejada, Michael Angelou L. Nada, Ruth Antoinette D. Chin, Janna Ysabelle O. Casidsid, Joseph B. Ancla, Marel Jan G. Joloro, Mark Christian C. Reterta, Anton Roi G. Collado, Sharmen C. Berlin, Arra B. Asejo, Nikka Marie R. Yadao, Virgilio Jr. P. De Paz, Ursela G. Bigol, Rommel J. Gestuveo,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:

The genus *Mosigvirus* currently includes 13 ICTV listed species.

Proposed taxonomic change(s):

Create one new species, *Mosigvirus lindsay*

Justification:
Escherichia phage vB_VIPECOMC06 was isolated from Masalasa Creek, Tarlac, Philippines. The genome is complete with direct terminal repeats based on an analysis with checkV [1] and is publicly available in NCBI Genbank database. Comparison to members of the genus *Mosigvirus* using VIRIDIC indicates that vB_VIPECOMC06 represents a new species in the genus.

Submitted: 04/12/2025; *Revised:* 29/08/2025

TABLE 56 - *Mosigvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Mosigvirus lindsay*	Escherichia phage vB_VIPECOMC06	PQ416618

2025.046B.Ac.v3.Motookavirus_1ng_2ns

Title: Create a new genus *(Motookavirus)* with two species in the Class *Caudoviricetes*

Authors: Ayesha Lone, Andrew M. Kropinski, Cristina Moraru, Jakub Barylski, Hany Anany

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

Description of current taxonomy: None for these phages

Proposed taxonomic change(s): To create a new genus *(Motookavirus)* containing two species

Justification: In accordance with the demarcation criteria of what constitutes a new genus and species these two *Bacillus cereus* phages are classified into a new genus (Motookavirus) of jumbo phages

Submitted: 15/06/2025; *Revised:* 27/08/2025

TABLE 57 - *Motookavirus*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Motookavirus*		
New taxon	Species	*Motookavirus edson*	Bacillus phage Edson	PV796108
New taxon	Species	*Motookavirus WH1*	Bacillus phage vB_BceM_WH1	LC597490

2025.047B.Ac.v3.Mweyongvirus_1ng_1ns

Title: Create one new genus *(Mweyongvirus)* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, *species*

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

Proposed taxonomic change(s):
Create one new genus, *Mweyongvirus* and a single species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Microcystis* phage Mwe-Yong1112-1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 58 - *Mweyongvirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Mweyongvirus*		
New taxon	Species	*Mweyongvirus yong1121*	Microcystis phage Mwe-Yong1112-1	MZ436628

2025.048B.Ac.v3.Mycobacterium_phages_1ng_8ns

Title: Create one new genus *(Peetremavirus)* of *Mycobacterium* phages with eight species (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: None. Mycobacterium phage P3MA is defined in the Actinobacteriophage Database as a singleton. The prophages have not been included in the database as of writing (18/08/2025)

Proposed taxonomic change(s): Create one new genus *Peetremavirus* with eight species

Justification: Phage P3MA was isolated on *Mycobacterium abscessus* 330 while the other proposed members of this genus were identified in the genomes of a variety of *M. abscessus* isolates. All of these temperate siphoviruses conform to the criteria which we have established for creation of a genera and associated species.

Submitted: —; *Revised:* 18/08/2025

TABLE 59 - *Mycobacterium*, 9 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Peetremavirus*		
New taxon	Species	*Peetremavirus P3MA*	Mycobacterium phage P3MA	PV089522
New taxon	Species	*Peetremavirus prophi621*	Mycobacterium phage prophi62-1	MW584194
New taxon	Species	*Peetremavirus phiGD342*	Mycobacterium phage phiGD34-2	MW314853
New taxon	Species	*Peetremavirus prophiGD211*	Mycobacterium phage prophiGD21-1	MW584205
New taxon	Species	*Peetremavirus prophiDG112*	Mycobacterium phage prophiGD11-2	MW584151
New taxon	Species	*Peetremavirus prophiGD161*	Mycobacterium phage prophiGD16-1	MW584149
New taxon	Species	*Peetremavirus prophiGD43A2*	Mycobacterium phage prophiGD43A-2	MW584198
New taxon	Species	*Peetremavirus phiGD891*	Mycobacterium phage phiGD89-1	MW314851

2025.049B.Ac.v3.Myosmarvirus_1ns

Title: Create one new species in the genus *Myosmarvirus* (class *Caudoviricetes,* family *Lindbergviridae)*

Authors: Michał J. Wójcicki, Dziyana Shymialevich, Iwona Gientka, Paulina Średnicka, Stanisław B. Błażejak, Barbara Sokołowska

Summary:

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

Description of current taxonomy:
Currently, in the *Lindbergviridae* family, 10 genera have been distinguished. The *Myosmarvirus* genus includes three species: *Myosmarvirus* MTx, Myosmarvirus myosmar, *and* Myosmarvirus SMP.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create one new species in the *genus Myosmarvirus.*

Justification:
Based on DNA and protein similarity, the one proposed new species is coherent and together with the three known species *(Myosmarvirus* MTx, Myosmarvirus myosmar, *and* Myosmarvirus *SMP)* can be classified in the genus *Myosmarvirus.*

Submitted: 20/03/2025; *Revised:* —

TABLE 60 - *Myosmarvirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Myosmarvirus Spe5P4*	Serratia phage Spe5P4	PP858852

2025.050B.A.v2.Nanchangvirus_1ng_1ns

Title: Create one new genus *(Nanchangvirus)* with a single species *(Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:

Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *(Nanchangvirus)* with one species. This virus is related to *Rhodococcus* phage Braxoaddie, a putative member of the *genus Pleakleyvirus*

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NC1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 61 - *Nanchangvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nanchangvirus*		
New taxon	Species	*Nanchangvirus NC1*	Nocardia phage NC1	MW452562

2025.051B.Ac.v3.Nanosmitevirus_1ng_1ns

Title: Create one new genus *(Nanosmitevirus)* with a single species (Caudoviricetes).

Authors: Andrew M. Kropinski, Ipek Kurtböke

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

Description of current taxonomy:
While the Actinobacteriophage Database groups temperate Mycobacterium phage Nanosmite in Cluster M/Subcluster M3 our BLASTN and VIRIDIC analysis reveals that it is sufficiently different from M Cluster viruses to deserve recognition as a separate genus. We have classified M Cluster phages to the subfamily *Mclasvirinae, family Vilmaviridae.*

Proposed taxonomic change(s):
Add new genus and one new species to the subfamily *Mclasvirinae,* family Vilmaviridae

Justification:
Mycobacterium phage Nanosmite is a unique, unclassified temperate virus. BLASTN analysis reveals that it shares 57.9% DNA sequence identity with Mycobacterium phage Rey.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 62 - *Nanosmitevirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Nanosmitevirus*		
New taxon	Species	*Nanosmitevirus nanosmite*	Mycobacterium phage Nanosmite	MW578836

2025.052B.Ac.v3.Nitrunavirus_1ng_1ns

Title: Create one new genus *(Nitrunavirus)* with a single species (Caudoviricetes).

Authors: Andrew M. Kropinski, Ipek Kurtböke, , , , ,

Summary:Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *Nitrunavirus* with one new species

Justification:
The bacteriophage NTR1 was isolated from activated sludge and infects three species of *Norcardia.* NTR1 exhibits a siphovirus morphology and possesses a 65.3 kb genome with 97 predicted protein-coding genes and a single tRNA. Analysis with VIRIDIC and ViPTree indicates that *Nocardia* phage NTR1 represents a new genus and species that conforms to the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 63 - *Nitrunavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nitrunavirus*		
New taxon	Species	*Nitrunavirus NTR1*	Nocardia phage NTR1	MF477236

2025.053B.Ac.v3.Nubrunavirus_1ng_2ns

Title: Create one new genus *(Nubrunavirus)* with a single species (class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: As far as we are aware no *Nocardia* phages have been classified by ICTV

Proposed taxonomic change(s): To create a new genus *Nubrunavirus* with two species

Justification:
Analysis with VIRIDIC and ViPTree indicates that *Nocardia phages* NBR1 and *Nocardia* phage *KYD2 represents* a new genus and species that conforms to the established demarcation criteria. BLASTN analysis reveals that these phages are peripherally related to *Nymphadoravirus bunnybear.*

Submitted: —; *Revised:* 09/01/2025

TABLE 64 - *Nubrunavirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Nubrunavirus*		
New taxon	Species	*Nubrunavirus NBR1*	Nocardia phage NBR1	JN116828
New taxon	Species	*Nubrunavirus KYD2*	Nocardia phage KYD2	MW654182

2025.054B.Uc.v3.Hirszfeldviridae_1nf_21ng_1mg_5mrs_46ns

Title: Create a new family, *Hirszfeldviridae,* with 22 genera, *Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, *Scipiovirus, Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus,* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Martyna A. Cieślik, Edyta Pawlak, Andrzej Górski, Ewa M. Jończyk-Matysiak

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

Description of current taxonomy:

According to the current taxonomy, the *Obolenskvirus* genus has been classified within the class *Caudoviricetes* without assignment to a family rank. Currently, the *Obolenskvirus* genus includes eight species: *Obolenskvirus AB1, Obolenskvirus AB2, Obolenskvirus AbC62, Obolenskvirus AbP2, Obolenskvirus AP22, Obolenskvirus LZ35, Obolenskvirus WCHABP1,* and *Obolenskvirus WCHABP12.*

Proposed taxonomic change(s):

Create a new family, *Hirszfeldviridae,* with 22 genera, *Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, *Scipiovirus, Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus,* for a group of *Acinetobacter-specific* phages.

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus.* Based on our analysis, we propose the creation of a new family for these phages along with 22 distinct genera.

To create a new family, *Hirszfeldviridae,* with 22 genera.
To create a new genus, *Nosocomialisvirus,* with two species.
To create a new single species genus, *Beijingvirus.*
To create a new single species genus, *Guangzhouvirus.*
To create a new single species genus, *Chinavirus.*
To create a new single species genus, *Pittiivirus.*
To move the genus *Obolenskvirus* to new family, *Hirszfeldviridae.*
To create four new species in genus *Obolenskvirus.*
To create a new single species genus, *Ganjingzivirus.*
To create a new single species genus, *Guizhouvirus.*
To create a new single species genus, *Brutusvirus.*
To create a new single species genus, *Walailakvirus.*
To create a new single species genus, *Scipiovirus.*
To move *Obolenskvirus AB1* from *Obolenskvirus* genus and rename to new *Wenzhouvirus* genus with two species.
To move *Obolenskvirus AbP2* from *Obolenskvirus* genus and rename to new *Burnvirus* genus with 11 species.
To create a new single species genus, *Ankaravirus.*
To create a new genus, *Polandvirus,* with two species.
To create a new single species genus, *Kenyavirus.*
To create a new genus, *Cairovirus,* with two species.
To create a new genus, *Helsinkivirus,* with two species.
To move *Obolenskvirus* WCHABP1 *and* Obolenskvirus *WCHABP12* from *Obolenskvirus* genus and rename to new *Sichuanvirus* genus with six species.
To create a new single species genus, *Pakistanvirus.*
To create a new single species genus, *Catovirus.*
To move *Obolenskvirus AP22* from *Obolenskvirus* genus and rename to new *Theraphagusvirus* genus with two species.

Justification:

After examination of 55 bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Hirszfeldviridae,* to accommodate 22 genera *(Nosocomialisvirus,* Beijingvirus, Guangzhouvirus, Chinavirus, Pittiivirus, Obolenskvirus, Ganjingzivirus, Guizhouvirus, Brutusvirus, Walailakvirus, Scipiovirus, *Wenzhouvirus, Burnvirus, Ankaravirus, Polandvirus, Kenyavirus, Cairovirus, Helsinkivirus, Sichuanvirus, Pakistanvirus, Catovirus,* and *Theraphagusvirus).*

Submitted: 20/06/2025; *Revised:* 23/10/2025

TABLE 65 - *Hirszfeldviridae*, 63 new taxa*. Table too large, see supplementary information sheet supp_info_tab_65

TABLE 66 - *Hirszfeldviridae*, 5 move; rename taxa*

Operation	Rank	New taxon name	New parent taxon	Old taxon name
Move; rename taxon	Species	*Wenzhouvirus AB1*	*Hirszfeldviridae*	*Obolenskvirus AB1*
Move; rename taxon	Species	*Burnvirus AbP2*	*Hirszfeldviridae*	*Obolenskvirus AbP2*
Move; rename taxon	Species	*Sichuanvirus WCHABP1*	*Hirszfeldviridae*	*Obolenskvirus WCHABP1*
Move; rename taxon	Species	*Sichuanvirus WCHABP12*	*Hirszfeldviridae*	*Obolenskvirus WCHABP12*
Move; rename taxon	Species	*Theraphagusvirus AP22*	*Hirszfeldviridae*	*Obolenskvirus AP22*

TABLE 67 - *Hirszfeldviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Obolenskvirus*	*Hirszfeldviridae*

2025.059B.Ac.v3.Peggyvirus_1ng_1ns

Title: Create a new genus *(Peggyvirus)* with a single species in the order *Autographivirales*

Authors: Ayesha Lone, Andrew M. Kropinski, Cristina Moraru, Hany Anany

Summary:
Taxonomic rank(s) affected: Subfamily, Genus

Description of current taxonomy: The family *Autographiviridae* (T7-like phages) has recently been replaced by the order *Autographivirales* which consists of four families, 13 subfamilies, 228 genera, and 968 species (ICTV Taxonomy Proposal 2024.045B.Autographivirales). This proposal affects the *subfamily Slopekvirinae*

Proposed taxonomic change(s): Addition of a new genus, *"Peggyvirus"* to this subfamily

Justification: In accordance with our definition of what constitutes a new genus and species [3] this Cronobacter phage is sufficiently different from other viruses to constitute a new genus in the subfamily *Slopekvirinae.*

Submitted: 15/06/2025; *Revised:* 27/08/2025

TABLE 68 - *Peggyvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Peggyvirus*		
New taxon	Species	*Peggyvirus peggy*	Cronobacter phage Peggy	PV796109

2025.060B.A.v2.Pepevirus_1ns

Title: Reinstatement of the species *Pepevirus spumicola*

Authors: Jānis Rūmnieks, , , , , , ,

Summary:Taxonomic rank(s) affected:
Species

Description of current taxonomy:
Genus *Pepevirus* currently holds six genera of bacterial single-stranded RNA viruses *(class Leviviricetes). Pseudomonas* virus LeviOr01 had previously been assigned to species *Pepevirus spumicola,* but this species is now abolished and in accordance with the current taxonomy, LeviOr01 is an unclassified *Pepevirus.*

Proposed taxonomic change(s):
Create species *"Pepevirus spumicola"* with *Pseudomonas* virus LeviOr01 as the exemplar *virus.* This *would* effectively reinstate a previously abolished species.

Justification:
Sequence analysis suggests that the abolishment of species *Pepevirus spumicola* was unjustified: according to the currently adopted demarcation criteria for *Leviviricetes, Pseudomonas* virus LeviOr01 belongs to genus *Pepevirus* but cannot be assigned to any of the currently recognized constituent species.

Submitted: 16/06/2025; *Revised:* —

TABLE 69 - *Pepevirus*, 1 new taxon*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Pepevirus spumicola*	ssRNA phage LeviOr01	LT821717

2025.061B.Uc.v3.Pituviridae_1nf_7ng_8ns

Title: Create a new family, *Pituviridae,* including seven new genera and eight new species (Class *Caudoviricetes)*

Authors: Michael Angelou L. Nada, Marel Jan G. Joloro, Ruth Antoinette D. Chin, Mark Christian C. Reterta, Janna Ysabelle O. Casidsid, Anton Roi G. Collado, Aubrey Joy P. Tejada, Sharmen C. Berlin, Joseph B. Ancla, Arra B. Asejo, Rommel J. Gestuveo

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

Description of current taxonomy:
Klebsiella phages are currently classified in the order *Autographivirales* and the families *Ackermannviridae, Casjensviridae, Demerecviridae, Drexlerviridae, Peduoviridae, Schitoviridae,* and *Straboviridae.* Our taxonomic analysis revealed *that Klebsiella* phage vB_VIPKPNMC05 does not belong to the existing phage families, thus, remains unclassified.

Proposed taxonomic change(s):

Create a new family, *Pituviridae*
Create a new single species *genus, Pituvirus*
Create a new single species *genus, Oxavirus*
Create a new single species *genus, Corunyavirus*
Create a new genus *Vimivirus,* with two species
Create a new single species *genus, Xubiasivirus*
Create a new single species *genus, Keypisivirus*
Create a new single species *genus, Samsivirus*

Justification:

As a result of detailed genomic, proteomic, and phylogenetic analyses using VIRIDIC, ViPTree, VirClust, we propose the creation a new phage family, *Pituviridae,* with seven genera *(Pituvirus, Oxavirus, Corunyavirus, Vimivirus, Xubiasivirus, Keypisivirus,* and *Samsivirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 30/05/2025; *Revised:* 09/01/2025

TABLE 70 - *Pituviridae*, 16 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Pituviridae*		
New taxon	Genus	*Pituvirus*		
New taxon	Species	*Pituvirus akira*	Klebsiella phage vB_VIPKPNMC05	PQ351753
New taxon	Genus	*Oxavirus*		
New taxon	Species	*Oxavirus ST13OXA48phi124*	Klebsiella phage ST13-OXA48phi12.4	MK422450
New taxon	Genus	*Corunyavirus*		
New taxon	Species	*Corunyavirus ST13OXA48phi122*	Klebsiella phage ST13-OXA48phi12.2	MK422452
New taxon	Genus	*Vimivirus*		
New taxon	Species	*Vimivirus ST147VIM1phi72*	Klebsiella phage ST147-VIM1phi7.2	MK448232
New taxon	Species	*Vimivirus Kp48873*	Klebsiella phage Kp4887-3	OK490474
New taxon	Genus	*Xubiasivirus*		
New taxon	Species	*Xubiasivirus EcoS733R5*	Escherichia phage vB_EcoS-733R5	ON470608
New taxon	Genus	*Keypisivirus*		
New taxon	Species	*Keypisivirus ST101KPC2phi63*	Klebsiella phage ST101-KPC2phi6.3	MK416017
New taxon	Genus	*Samsivirus*		
New taxon	Species	*Samsivirus Kp48802*	Klebsiella phage Kp4880-2	OK490458

2025.065B.Ac.v3.Rcapmuvirus_1ng_2ns

Title: Create one new genus *Rcapmuvirus* with two species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:

Genus, species

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

Proposed taxonomic change(s):
Create a new genus, *"Rcapmuvirus"* with two new species

Justification: The bacterial viruses RcapMu and RcWaterboi are both temperate siphoviruses that infect *Rhodobacter capsulatus.* VIRIDIC analysis shows that these phages exhibit approximately 83% intergenomic similarity warranting their inclusion within a single genus.

Submitted: —; *Revised:* 09/01/2025

TABLE 71 - *Rcapmuvirus*, 3 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Rcapmuvirus*		
New taxon	Species	*Rcapmuvirus capmu*	Rhodobacter phage RcapMu	JN190960
New taxon	Species	*Rcapmuvirus waterboi*	Rhodobacter phage RcWaterboi	MW677528

2025.066B.A.v2.Rename_taxa

Title: Rename three genera within the class *Caudoviricetes*

Authors: Andrew M. Kropinski, , , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus

Description of current taxonomy:
The three affected taxons are *Orchidvirus, Apricotvirus* and *Vhmlvirus.* These taxa are floating genera within the *class Caudoviricetes.*

Proposed taxonomic change(s):
Change the names of the genera *Orchidvirus, Apricotvirus and Vhmlvirus*

Justification:
The names *Apricotvirus* and *Orchidvirus* might lead to a misinterpretation that these viruses infect apricot trees and orchids. *Vhmlvirus* is unpronounceable.

Submitted: —; *Revised:* —

TABLE 72 - *Rename*, 8 rename taxa*

Operation	Rank	New taxon name	Previous taxon name
Rename taxon	Genus	*Kampevirus*	*Apricotvirus*
Rename taxon	Genus	*Cratervirus*	*Orchidvirus*
Rename taxon	Genus	*Oonoonbavirus*	*Vhmlvirus*
Rename taxon	Species	*Kampevirus apricot*	*Apricotvirus apricot*
Rename taxon	Species	*Cratervirus orchid*	*Orchidvirus orchid*

Rename taxon	Species	*Oonoonbavirus VHML*	*Vhmlvirus VHML*
Rename taxon	Species	*Oonoonbavirus VP85*	*Vhmlvirus VP585*
Rename taxon	Species	*Oonoonbavirus mar*	*Vhmlvirus mar*

2025.067B.Ac.v3.Rhodococcus_phages_2ng_2ns

Title: Create two new genera of *Rhodococcus* phages (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected: genus and species

Description of current taxonomy: The viruses described in this proposal are currently unclassified. They are defined in the Actinobacteriophage Database as singletons

Proposed taxonomic change(s): Create two new genera, *"Docdeeseptimavirus"* and *"Eetrevirus"* each with a single species

Justification: Rhodococcus phages Reqi DocB7 and E3 show little similarity to other phages in the extant nucleotide sequence databases when examined using BLASTN. Based on this, we propose that each represents a new species and genus.

Submitted: —; *Revised:* 09/01/2025

TABLE 73 - *Rhodococcus*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Docdeeseptimavirus*		
New taxon	Species	*Docdeeseptimavirus Doc7*	Rhodococcus phage ReqiDocB7	GU580940
New taxon	Genus	*Eetrevirus*		
New taxon	Species	*Eetrevirus E3*	Rhodococcus phage E3	HM114277

2025.068B.Ac.v3.Ricunavirus_1ng_1ns

Title: Create one new genus *Ribunavirus* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Ribunavirus* with a single species

Justification: *Rhizobium* phage RR1-B is a temperate myovirus with a 37.4 kb genome. Analysis of the genome sequence with VIRIDIC supports the creation of a new genus based on the established demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 74 - *Ricunavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Ribunavirus*		
New taxon	Species	*Ribunavirus RR1B*	Rhizobium phage RR1-B	JF974315

2025.069B.Ac.v3.Ricunavirus_1ng_1ns

Title: Create one new genus *(Ricunavirus)* with one species (Class: *Caudoviricetes)*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified

Proposed taxonomic change(s):
Create a new genus, *Ricunavirus* and a single species

Justification:
Rhodobacter phage RC1 is a temperate siphovirus with a 39.6 kb genome. Analysis of the genome sequence with VIRIDIC shows it exhibits little similarity to other phages infecting this bacterial genus and supports the establishment of a new genus based on the current demarcation criteria.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 75 - *Ricunavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Ricunavirus*		
New taxon	Species	*Ricunavirus RC1*	Rhodobacter phage RC1	JF974308

2025.070B.Ac.v3.Riverraidervirus_1ng_1ns

Title: Create one new genus *(Riverraidervirus)* with a single species (Class: *Caudoviricetes,* Family: *Stackebrandtviridae).*

Authors: Andrew M. Kropinski, Cristina Moraru, Ipek Kurtböke

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The bacterial virus described in this proposal is currently unclassified.

Proposed taxonomic change(s):
Create one new genus, *"Riverraidervirus"* and one new species within the family *Stackebrandtviridae.*

Justification:
Gordonia phage RiverRaider is a lytic siphovirus with a 59.6 kb genome. VIRIDIC analysis shows that it shares considerable intergenomic similarity with species of the genera *Vividuovirus* and *Kroosvirus* but is sufficiently different to establish a new genus under the current demarcation criteria.

Submitted: —; *Revised:* 09/01/2025

TABLE 76 - *Riverraidervirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Riverraidervirus*		
New taxon	Species	*Riverraidervirus riverraider*	Gordonia phage RiverRaider	PQ184823

2025.071B.Ac.v3.Santaclaravirinae_1nsf_3ng_6ns

Title: Create a new subfamily, *Santaclaravirinae* with three genera (Class *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected: subfamily, genus and species

Description of current taxonomy: Phage-plasmids are a novel, hybrid class of mobile genetic element which retain aspects of both phages and plasmids. These genetic elements have not been previously classified by ICTV.

Proposed taxonomic change(s): Create a new subfamily, *Santaclaravirinae* with three genera *Cyranovirus, Westmeadvirus and Suquintavirus*

Justification: These phages represent phage-plasmids, those that exhibit characteristics of both phages as plasmids. These mobile genetic elements can exist as circular replicons and often encode homologs of the ParA/ParB plasmid partitioning proteins. They also have the ability to form virions enabling the lysis and infection of bacteria. The phages described in this proposal share a significant number of protein homologs (c. 83 proteins) and exhibit >50% intergenomic nucleotide sequence similarity, supporting the creation of a new subfamily.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 77 - *Santaclaravirinae*, 8 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Subfamily	*Santaclaravirinae*		
New taxon	Species	*Westmeadvirus pJN226*	Klebsiella phage pJN2-26	MZ779062
New taxon	Genus	*Suquintavirus*		
New taxon	Species	*Suquintavirus SSU5*	Salmonella phage SSU5	JQ965645

New taxon	Genus	*Cyranovirus*		
New taxon	Species	*Cyranovirus cryano*	Escherichia phage Cyrano	OV696614
New taxon	Species	*Cyranovirus CMS2020a*	Escherichia phage CMS-2020a	CP054387
New taxon	Species	*Cyranovirus CMS2020b*	Escherichia phage CMS-2020b	CP053388

TABLE 78 - *Santaclaravirinae*, 1 move; rename taxon*

Operation	**Rank**	**New taxon name**	**New parent taxon**	**Old taxon name**
Move; rename taxon	Genus	*Westmeadvirus*	*Santaclaravirinae*	*Sourvirus*

2025.072B.Ac.v4.Schitoviridae_4_nsf_16ng_78_ns

Title: Create four (4) new subfamilies, sixteen (16) new genera and sixty-one (78) new species in the family *Schitoviridae* (Class *Caudoviricetes)*

Authors: Johannes Wittmann, Dann Turner

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

Description of current taxonomy:
The family *Schitoviridae* was created in 2020 (Taxonomy Proposal). The family is comprised of nine subfamilies, 57 genera and 106 species

Proposed taxonomic change(s):
Here, we propose to create four (4) new subfamilies:
Waldeevirinae, containing three (3) new genera, *Mifoctavirus, Sabivirus* and *Ekoctavirus,* alongside the existing genera *Cbunavirus* and *Efbeekayvirus*
Gaffkyvirinae, containing two (2) genera, *Pacinivirus* and *Vicoquintavirus*
Gebvirinae, containing one (1) new genus, *Dowsonvirus,* and the existing genera *Riverridervirus, Pokkenvirus, Philippevirus* and *Cavevirus*
Brisouvirinae, containing two (2) new genera, *Nacbunavirus* and *Atduovirus* and the existing genus *Exceevirus.*
Additionally, we intend to create ten (10) new genera, *Aracevirus, Axvirus, Dongfangvirus, Aquintavirus, Geeundevigintivirus, Pastisvirus, Peegeeundecimvirus, Manannanvirus,* Roskoffvirus *and Viundeviginityvirus.*

Justification:
Using different tools like VIRIDIC [1], VICTOR [2] or ViPTree [3] (Fig 1. and 2) for pairwise nucleotide identity or whole genome analyses of schitoviruses we propose 4 new subfamilies, *Brisouvirinae, Gaffkyvirinae, Gebvirinae,* and *Waldeevirinae* and 16 new genera. We used 95% and 70% nucleotide sequence identity over the entire length of the genome as criteria for delimiting species and genera, respectively. At the subfamily level, members of the subfamily share at least 20 % intergenomic distance as determined by VIRIDIC analysis.

Submitted: 06/02/2025; *Revised:* 09/02/2025

TABLE 79 - *Schitoviridae*, 98 new taxa*. Table too large, see supplementary information sheet supp_info_tab_79

TABLE 80 - *Schitoviridae*, 10 move taxa*

Operation	Rank	Taxon name	New parent taxon	Old parent taxon
Move taxon	Genus	*Vicoquintavirus*	*Gaffkyvirinae*	*Schitoviridae*
Move taxon	Genus	*Pacinivirus*	*Gaffkyvirinae*	*Schitoviridae*
Move taxon	Genus	*Cavevirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Philippevirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Pokkenvirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Riverridervirus*	*Gebvirinae*	*Schitoviridae*
Move taxon	Genus	*Exceevirus*	*Brisouvirinae*	*Schitoviridae*
Move taxon	Genus	*Cbunavirus*	*Waldeevirinae*	*Schitoviridae*
Move taxon	Genus	*Efbeekayvirus*	*Waldeevirinae*	*Schitoviridae*
Move taxon	Genus	*Triduovirus*	*Humphriesvirinae*	*Schitoviridae*

2025.075B.Ac.v3.Tabiovirus_1ng_8ns

Title: Create a new genus *(Tabiovirus)* with eight species in the Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s):
To create one new genus *Tabiovirus* with eight species of *Xanthomonas phages*

Justification: Based on analysis with ViPTree and VIRIDIC, we propose the creation of one new genus, *Tabiovirus* and eight new species of *Xanthomonas* phages.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 81 - *Tabiovirus*, 9 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Tabiovirus*		
New taxon	Species	*Tabiovirus JUN5*	Xanthomonas phage JUN5	OK913679
New taxon	Species	*Tabiovirus tenjo*	Xanthomonas phage Tenjo	LR743531
New taxon	Species	*Tabiovirus tabio*	Xanthomonas phage Tabio	LR743528
New taxon	Species	*Tabiovirus 10KY502B*	Xanthomonas phage 10KY502B	OQ622092
New taxon	Species	*Tabiovirus MET23P3*	Xanthomonas phage MET23-P3	OK913680
New taxon	Species	*Tabiovirus olaya*	Xanthomonas phage Olaya	MW802488
New taxon	Species	*Tabiovirus Cp2*	Xanthomonas citri phage Cp2	AB720064
New taxon	Species	*Tabiovirus SAC*	Xanthomonas phage SAC	PV012638

2025.076B.A.v2.Tequintavirus_1ns

Title: Create one new species in the genus *Tequintavirus*

Authors: Emilia Andrea V. Sabban, Stephen Kyle C. Arcan, Adonis N. Eclipse, Dexter Bryan L. Esliza, Paul Jeremy C. Lanete, Lindley C. Susi, Gelito Joseph M. Sikat,

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Tequintavirus* is classified within the subfamily *Markadamsvirinae,* family *Demerecviridae.* The genus is currently comprised of 70 species.

Proposed taxonomic change(s):
Create one new species *Tequintavirus vipecosubii* in the *genus Tequintavirus.*

Justification:
A new species, represented by Escherichia phage vB_EcoS_I14, is proposed based on a 95% intergenomic similarity threshold. This newly identified species is most closely related to *Tequintavirus S131* (GenBank MH370378.1), sharing 80.1% similarity. This taxonomic proposal is grounded in the principles of phylogenetic analysis and genomic comparison, providing a robust classification for this newly isolated bacteriophage.

Submitted: 29/08/2024; *Revised:* —

TABLE 82 - *Tequintavirus*, 1 new taxon*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Species	*Tequintavirus vipecosubii*	Escherichia phage vB_EcoS_I14	PP892525

2025.078B.Ac.v3.Vibrio_phages_2ng_3ns

Title: Create two new genera of *Vibrio* phages (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

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

Proposed taxonomic change(s): Create two new genera *Strymvirus* and Baybaevirus

Justification: The phages described in this proposal are temperate siphoviruses infecting *Vibrio* spp. Analysis with VIRIDIC and ViPTree support the creation of two new genera and three new species in accordance with the established demarcation criteria.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 83 - *Vibrio*, 5 new taxa*

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

New taxon	Species	*Strymvirus H2*	Vibrio phage H2 PGK-2017	KY658673
New taxon	Species	*Strymvirus strym*	Vibrio phage Strym	KX581099
New taxon	Genus	*Baybaevirus*		
New taxon	Species	*Baybaevirus baybae*	Vibrio phage Baybae	OQ079154

2025.079B.Ac.v3.Wallmarkvirinae_1nsf_3ng_9ns

Title: Create a new subfamily *Wallmarkvirinae* with three new genera, *Machiasvirus*

Authors: Andrew M. Kropinski, Cristina Moraru, Jumpei Uchiyama, Małgorzata Łobocka, Andrew D. Millard

Summary:
Taxonomic rank(s) affected:
Subfamily, genus

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

Proposed taxonomic change(s):
To create a new subfamily *"Wallmarkvirinae"* with three new genera, *"Machiasvirus", "Lentusvirus"* and *"Madawaskavirus"* of jumbo *Staphylococcus myophages*

Justification: This proposal covers a clade of bacterial viruses with genomes of greater than 250 kb that infect *Staphylococcus* spp. Comparative analysis at the nucleotide level indicates that this clade of phages exhibit a minimum of 54% inter-genomic similarity. At the protein level, these bacteriophages 163 proteins. This indicates that approximately 60.8% of the phage-encoded proteins are conserved. In accordance with the demarcation criteria, we propose one new subfamily that includes three new genera and nine new species.

Submitted: 15/06/2025; *Revised:* 19/08/2025

TABLE 84 - *Wallmarkvirinae*, 13 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Subfamily	*Wallmarkvirinae*		
New taxon	Genus	*Machiasvirus*		
New taxon	Species	*Machiasvirus AH12*	Staphylococcus phage AH12	OR455461
New taxon	Species	*Machiasvirus machias*	Staphylococcus phage Machias	MW349128
New taxon	Species	*Machiasvirus PB50*	Staphylococcus phage vB_StaM_PB50	OR770614
New taxon	Genus	*Lentusvirus*		
New taxon	Species	*Lentusvirus SA1*	Staphylococcus phage vB_StaM_SA1	MW218148
New taxon	Genus	*Madawaskavirus*		
New taxon	Species	*Madawaskavirus LY01*	Staphylococcus phage LY01	OR836606
New taxon	Species	*Madawaskavirus PALS2*	Staphylococcus phage PALS2	MN091626
New taxon	Species	*Madawaskavirus DC4*	Staphylococcus phage vB_SauM-UFV_DC4	MZ779063
New taxon	Species	*Madawaskavirus marshill*	Staphylococcus phage MarsHill	MW248466
New taxon	Species	*Madawaskavirus madawaska*	Staphylococcus phage Madawaska	MW349129

2025.080B.A.v2.Justusliebigvirus_4ns

Title: Create four new species in the genus *Justusliebigvirus* (class *Caudoviricetes,* subfamily *Stephanstirmvirinae)*

Authors: Michał J. Wójcicki, Iwona Gientka, Barbara Sokołowska

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

Description of current taxonomy:
The subfamily *Stephanstirmvirinae* comprises two genera, *Justusliebigvirus* and *Phapecoctavirus,* and 19 species. Currently, the *Justusliebigvirus* genus includes six species: *Justusliebigvirus* VEcB, *Justusliebigvirus* PHB05, Justusliebigvirus PD06, Justusliebigvirus alia, Justusliebigvirus phi92, *and* Justusliebigvirus muut.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create four new species in the genus *Justusliebigvirus* (class *Caudoviricetes, subfamily Stephanstirmvirinae).*

Justification:
Based on DNA and protein similarity, the proposed four new species are coherent and together with the six known species *(Justusliebigvirus* VEcB, *Justusliebigvirus* PHB05, Justusliebigvirus PD06, Justusliebigvirus alia, Justusliebigvirus phi92, *and* Justusliebigvirus *muut)* can be classified in the genus *Justusliebigvirus.*

Submitted: 27/03/2025; *Revised:* —

TABLE 85 - *Justusliebigvirus*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Justusliebigvirus UAB1*	Salmonella phage UAB_1	OL656106
New taxon	Species	*Justusliebigvirus SD2*	Escherichia phage SD2	PQ821640
New taxon	Species	*Justusliebigvirus KKP3264*	Serratia phage KKP_3264	OK210077
New taxon	Species	*Justusliebigvirus JLBYU50*	Escherichia phage JLBYU50	OK272470

2025.081B.Ac.v3.Yuavirus_12ns

Title: Add 12 new species to the genus *Yuavirus,* Class *Caudoviricetes*

Authors: Andrew M. Kropinski, Cristina Moraru

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The genus *Yuavirus* currently consists of five species. Previous proposals related to this genus are 2012.008a-dB.A.v3.Yualikevirus and 2015.006aB.A.v2.Phage_Genera_ren.

Proposed taxonomic change(s):
To create 12 new species in the *genus Yuavirus*

Justification:
Species classified in the genus *Yuavirus* represent lytic siphoviruses with genomes of approximately 60kb and a characteristic elongated head structure. This proposal adds 12 new species to the genus, based on intergenomic similarity calculated using VIRIDIC.

Submitted: 15/06/2025; *Revised:* 09/01/2025

TABLE 86 - *Yuavirus*, 12 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Yuavirus PC1*	Pseudomonas phage PC1	PP596838
New taxon	Species	*Yuavirus bella*	Pseudomonas phage Bella	PP661417
New taxon	Species	*Yuavirus jack*	Pseudomonas phage Jack	PP661418
New taxon	Species	*Yuavirus JM2*	Pseudomonas phage JM2	PP944331
New taxon	Species	*Yuavirus PAC4*	Pseudomonas phage vB_Pa-PAC4	PP408251
New taxon	Species	*Yuavirus PAC6*	Pseudomonas phage vB_Pa-PAC6	PP408253
New taxon	Species	*Yuavirus Epa38*	Pseudomonas phage Epa38	MT118302
New taxon	Species	*Yuavirus PSA20*	Pseudomonas phage PSA20,	MZ089734
New taxon	Species	*Yuavirus PSP2*	Pseudomonas phage PSP2	OR538761
New taxon	Species	*Yuavirus NEU2024*	Pseudomonas phage NEU2024	PQ144889
New taxon	Species	*Yuavirus clover*	Pseudomonas phage Clover	OQ992553
New taxon	Species	*Yuavirus HLL23*	Pseudomonas phage vB_Pae_HLL23	PP760143

2025.082B.A.v2.Yuavirus_2ns

Title: Create two new species in the genus *Yuavirus* (class *Caudoviricetes)*

Authors: Aaryan Harshith, Paul Bollyky, Jessica C. Sacher, Carlo Armijo

Summary:
Taxonomic rank(s) affected:
Species

Description of current taxonomy:
The genus *Yuavirus* was established under proposal 2012.008a-dB.A.v3.Yualikevirus. The genus currently consists of five species.

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

Justification:
VIRIDIC analysis indicates that both phages satisfy the species similarity threshold proposed by the ICTV Bacterial Viruses Subcommittee. Proteomic and phylogenetic evidence further supports the placement of phages Vanta and Luminis in the genus *Yuavirus.*

Submitted: 22/01/2025; *Revised:* —

TABLE 87 - *Yuavirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Yuavirus vanta*	Pseudomonas phage vanta	PQ628237
New taxon	Species	*Yuavirus luminis*	Pseudomonas phage Luminis	PQ632788

2025.083B.Uc.v3.Zimmerviridae_1nf_3nsf_4ng_9ns

Title: Create a new family *Zimmerviridae* (Class: *Caudoviricetes)*

Authors: Julien Lossouarn , Susan (M) Lehman , Igor Tolstoy, Andrew (M) Kropinski, Evelien Adriaenssens , Marie-Agnès Petit

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

Description of current taxonomy:
Since its discovery in the early 1950's to the mid 1980's, the temperate bacterial virus (phage) lambda was at the heart of the research which played a crucial role in our current understanding of molecular genetics. Over the years, many phages related to lambda, and susceptible to recombine with it, were isolated and named « lambdoids » (or « lambda-like »). Until recently, lambda and most of the lambdoid phages were taxonomically assigned into the family Siphoviridae, according to a classification scheme based on prokaryotic virion morphotype. In the last years, this morphological taxonomy was abandoned in favor of a molecular taxonomy, based upon overall DNA and protein similarity, for which lambda still remains unclassified at the family level.

Proposed taxonomic change(s):
Create a new family, *Zimmerviridae,* with two new subfamilies, six new genera and eight new species Move the genera *Jouyvirus,* Bievrevirus, Glaedevirus, Nesevirus, Alegriavirus, Radostvirus and *Lambdavirus* into the newly created *Jacobvirinae subfamily*

Justification:
We have applied whole proteome and phylogenetic approaches to analyse a set of 98 lambdoid genomes and 2 outliers, *Escherichia* phage T1 *(Tunavirus T1)* and T7 *(Teseptimavirus T7).* Based on these results, 22 of the 98 genomes form a cohesive and monophyletic group; we consequently propose a new family, named *"Zimmerviridae"* to honour microbiologist Esther Zimmer Lederberg. We propose to divide this family into two subfamilies, forming distinct monophyletic clades. We propose to name them *"Jacobvirinae"* and *"Wollmanvirinae"* to celebrate respectively microbiologists François Jacob and Elie Wollman. Seven previously defined genera and 14 previously defined species are clustered in the *"Jacobvirinae",* while intergenomic nucleotide similarities helped us to define three more genera and five species within the *"Wollmanvirinae"* subfamily.

Submitted: —; *Revised:* 11/03/2025

TABLE 88 - *Zimmerviridae*, 17 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Zimmerviridae*		
New taxon	Subfamily	*Jacobvirinae*		
New taxon	Subfamily	*Wollmanvirinae*		

New taxon	Genus	*Limmatquaivirus*		
New taxon	Species	*Limmatquaivirus mEp460*	Enterobacteria phage mEp460	JQ182728
New taxon	Species	*Limmatquaivirus mEp460_4F5*	Escherichia virus mEp460_4F5	LR595868
New taxon	Genus	*Dotonborivirus*		
New taxon	Species	*Dotonborivirus cdtl*	Enterobacteria phage cdtl	AB285204
New taxon	Species	*Dotonborivirus Ayreon*	Escherichia phage Ayreon	MF807953
New taxon	Genus	*Vilvertvirus*		
New taxon	Species	*Vilvertvirus mEp460ev081*	Escherichia phage mEp460_ev081	LR597641
New taxon	Genus	*Yvettevirus*		
New taxon	Species	*Yvettevirus Gifsy1*	Salmonella typhimurium phage Gifsy-1	NC_010392
New taxon	Genus	*Essonnevirus*		
New taxon	Species	*Essonnevirus Gifsy2*	Salmonella typhimurium phage Gifsy-1	NC_010393
New taxon	Genus	*Schuylkillvirus*		
New taxon	Species	*Schuylkillvirus Fels1*	Salmonella phage Fels-1	NC_010391

TABLE 89 - *Zimmerviridae*, 7 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Jouyvirus*	*Zimmerviridae*
Move taxon	Genus	*Bievrevirus*	*Zimmerviridae*
Move taxon	Genus	*Glaedevirus*	*Zimmerviridae*
Move taxon	Genus	*Nesevirus*	*Zimmerviridae*
Move taxon	Genus	*Alegriavirus*	*Zimmerviridae*
Move taxon	Genus	*Radostvirus*	*Zimmerviridae*
Move taxon	Genus	*Lambdavirus*	*Zimmerviridae*

2025.084B.Ac.v3.Zizhuyuanvirus_1ng_1ns

Title: Create one new genus, *Zizhuyuanvirus,* with one species (Class: *Caudoviricetes).*

Authors: Andrew M. Kropinski, Cristina Moraru, , , , , ,

Summary:

Taxonomic rank(s) affected:

Genus, species

Description of current taxonomy:

The bacterial viruses described in this proposal are currently unclassified

Proposed taxonomic change(s):

Create one new genus, *Zizhuyuanvirus* and a single species

Justification:

Leptolyngbya phage Lsp-JY19 is a temperate siphovirus with a 37.4 kb genome. Analysis of the genome sequence with VIRIDIC reveals very low intergenomic similarity (<20%) to two phages which infect *Stenotrophomonas* sp. Based on the lack of similarity to other phages, we propose that the creation of a new species and genus, *Zizhuyuanvirus.*

Submitted: —; *Revised:* 09/01/2025

TABLE 90 - *Zizhuyuanvirus*, 2 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Zizhuyuanvirus*		
New taxon	Species	*Zizhuyuanvirus JY19*	Leptolyngbya phage Lsp-JY19	PP438411

2025.085B.A.v2.Friunavirus_32ns

Title: Create 32 new species in the genus *Friunavirus* (class *Caudoviricetes, order* Autographivirales, *family* Autoscriptoviridae, *subfamily Beijerinckvirinae)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Edyta Pawlak, Iwona Gientka, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:

Taxonomic rank(s) affected:
Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes, order* Autographivirales, *family* Autoscriptoviridae, *subfamily Beijerinckvirinae.*

Description of current taxonomy:
The subfamily *Beijerinckvirinae* comprises four genera (i.e., *Aristophanesvirus,* Daemvirus, Friunavirus, *Pettyvirus) and* 68 species. Currently, the *Friunavirus* genus includes 65 species.

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create 32 new species in the *genus Friunavirus.*

Justification:
Based on DNA and protein similarity, the 32 proposed new species are coherent and together with the 65 known species can be classified in the genus *Friunavirus.*

Submitted: 20/06/2025; *Revised:* —

TABLE 91 - *Friunavirus*, 32 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Species	*Friunavirus AB3*	Acinetobacter phage AB3	KC311669
New taxon	Species	*Friunavirus 1137KEN02*	Acinetobacter phage vB_Ab_1137_KEN_02	PP841130
New taxon	Species	*Friunavirus 1137KEN05*	Acinetobacter phage vB_Ab_1137_KEN_05	PP841136
New taxon	Species	*Friunavirus 1137KEN03*	Acinetobacter phage vB_Ab_1137_KEN_03	PP841131
New taxon	Species	*Friunavirus 5899STDY8049184*	Acinetobacter phage MD-2021b strain 5899STDY8049184	OV298668
New taxon	Species	*Friunavirus NC12*	Acinetobacter phage AB_NC12	PV022100
New taxon	Species	*Friunavirus SWHAb1*	Acinetobacter phage SWH-Ab-1	NC_047896
New taxon	Species	*Friunavirus 5899STDY8049183*	Acinetobacter phage MD-2021b strain 5899STDY8049183	OV298628
New taxon	Species	*Friunavirus TCUAN2*	Acinetobacter phage TCUAN2	ON531987
New taxon	Species	*Friunavirus 5899STDY8049180*	Acinetobacter phage MD-2021b strain 5899STDY8049180	OV298791

New taxon	Species	*Friunavirus 1137KEN06*	Acinetobacter phage vB_Ab_1137_KEN_06	PP841137
New taxon	Species	*Friunavirus Margaret*	Acinetobacter phage vB_AbaP_Margaret	OZ038333
New taxon	Species	*Friunavirus phiAB440*	Acinetobacter phage phiAB440	PP792915
New taxon	Species	*Friunavirus Tama*	Acinetobacter phage vB_AbaP_Tama	OZ038331
New taxon	Species	*Friunavirus Fanak*	Acinetobacter phage vB_AbaP_Fanak	OZ075095
New taxon	Species	*Friunavirus Bhz16*	Acinetobacter phage vB_AbaS-Bhz16	PV067733
New taxon	Species	*Friunavirus A43Y*	Acinetobacter phage A43Y	PV467368
New taxon	Species	*Friunavirus Acba19*	Acinetobacter phage Acba_19	PV067698
New taxon	Species	*Friunavirus APK44*	Acinetobacter phage vB_AbaP_APK44	MN604238
New taxon	Species	*Friunavirus ZC2*	Acinetobacter phage vB_Aba_ZC2	PQ351672
New taxon	Species	*Friunavirus 164KEN02*	Acinetobacter phage vB_Ab_164_KEN_02	PP841133
New taxon	Species	*Friunavirus 5899STDY8049177*	Acinetobacter phage MD-2021b strain 5899STDY8049177	OV298630
New taxon	Species	*Friunavirus 5899STDY8049181*	Acinetobacter phage MD-2021b strain 5899STDY8049181	OV298725
New taxon	Species	*Friunavirus Fishpie*	Acinetobacter phage vB_AbaP_Fishpie	OZ038332
New taxon	Species	*Friunavirus EAB11*	Acinetobacter phage vB_AbaA_EAB11	PV208534
New taxon	Species	*Friunavirus 02KEN01*	Acinetobacter phage vB_Ab_02_KEN_01	PP841128
New taxon	Species	*Friunavirus ABW132*	Acinetobacter phage vB_AbaP_ABW132	OZ038338
New taxon	Species	*Friunavirus A31Y*	Acinetobacter phage A31Y	PV467367
New taxon	Species	*Friunavirus ABW311*	Acinetobacter phage vB_AbaP_ABW311	OZ038334
New taxon	Species	*Friunavirus W8*	Acinetobacter phage vB_AbaP_W8	PP174318
New taxon	Species	*Friunavirus Ab11*	Acinetobacter phage Ab11	PP763255
New taxon	Species	*Friunavirus AbaSI4*	Acinetobacter phage vB_AbaSI_4	PQ382035

2025.086B.Uc.v3.Luriaviridae_1nf_3ng_1mg_12ns

Title: Create a new family, *Luriaviridae,* with four genera, *Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus,* for a group of *Acinetobacter-specific* phages (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Dann Turner, Iwona Gientka, Martyna A. Cieślik, Andrzej Górski, Ewa M. Jończyk-Matysiak

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

Description of current taxonomy:
Currently, the *Saclayvirus* genus includes three species: *Saclayvirus Aci011, Saclayvirus Aci022,* and *Saclayvirus Aci05.*

Proposed taxonomic change(s):
We performed a genomic analysis of phages deposited in the NCBI database. We propose to create a new family *(Luriaviridae)* with four genera *(Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus)* for a group of *Acinetobacter-specific* phages (realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Saclayvirus.* Based on our analysis, we propose the creation of a new family for these phages along with four distinct genera.

To create a new family, *Luriaviridae,* with four genera.
To create a new single species genus, *Queenastridvirus.*
To create a new genus, *Wulsvirus,* with three species.
To move the genus, *Saclayvirus,* to a new family, *Luriaviridae.*
To create six new species in genus *Saclayvirus.*
To create a new genus, *Dalianvirus,* with two species.

Justification:
After examination of bacteriophages based on nucleotide sequence similarity, tblastx distances and core gene phylogeny, we propose the creation of a new family, *Luriaviridae,* to accommodate four genera *(Queenastridvirus, Wulsvirus, Saclayvirus,* and *Dalianvirus).* The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 20/06/2025; *Revised:* 17/10/2025

TABLE 92 - *Luriaviridae*, 16 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Family	*Luriaviridae*		
New taxon	Genus	*Queenastridvirus*		
New taxon	Species	*Queenastridvirus Acibel004*	Acinetobacter phage vB_AbaM_Acibel004	KJ473422
New taxon	Genus	*Wulsvirus*		
New taxon	Species	*Wulsvirus Acba22*	Acinetobacter phage Acba_22	PV067693
New taxon	Species	*Wulsvirus KissB*	Acinetobacter phage vB_AbaM_KissB	OZ038335
New taxon	Species	*Wulsvirus Rocket*	Acinetobacter phage vB_AbaM_Rocket	OZ038337
New taxon	Species	*Saclayvirus Ab121*	Acinetobacter phage Ab_121	MT623546
New taxon	Species	*Saclayvirus CP14*	Acinetobacter phage vB_AbaM_CP14	OP585105
New taxon	Species	*Saclayvirus Liucustia*	Acinetobacter phage Liucustia	MW349133
New taxon	Species	*Saclayvirus phi1092033*	Acinetobacter phage phi1_092033	PQ859668
New taxon	Species	*Saclayvirus TAC1*	Acinetobacter phage TAC1	MK170160
New taxon	Species	*Saclayvirus 14CRR8*	Acinetobacter phage vB_AbaM_14/CRR8	PV611675
New taxon	Genus	*Dalianvirus*		
New taxon	Species	*Dalianvirus D22*	Acinetobacter phage vB_AbaM_D22	MT188223
New taxon	Species	*Dalianvirus P1*	Acinetobacter phage vB_AbaM_P1	OL960030

TABLE 93 - *Luriaviridae*, 1 move taxon*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Saclayvirus*	*Luriaviridae*

2025.088B.Uc.v3.Caudoviricetes_2ng_2ns

Title: Create two new single-species genera – *Odravirus* and *Solivirus* (class *Caudoviricetes)*

Authors: Michał J. Wójcicki, Martyna A. Cieślik, Edyta Pawlak, Andrzej Górski, Ewa M. Jończyk-Matysiak

Summary:
Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy:
The Acinetobacter phage Acjo_20 and Acinetobacter phage phiAC-1 have not yet been classified by the ICTV. Analysis of the NCBI database indicates their closest similarity to phages from the *Obolenskvirus* genus, but the degree of relatedness is too low to link them to the *Obolenskvirus genus.*

Proposed taxonomic change(s):
To create two new single-species genera – *Odravirus* and *Solivirus* (class *Caudoviricetes).*

We performed a genomic analysis of several *Acinetobacter-specific* phages deposited in the NCBI database, all of which have been classified within the genus *Obolenskvirus.* Based on our analysis, we propose the creation of a two distinct genera, not classified to the family level.

To create a new single species genus, *Odravirus.*
To create a new single species *genus, Solivirus.*

Justification:
Analysis performed using VIRIDIC and ViPTree indicates that the Acinetobacter phage Acjo_20 and Acinetobacter phage phiAC-1 each form a single species in two new genera. The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

Submitted: 20/06/2025; *Revised:* 23/10/2025

TABLE 94 - *Caudoviricetes*, 4 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Genus	*Odravirus*		
New taxon	Species	*Odravirus Acjo20*	Acinetobacter phage Acjo_20	PV067699
New taxon	Genus	*Solivirus*		
New taxon	Species	*Solivirus phiAC1*	Acinetobacter phage phiAC-1	JX560521

2025.089B.Ac.v3.Acarajevirus_1ng_1ns

Title: Proposal of a new genus, *Acarajevirus,* harboring a new species belonging to the *Peduoviridae* family

Authors: Poliane Alfenas-Zerbini, Rafael R. Rezende , ,

Summary:

Taxonomic rank(s) affected:
Genus, species

Description of current taxonomy: *Peduoviridae* is orphan family associated with *Caudoviricetes* order harboring a total of 58 genera and 126 species.

Proposed taxonomic change(s): We proposed the Ralstonia phage AB1 be classified as new species “Acarajevirus bahia” belonging to a new genus named “Acarajevirus” associated with the family *Peduoviridae (Caudoviricetes class)*

Justification:
According to recommendation of ICTV to bacterial viruses taxonomy, the Ralstonia phage AB1 is related to other viruses from *Peduoviridae* family, but no sharing intergenomic similarity enough to be classified to establish species or genus.

Submitted: —; *Revised:* —

TABLE 95 - *Acarajevirus*, 2 new taxa*

Operation	**Rank**	**New taxon name**	**Virus name**	**Exemplar**
New taxon	Genus	*Acarajevirus*		
New taxon	Species	*Acarajevirus bahia*	Ralstonia phage AB1	PP316168

2025.090B.Ac.v3.Anamaviridae_1nf

Title: The description of new *Ralstonia* phage and its related phage fill some gaps on *Caudoviricetes* taxonomy

Authors: Poliane Alfenas-Zerbini, Rafael R. Rezende

Summary:

Taxonomic rank(s) affected:
Genus, species, subfamily, family.

Description of current taxonomy: The *Bakolyvirus* and *Naesvirus* comprise genera unrelated to any family. As for *Tsukubavirus, Beograduvirus* and *Xanthovirus* are associated with the subfamily *Kantovirinae,* which is not associated with any family.

Proposed taxonomic change(s): Recently, we described a new temperate phage named Ralstonia phage CA1 that infects bacteria *Ralstonia solanacearum* and *Ralstonia pseudosolanacearum.* The taxonomy classification of this virus results in the proposal of a new family, *“Anamaviridae”,* harboring the subfamilies *“Mascarenevirinae”* a new family, and *Kantovirinae,* previously not associated with the established family. Also, we proposed the creation of “Cocadavirus alagoinhas” species *(Cocadavirus* genus) related to the “Mascarenevirinae” subfamily. At last, we proposed moving the “Cocadavirus”, *Bakolyvirus,* and *Naesvirus* to the new subfamily “Mascarenevirinae”.

Justification: Based on whole-sequence intergenomic similarity analysis, it was possible to reclassify 28 isolates into species associated with a new genus and other established genera and further, based on the sharing of protein orthogroups, a new subfamily was created, which was associated with a new family and established as a subfamily. This proposal eliminated some taxonomic gaps in families and genera from the *Caudoviricetes* class.

Submitted: —; *Revised: —*

TABLE 96 - *Anamaviridae*, 21 new taxa*

Operation	Rank	New taxon name	Virus name	Exemplar
New taxon	Family	*Anamaviridae*		
New taxon	Subfamily	*Mascarenevirinae*		
New taxon	Genus	*Cocadavirus*		
New taxon	Species	*Cocadavirus alagoinhas*	Ralstonia phage CA1	PP316168
New taxon	Species	*Bakolyvirus elie*	Ralstonia phage Elie	MT740735
New taxon	Species	*Bakolyvirus adzire*	Ralstonia phage Adzire	MT740725
New taxon	Species	*Bakolyvirus sarlave*	Ralstonia phage Sarlave	MT740746
New taxon	Species	*Bakolyvirus jenny*	Ralstonia phage Jenny	MT740744
New taxon	Species	*Tsukubavirus xpp6*	Xanthomonas phage XPP6	MG944231
New taxon	Species	*Tsukubavirus xpp2*	Xanthomonas phage XPP2	MG944228
New taxon	Species	*Tsukubavirus xpp3*	Xanthomonas phage XPP3	MG944229
New taxon	Species	*Tsukubavirus xpp8*	Xanthomonas phage XPP8	MG944232
New taxon	Species	*Tsukubavirus xpp9*	Xanthomonas phage XPP9	MG944233
New taxon	Species	*Tsukubavirus pxoo2107*	Xanthomonas phage pXoo2107	OP067662
New taxon	Species	*Tsukubavirus x2*	Xanthomonas phage X2	MW435566
New taxon	Species	*Tsukubavirus xpv3*	Xanthomonas phage XPV3	MG944236
New taxon	Species	*Tsukubavirus xpv2*	Xanthomonas phage XPV2	MG944235
New taxon	Species	*Beograduvirus BsXeu*	Xanthomonas phage BsXeu269p/3	ON996340
New taxon	Species	*Beograduvirus myk3*	Xanthomonas phage MYK3	OK275494
New taxon	Genus	*Xanthovirus*		
New taxon	Species	*Xanthovirus neb7*	Xanthomonas phage NEB7	OQ676962

TABLE 97 - *Anamaviridae*, 3 move taxa*

Operation	Rank	Taxon name	New parent taxon
Move taxon	Genus	*Bakolyvirus*	*Anamaviridae*
Move taxon	Genus	*Naesvirus*	*Anamaviridae*
Move taxon	Subfamily	*Kantovirinae*	*Anamaviridae*