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

## Main Text

## Contents

**2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns**

**Title:** Create three new families *(Alisviridae, Ludisviridae*, and *Nixviridae)* with seven new genera and 24 new species

**Authors:** Matrishin CB, Kauffman KM (kmkauffm@buffalo.edu)

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

Realm *Duplodnaviria,* kingdom *Heunggongvirae,* phylum *Uroviricota,* class *Caudoviricetes*

***Description of current taxonomy:***

The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
Creation of three new families *(Alisviridae, Ludisviridae*, and *Nixviridae)* with seven new genera *(Honmavirus, Ludisvirus, Dewhirstvirus, Nixvirus, Haasevirus*, *Excelsiorvirus,* and *Schifferlevirus)* and 24 new species.

***Justification:***

A comprehensive analysis of publicly available NCBI *Porphryomonas gingivalis* genomes revealed three new families of viruses, containing seven new genera and 24 new species. This discovery, using a rigorous, complementary bioinformatic approach, revealed what we believe to be precise nucleotide start and end points of the prophage genomes within bacterial contigs (see Figure 1). These novel prophages represent the first systematically described phages of *P. gingivalis.* This work, including the proposed taxonomic classifications and figures shown in this proposal, are described in Matrishin et al. (2023) {37491415} . Phage genomes are available on NCBI within BioProject PRJNA874424.

*Submitted:* 05/29/2024; *Revised:* -

**TABLE 1** - *Alisviridae*, 34 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Alisviridae* | | |
| New taxon | genus | *Honmavirus* | | |
| New taxon | species | *Honmavirus pging00B* | Porphyromonas phage phage006a_EM3 | BK068089 |
| New taxon | species | *Honmavirus pging00C* | Porphyromonas phage phage007a_Bg4 | PP754929 |
| New taxon | species | *Honmavirus pging00D* | Porphyromonas phage phage008a_KCOM2795 | BK068090 |
| New taxon | species | *Honmavirus pging00E* | Porphyromonas phage phage010a_HG1691old | PP754930 |
| New taxon | species | *Honmavirus pging00F* | Porphyromonas phage phage011a_WW2952 | BK068092 |
| New taxon | species | *Honmavirus pging00G* | Porphyromonas phage phage012a_381OKJP | BK068093 |
| New taxon | species | *Honmavirus pging00H* | Porphyromonas phage phage013a_WW2885 | BK068094 |
| New taxon | species | *Honmavirus pging00I* | Porphyromonas phage phage014a_Kyudai4 | BK068095 |

| | | | | |
|---|---|---|---|---|
| New taxon | family | *Ludisviridae* | | |
| New taxon | genus | *Ludisvirus* | | |
| New taxon | species | *Ludisvirus pging00A* | Porphyromonas phage phage005b_ATCC49417 | PP754928 |
| New taxon | family | *Nixviridae* | | |
| New taxon | genus | *Dewhirstvirus* | | |
| New taxon | species | *Dewhirstvirus pging00J* | Porphyromonas phage phage016a_WW2866 | BK068097 |
| New taxon | species | *Dewhirstvirus pging00K* | Porphyromonas phage phage017a_JCVISC001 | BK068098 |
| New taxon | species | *Dewhirstvirus pging00L* | Porphyromonas phage phage018a_AFR5B1 | BK068099 |
| New taxon | species | *Dewhirstvirus pging00M* | Porphyromonas phage phage019b_ATCC49417 | PP754931 |
| New taxon | genus | *Nixvirus* | | |
| New taxon | species | *Nixvirus pging00X* | Porphyromonas phage phage032a_KCOM2801 | BK068113 |
| New taxon | genus | *Haasevirus* | | |
| New taxon | species | *Haasevirus pging00R* | Porphyromonas phage phage025a_SJD11 | BK068106 |
| New taxon | species | *Haasevirus pging00T* | Porphyromonas phage phage027a_F0568 | BK068108 |
| New taxon | species | *Haasevirus pging00U* | Porphyromonas phage phage028a_KCOM2799 | BK068109 |
| New taxon | species | *Haasevirus pging00V* | Porphyromonas phage phage029a_Kyudai3 | BK068110 |
| New taxon | species | *Haasevirus pging00W* | Porphyromonas phage phage030a_KCOM2803 | BK068111 |
| New taxon | genus | *Excelsiorvirus* | | |
| New taxon | species | *Excelsiorvirus pging00S* | Porphyromonas phage phage026a_KCOM2802 | BK068107 |
| New taxon | genus | *Schifferlevirus* | | |
| New taxon | species | *Schifferlevirus pging00N* | Porphyromonas phage phage020a_SJD2 | BK068101 |
| New taxon | species | *Schifferlevirus pging00O* | Porphyromonas phage phage022a_WW2931 | BK068103 |
| New taxon | species | *Schifferlevirus pging00P* | Porphyromonas phage phage023a_KCOM2797 | BK068104 |
| New taxon | species | *Schifferlevirus pging00Q* | Porphyromonas phage phage024a_F0570 | BK068105 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.001B.A.v1.Alisviridae_Ludisviridae_Nixviridae_3nf_7ng_24ns.xlsx

## 2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns

**Title:** Create a new family, *Andersonviridae* for the *FelixO1-like* phages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
At present the following taxa exist as floating genera in the class *Caudoviricetes: Felixounavirus,*

*Kolesnikvirus, Suspvirus*, and *Mooglevirus*.

***Proposed taxonomic change(s):***
We propose the creation of one new *family, Andersonviridae.*
To update the genus *Felixounavirus* with 80 new species
To update the genus *Mooglevirus* with 11 new species
To add one new species to the genus *Kolesnikvirus*
To create a new genus *Daniellevirus* with two species
To create a new genus *Arnovirus* with three species

***Justification:***
We investigated the evolutionary relationships of 123 bacteriophages. Analysis of conserved genes revealed that these phages form a deeply branching monophyletic clade with a distance commensurate with the creation of a new family.

*Submitted:* 01/06/2024; *Revised:* 30/09/2024

**TABLE 2 -** *Andersonviridae*, 100 new taxa*. Table too large, see supplementary information sheet supp_info_tab_2

**TABLE 3 -** *Andersonviridae*, 6 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Kolesnikvirus* | *Andersonviridae* |
| Move taxon | genus | *Felixounavirus* | *Andersonviridae* |
| Move taxon | genus | *Kolesnikvirus* | *Andersonviridae* |
| Move taxon | genus | *Mooglevirus* | *Andersonviridae* |
| Move taxon | genus | *Felixounavirus* | *Andersonviridae* |
| Move taxon | subfamily | *Ounavirinae* | *Andersonviridae* |

**TABLE 4 -** *Andersonviridae*, 2 move; rename taxa*

| Operation | Rank | New taxon name | New parent taxon | Old taxon name |
|---|---|---|---|---|
| Move; rename taxon | species | *Mooglevirus susp1* | *Andersonviridae* | *Suspvirus SUSP1* |
| Move; rename taxon | species | *Mooglevirus susp2* | *Andersonviridae* | *Suspvirus SUSP2* |

**TABLE 5 -** *Andersonviridae*, 1 abolish taxon*

| Operation | Rank | Abolished taxon name |
|---|---|---|
| Abolish taxon | genus | *Suspvirus* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.002B.A.v2.Andersonviridae_1nf_2ng_98ns.xlsx

## 2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns

**Title:** Create a new family, *Berryhillviridae,* for a group of lytic *Arthrobacter* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

***Summary:***

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

***Description of current taxonomy:***
At present the following taxa exist as floating genera in the class *Caudoviricetes*:
genera *Marthavirus, Vibakivirus, Jawnskivirus* and *Ayohtrevirus*

***Proposed taxonomic change(s):***
We propose the created of a new family, *Berryhillviridae,* containing the existing genera *Marthavirus, Vibakivirus,* and *Ayohtrevirus* in addition to six new genera, *Jinkiesvirus, Jawnskivirus*, *Lilmacvirus, Altadenavirus, Eastwestvirus* and *Sicariusvirus*

***Justification:*** We investigated the evolutionary relationships of 21 bacteriophages. Analysis of conserved genes and tblastx distances revealed that these phages form a deeply branching clade at a distance commensurate with the creation of a new family.

*Submitted:* 25/05/2024; *Revised:* -

**TABLE 6 -** *Berryhillviridae*, 18 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Berryhillviridae* | | |
| New taxon | genus | *Jawnskivirus* | | |
| New taxon | species | *Jawnskivirus king2* | Arthrobacter phage King2 | MT776811 |
| New taxon | genus | *Jinkiesvirus* | | |
| New taxon | species | *Jinkiesvirus jinkies* | Arthrobacter phage Jinkies | MT498043 |
| New taxon | genus | *Lilmacvirus* | | |
| New taxon | species | *Lilmacvirus lilmac1015* | Arthrobacter phage Lilmac1015 | OL742560 |
| New taxon | species | *Lilmacvirus bolt007* | Arthrobacter phage Bolt007 | OP985600 |
| New taxon | species | *Lilmacvirus prairie* | Arthrobacter phage Prairie | MW601223 |
| New taxon | species | *Lilmacvirus klevey* | Arthrobacter phage Klevey | MZ747522 |
| New taxon | genus | *Altadenavirus* | | |
| New taxon | species | *Altadenavirus altadena* | Arthrobacter phage Altadena | OR521058 |
| New taxon | species | *Altadenavirus bumble* | Arthrobacter phage Bumble | MT498055 |
| New taxon | genus | *Eastwestvirus* | | |
| New taxon | species | *Eastwestvirus eastwest* | Arthrobacter phage EastWest | OK999980 |
| New taxon | genus | *Sicariusvirus* | | |
| New taxon | species | *Sicariusvirus sicarius2* | Arthrobacter phage Sicarius2 | MW862982 |
| New taxon | species | *Sicariusvirus wyborn* | Arthrobacter phage Wyborn | OR475274 |

**TABLE 7 -** *Berryhillviridae*, 4 move; rename taxa*

| Operation | Rank | New taxon name | New parent taxon | Old taxon name |
|---|---|---|---|---|
| Move; rename taxon | species | *Jawnskivirus jawnski* | *Berryhillviridae* | *Marthavirus jawnski* |
| Move; rename taxon | species | *Jawnskivirus beans* | *Berryhillviridae* | *Marthavirus beans* |
| Move; rename taxon | species | *Jawnskivirus piccoletto* | *Berryhillviridae* | *Marthavirus piccoletto* |
| Move; rename taxon | species | *Jawnskivirus brent* | *Berryhillviridae* | *Marthavirus brent* |

**TABLE 8 -** *Berryhillviridae*, 3 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Vibakivirus* | *Berryhillviridae* |
| Move taxon | genus | *Ayohtrevirus* | *Berryhillviridae* |
| Move taxon | genus | *Marthavirus* | *Berryhillviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.003B.A.v1.Berryhillviridae_1nf_7ng_3mg_10ns.xlsx

## 2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns

**Title:** Create a new family, *Casidaviridae,* for a group of *Arthrobacter-Microbacterium* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
At present the following taxa exist as floating genera in the order *Caudoviricetes:*
*Zetavirus, Baileybluvirus, Yangvirus*, *Manhattanvirus* and *Liebevirus*

***Proposed taxonomic change(s):***
To create a new genus, *Gardenstatevirus,* with two species
To create a new genus, *Percivalvirus,* with two species
To create a new single species genus *Mabodamacavirus*
To create a new genus, *Barnstormervirus* with two species
To create a new single species genus *Honkvirus*
To create a new single species genus *Cenunavirus*
To create a new species in *Baileybluvirus*
To create seven new species in the genus *Yangvirus*
To create two new species in the genus *Manhattanvirus*
To create a new single species genus, *Emotionvirus*
To create a new single species genus, *Hilgardvirus*
To create a new single species genus, *Swepdovirus*
To create one new species in the genus *Liebevirus*
To create a new family, *Casidaviridae*

***Justification:***
We propose the creation of a new *family, Casidaviridae,* after examination of 21 bacteriophages related to the genera *Zetavirus, Baileybluvirus, Yangvirus*, *Manhattanvirus* and *Liebevirus* on the basis of nucleotide sequence similarity, tblastx distances and core gene phylogeny.

*Submitted:* 20/05/2024; *Revised:* 30/09/2024

**TABLE 9 -** *Casidaviridae*, 33 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Casidaviridae* | | |
| New taxon | species | *Baileybluvirus callinallbarbz* | Arthrobacter phage CallinAllBarbz | OR553891 |

| | | | | |
|---|---|---|---|---|
| New taxon | species | *Yangvirus janeemi* | Arthrobacter phage Janeemi | ON970616 |
| New taxon | species | *Yangvirus tuck* | Arthrobacter phage Tuck | OP820474 |
| New taxon | species | *Yangvirus berrie* | Arthrobacter phage Berrie | PP208921 |
| New taxon | species | *Yangvirus ascela* | Arthrobacter phage Ascela | OQ709218 |
| New taxon | species | *Yangvirus cassia* | Arthrobacter phage Cassia | OQ709212 |
| New taxon | species | *Yangvirus tfortroy* | Arthrobacter phage TforTroy | PP208923 |
| New taxon | species | *Yangvirus nitro* | Arthrobacter phage Nitro | OR553895 |
| New taxon | species | *Manhattanvirus vresidence* | Arthrobacter phage VResidence | OP434455 |
| New taxon | species | *Manhattanvirus wildwest* | Arthrobacter phage Wildwest | OR521060 |
| New taxon | species | *Liebevirus maguco* | Arthrobacter phage MaGuCo | OQ709203 |
| New taxon | genus | *Gardenstatevirus* | | |
| New taxon | species | *Gardenstatevirus gardenstate* | Microbacterium phage GardenState | MT952845 |
| New taxon | species | *Gardenstatevirus iamgroot* | Microbacterium phage IAmGroot | MK880124 |
| New taxon | genus | *Percivalvirus* | | |
| New taxon | species | *Percivalvirus percival* | Microbacterium phage Percival | MH271308 |
| New taxon | species | *Percivalvirus floof* | Microbacterium phage Floof | MH271298 |
| New taxon | genus | *Mabodamacavirus* | | |
| New taxon | species | *Mabodamacavirus mabodamaca* | Microbacterium phage Mabodamaca | OR613467 |
| New taxon | genus | *Barnstormervirus* | | |
| New taxon | species | *Barnstormervirus barnstormer* | Microbacterium phage Barnstormer | OQ190478 |
| New taxon | species | *Barnstormervirus caron* | Microbacterium phage Caron | OQ190481 |
| New taxon | genus | *Honkvirus* | | |
| New taxon | species | *Honkvirus honk* | Microbacterium phage Honk | MW862981 |
| New taxon | genus | *Cenunavirus* | | |
| New taxon | species | *Cenunavirus Cen1621* | Microbacterium phage Cen1621 | ON970568 |
| New taxon | genus | *Emotionvirus* | | |
| New taxon | species | *Emotionvirus emotion* | Arthrobacter phage Emotion | OQ709216 |
| New taxon | genus | *Hilgardvirus* | | |
| New taxon | species | *Hilgardvirus vroomvroom* | Arthrobacter phage VroomVroom | OQ938592 |
| New taxon | genus | *Swepdovirus* | | |
| New taxon | species | *Swepdovirus SWEP2* | Arthrobacter phage SWEP2 | ON528933 |

**TABLE 10 -** *Casidaviridae*, 5 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Zetavirus* | *Casidaviridae* |
| Move taxon | genus | *Baileybluvirus* | *Casidaviridae* |
| Move taxon | genus | *Yangvirus* | *Casidaviridae* |
| Move taxon | genus | *Manhattanvirus* | *Casidaviridae* |
| Move taxon | genus | *Liebevirus* | *Casidaviridae* |

**TABLE 11 -** *Casidaviridae*, 1 abolish taxon*

| Operation | Rank | Abolished taxon name |
|---|---|---|
| Abolish taxon | subfamily | *Azeevirinae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.005B.Uc.v2.Casidaviridae_1nf_9ng_23ns.xlsx

## 2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns

**Title:** Create a new genus, *Cepavirus,* with two species (*Caudoviricetes*; *Autographiviridae; Slopekvirinae)* and a new species in the genera *Suseptimavirus (Caudoviricetes; Gordonclarkvirinae)* and *Uetakevirus (Caudoviricetes).*

**Authors:** Pas C, Fieseler L, Briers Y (yves.briers@ugent.be)

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

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

***Proposed taxonomic change(s):***
Creation of a new genus, *Cepavirus,* within the subfamily *Slopekvirinae,* family *Autographiviridae.*
Assign Escherichia phage vB_EcoP_PAS7 as a new species in the new genus, *Cepavirus*
Assign Escherichia phage vB_EcoP_PAS59 as a new species in the genus *Suseptimavirus,* subfamily *Gordonclarkvirinae.*
Assign Escherichia phage vB_EcoP_PAS6 as a new species within the genus *Uetakevirus.*

***Justification:***
These bacterial viruses fall within current genus and species demarcation criteria for inclusion within existing genera.

*Submitted:* 27/11/2023; *Revised:* -

**TABLE 12 -** *Cepavirus*, 4 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | genus | *Cepavirus* | | |
| New taxon | species | *Cepavirus PAS7* | Escherichia phage vB_EcoP_PAS7 | OQ921331 |
| New taxon | species | *Suseptimavirus PAS59* | Escherichia phage vB_EcoP_PAS59 | OQ921332 |
| New taxon | species | *Uetakevirus PAS61* | Escherichia phage vB_EcoP_PAS61 | OQ921333 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.006B.A.v1.Cepavirus_Suseptimavirus_Uetakevirus_1ng_3ns.xlsx

## 2024.007B.A.v1.Chimalliviridae_16mg

**Title:** Move newly classified viral genera into *Chimalliviridae* family and fix previous error

**Authors:** Prichard A, Pogliano J (jpogliano@ucsd.edu)

***Summary:***
***Taxonomic rank(s) affected:***
We propose to move fifteen genera into the *Chimallivirdae* family and remove one genus from this family.

***Description of current taxonomy:***

Last year, we submitted a proposal to create a new viral family called *Chimallivirdae* and re-assigned currently classified viruses into this family. This proposal was accepted, but in the meantime, more viruses that belong in this family have been officially recognized and classified by the ICTV. Since these proposals were submitted in the same year as ours, and there was no existing family that was appropriate for them to be assigned to at the time, these viruses were not assigned to any viral families. However, we believe that these viruses belong to the now-recognized *Chimallivirdae* family.

***Proposed taxonomic change(s):***

Members of the newly created genera *Miamivirus, Nimduovirus, Meadowvirus, Branisovskavirus, Ferozepurvirus, Chaoshanvirus, Ludhianavirus, Siatvirus, Maaswegvirus, Eowynvirus, Miltoncavirus, Phabiovirus, Serwervirus, Tepukevirus,* and *Pawinskivirus* should be added to the family *Chimallivirdae.* Additionally, the genus *Takahashivirus* should be removed from the family Chimallivirus, as it was included in our proposal excel sheet last year by mistake and should not belong to this family.

***Justification:***

We have redone the phylogenetic analysis used to support the creation of the *Chimallivirdae* family and included these newly classified genera. This shows that these new genera belong in the family *Chimallivirdae,* while *Takahashivirus PBS1,* which we included by mistake, does not.

*Submitted:* **-** ; *Revised:* **-**

**TABLE 13 -** *Chimalliviridae*, 16 move taxa*

| Operation | Rank | Taxon name | Old parent taxon | New parent taxon |
|---|---|---|---|---|
| Move taxon | genus | *Takahashivirus* | *Chimalliviridae* | |
| Move taxon | genus | *Branisovskavirus* | | *Chimalliviridae* |
| Move taxon | genus | *Chaoshanvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Eowynvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Ferozepurvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Ludhianavirus* | | *Chimalliviridae* |
| Move taxon | genus | *Maaswegvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Meadowvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Miamivirus* | | *Chimalliviridae* |
| Move taxon | genus | *Miltoncavirus* | | *Chimalliviridae* |
| Move taxon | genus | *Nimduovirus* | | *Chimalliviridae* |
| Move taxon | genus | *Pawinskivirus* | | *Chimalliviridae* |
| Move taxon | genus | *Phabiovirus* | | *Chimalliviridae* |
| Move taxon | genus | *Serwervirus* | | *Chimalliviridae* |
| Move taxon | genus | *Siatvirus* | | *Chimalliviridae* |
| Move taxon | genus | *Tepukevirus* | | *Chimalliviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.007B.A.v1.Chimalliviridae_16mg.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.007B.A.v1.Chimalliviridae_16mg.xlsx

## 2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns

**Title:** Create a new family, *Colingsworthviridae,* of *Streptomyces* temperate phages (Class *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
Three taxa of temperate *Streptomyces* phages exist as floating genera in the class *Caudoviricetes, Vashvirus*, *Tigunavirus* and *Lomovskayavirus.* Up to the present no effort has been made to generate higher taxa.

***Proposed taxonomic change(s):***
Create a new single species genus *Shadyvirus*Create a new single species genus *Sycamorevirus*
Create a new single species genus *Shaekyvirus*
Create a new genus *Sebastisaurusvirus* with three species
To add a single new species to the genus *Vashvirus*
To add a single new species to the genus *Lomovskayavirus*
To create a new family, *Colingsworthviridae,* for these genera
To transfer *Vashvirus, Tigunavirus* and *Lomovskayavirus* to this new family

***Justification***
As a result of detailed genomic, proteomic and phylogenetic analyses using VIRIDIC, ViPTree, VirClust we propose to create four new genera of Phi-C31-like temperate siphoviruses, in a new family named in honour of the first person to isolate a *Streptomyces* bacteriophage, Dr. Donald Colingsworth.

*Submitted:* 15/05/2024; *Revised:* 30/09/2024

**TABLE 14 -** *Colingsworthviridae*, 13 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Colingsworthviridae* | | |
| New taxon | genus | *Shadyvirus* | | |
| New taxon | species | *Shadyvirus shady* | Streptomyces phage Shady | MT701596 |
| New taxon | genus | *Sycamorevirus* | | |
| New taxon | species | *Sycamorevirus sycamore* | Streptomyces phage Sycamore | MT701593 |
| New taxon | genus | *Shaekyvirus* | | |
| New taxon | species | *Shaekyvirus shaeky* | Streptomyces phage Shaeky | MT701595 |
| New taxon | genus | *Sebastisaurusvirus* | | |
| New taxon | species | *Sebastisaurusvirus sebastisaurus* | Streptomyces phage Sebastisaurus | MK450433 |
| New taxon | species | *Sebastisaurusvirus heather* | Streptomyces phage Heather | MK686069 |
| New taxon | species | *Sebastisaurusvirus remusloopin* | Streptomyces phage RemusLoopin | MK686068 |
| New taxon | species | *Vashvirus euratis* | Streptomyces phage Euratis | MK450426 |
| New taxon | species | *Lomovskayavirus shawty* | Streptomyces phage Shawty | MK433266 |

**TABLE 15 -** *Colingsworthviridae*, 3 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Vashvirus* | *Colingsworthviridae* |
| Move taxon | genus | *Lomovskayavirus* | *Colingsworthviridae* |
| Move taxon | genus | *Tigunavirus* | *Colingsworthviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.008B.A.v2.Colingsworthviridae_1nf_4ng_3mg_8ns.xlsx

## 2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns

**Title:** Create a new family, *Connertonviridae* for a group of *Campylobacter* phages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

***Summary:***

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

***Description of current taxonomy:***
At present the following taxa exist as genera within the floating subfamily *Eucampyvirinae,* order *Caudoviricetes: Fletchervirus* and *Firehammervirus*.

***Proposed taxonomic change(s):***
To create eight new species in the genus *Fletchervirus*
To create four new species in the genus *Firehammervirus*
To create a new family *Connertonviridae* and abolish the subfamily *Eucampyvirinae.*

***Justification:***
We propose the abolishment of the subfamily *Eucampyvirinae* and the creation of a new family *Connertonviridae* based on analysis of the genera *Fletchervirus* and *Firehammervirus* using VIRIDIC, ViPTree, VirClust and phylogeny of 16 core proteins shared between the member species.

*Submitted:* 30/05/2024; *Revised:* -

**TABLE 16 -** *Connertonviridae*, 13 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Connertonviridae* | | |
| New taxon | species | *Fletchervirus F341* | Campylobacter phage F341 | OQ864999 |
| New taxon | species | *Fletchervirus QDYZ* | Campylobacter phage vB_Cj_QDYZ | OQ515481 |
| New taxon | species | *Fletchervirus PC5* | Campylobacter phage PC5 | KX229736 |
| New taxon | species | *Fletchervirus F336* | Campylobacter phage F336 | MT863715 |
| New taxon | species | *Fletchervirus CJLB7* | Campylobacter phage CJLB-7 | MW057933 |
| New taxon | species | *Fletchervirus CJLB10* | Campylobacter phage CJLB-10 | MW074124 |
| New taxon | species | *Fletchervirus F372* | Campylobacter phage F372 | MT863729 |
| New taxon | species | *Fletchervirus F207* | Campylobacter phage F207 | MT863714 |
| New taxon | species | *Firehammervirus CJLB15* | Campylobacter phage CJLB-15 | MW365733 |
| New taxon | species | *Firehammervirus F379* | Campylobacter phage F379 | MT932329 |
| New taxon | species | *Firehammervirus CJLB12* | Campylobacter phage CJLB-12 | MW074125 |
| New taxon | species | *Firehammervirus CJLB14* | Campylobacter phage CJLB-14 | MW074126 |

**TABLE 17 -** *Connertonviridae*, 2 move taxa*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | genus | *Fletchervirus* | *Connertonviridae* |
| Move taxon | genus | *Firehammervirus* | *Connertonviridae* |

**TABLE 18 -** *Connertonviridae*, 1 abolish taxon*

| **Operation** | **Rank** | **Abolished taxon name** |
|---|---|---|
| Abolish taxon | subfamily | *Eucampyvirinae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.009B.A.v1.Connertonviridae_1nf_2mg_12ns.xlsx

## 2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns

**Title:** Create a new subfamily, *Dovevirinae,* with two genera for a group of lytic *Gordonia* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
Currently phages of this type are recognized in the genus *Lambovirus.* These are lytic siphophages with circularly permuted genomes infecting *Gordonia* species.

***Proposed taxonomic change(s):***
The creation of a new subfamily, *Dovevirinae,* composed of two genera, *Lambovirus* and *Xeniaduovirus* is proposed.

***Justification:***
Constituent species in these genera exhibit greater than 50% nucleotide sequence similarity supporting their assignment to a new subfamily

*Submitted:* 01/06/2024; *Revised:* -

**TABLE 19 -** *Dovevirinae*, 14 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | subfamily | *Dovevirinae* | | |
| New taxon | genus | *Xeniaduovirus* | | |
| New taxon | species | *Xeniaduovirus xenia2* | Gordonia phage Xenia2 | PP725409 |
| New taxon | species | *Lambovirus wojtek* | Gordonia phage Wojtek | OL455890 |
| New taxon | species | *Lambovirus genamy16* | Gordonia phage Genamy16 | ON755185 |
| New taxon | species | *Lambovirus novasharks* | Gordonia phage NovaSharks | ON755187 |
| New taxon | species | *Lambovirus zany* | Gordonia phage Zany | OL455887 |
| New taxon | species | *Lambovirus erutan* | Gordonia phage Erutan | OR475273 |
| New taxon | species | *Lambovirus jalebi* | Gordonia phage Jalebi | OL455895 |
| New taxon | species | *Lambovirus birthdayboy* | Gordonia phage BirthdayBoy | OR475261 |
| New taxon | species | *Lambovirus fulcrum* | Gordonia phage Fulcrum | OR521071 |
| New taxon | species | *Lambovirus parvustarda* | Gordonia phage ParvusTarda | OP172868 |
| New taxon | species | *Lambovirus otterstedtS21* | Gordonia phage OtterstedtS21 | OP172870 |
| New taxon | species | *Lambovirus patos* | Gordonia phage Patos | OP172876 |

**TABLE 20 -** *Dovevirinae*, 1 move taxon*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Lambovirus* | *Dovevirinae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.010B.A.v1.Dovevirinae_1nsf_1ng_12ns.xlsx

## 2024.011B.A.v2.Durnavirales_1nf_1ng_1ns

**Title:** Create a new family, *"Soropartitiviridae"*, within the order *Durnavirales* for classification of partiti-like virus infecting thermoacidophilic bacteria

**Authors:** Syun-ichi Urayama (urayama.shunichi.gn@u.tsukuba.ac.jp ), Akihito Fukudome, Eugene V. Koonin, Takuro Nunoura, Mart Krupovic (mart.krupovic@pasteur.fr )

***Summary:***
***Taxonomic rank(s) affected:***
*Riboviria, Orthornavirae, Pisuviricota, Duplopiviricetes, Durnavirales*

***Description of current taxonomy:***
Order *Durnavirales* includes six families of viruses with double-stranded RNA genomes. Most of the durnavirals infect fungal hosts, with the exception of partitivirids, which beside fungi, infect plants and protozoa, and picobirnavirids, which appear to infect bacteria.

***Proposed taxonomic change(s):***
Create a new family, *"Soropartitiviridae"*, with a genus, *"Caliparnavirus", within* the order *Durnavirales* to classify partiti-like viruses discovered in the hot spring samples and infecting thermoacidophilic bacteria.

***Justification:***
Phylogenetic analysis based on the RNA-dependent RNA polymerase (RdRP) placed the new group of bacterial partiti-like viruses outside of the established *Partitiviridae* genera. Furthermore, unlike all other classified partititivirids, one of the two segments of "soropartitivirids" is bicistronic.

*Submitted:* 21/06/2024; *Revised:* -

**TABLE 21 -** *Durnavirales*, 6 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Soropartitiviridae* | | |
| New taxon | genus | *Caliparnavirus* | | |
| New taxon | species | *Caliparnavirus acidus* | hot spring partiti-like virus 1 | RNA1: BTCP01000001;<br>RNA2: BTCP01000004 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.011B.A.v3.Durnavirales_1nf_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.011B.A.v3.Durnavirales_1nf_1ng_1ns.xlsx

## 2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns

**Title:** Create a new family, *Ehrlichviridae,* for a group of *Bacillus* Andromeda-like phages (Class: *Caudoviricetes)*

**Authors:** Barylski J (b54026@amu.edu.pl), Moraru C, Tolstoy I, Kropinski AM

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

***Description of current taxonomy:***

The genus *Andromedavirus* currently exists as a floating genus in the class *Caudoviricetes*

***Proposed taxonomic change(s):***
To create a new genus *Suttonboningtonvirus* with one species
To create a new genus *Gettysburgvirus* with three species
To add three new species to the genus *Andromedavirus*
To create a new single species genus *Anathvirus*
To create a new single species genus *Dazunavirus*
To create a new single species genus *Chennaivirus*
To create a new single species genus *Nairobivirus*
To create a new family, *Ehrlichviridae,* for the above-mentioned taxa.

***Justification:***
The phages comprising these taxa form a deep branching clade using tblastx distances and single gene phylogeny. Core gene analysis shows the presence of 15 proteins conserved across all members of the proposed family.

*Submitted:* 19/04/2024; *Revised:* -

**TABLE 22 -** *Ehrlichviridae*, 16 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Ehrlichviridae* | | |
| New taxon | species | *Andromedavirus leo2* | Bacillus phage Leo2 | KU836751 |
| New taxon | genus | *Suttonboningtonvirus* | | |
| New taxon | species | *Suttonboningtonvirus sv1ICo2020* | Bacillus phage 1_ICo-2020 | MT700412 |
| New taxon | genus | *Gettysburgvirus* | | |
| New taxon | species | *Gettysburgvirus gv056SW001B* | Bacillus phage 056SW001B | MN176230 |
| New taxon | species | *Gettysburgvirus gv268TH004* | Bacillus phage 268TH004 | MW394467 |
| New taxon | species | *Gettysburgvirus gv019DV002* | Bacillus phage 019DV002 | MN176220 |
| New taxon | genus | *Anathvirus* | | |
| New taxon | species | *Anathvirus anath* | Bacillus phage Anath | MG983742 |
| New taxon | genus | *Dazunavirus* | | |
| New taxon | species | *Dazunavirus DZ1* | Bacillus phage DZ1 | OR338916 |
| New taxon | genus | *Chennaivirus* | | |
| New taxon | species | *Chennaivirus MVCVPHSA1* | Staphylococcus phage MVC_VPHSA1 | OR670591 |
| New taxon | genus | *Nairobivirus* | | |
| New taxon | species | *Nairobivirus nv36* | Bacillus phage vB_BpsS-36 | MH884513 |

**TABLE 23 -** *Ehrlichviridae*, 1 move taxon*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | genus | *Andromedavirus* | *Ehrlichviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.012B.A.v1.Ehrlichviridae_1nf_6ng_1mg_9ns.xlsx

### 2024.013B.A.v1.Ferrettivirinae_1nsf_3ng_38ns

**Title:** To create a new subfamily, *Ferrettivirinae,* for *Streptococcus* prophages [Class: *Caudoviricetes]*

**Authors:** Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
We propose a new subfamily in the class *Caudoviricetes,* named in honour of Professor Joseph J. Ferretti, of *Streptococcus* temperate siphoprophages containing three genera: *Spinunavirus, Norfolkplacevirus* and *Hinxtonvirus.*

***Justification:***
Collectively these phages share ≥29.7% DNA sequence similarity and 14 homologous proteins (22.2% in common).

*Submitted:* 07/05/2024; *Revised:* -

**TABLE 24 -** *Ferrettivirinae*, 42 new taxa*. Table too large, see supplementary information sheet supp_info_tab_24*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.013B.A.v1.Ferrettivirinae_1nsf_3ng_38ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.013B.A.v2.Ferrettivirinae_1nsf_3ng_38ns.xlsx

## 2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns

**Title:** Create one new order *Grandevirales (Duplodnaviria)*

**Authors:** Cook R, Pye HV, Crisci MA, Telatin A, Santini JM (j.santini@ucl.ac.uk ), Adriaenssens EM (Evelien.adriaenssens@quadram.ac.uk )

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

***Description of current taxonomy:*** The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):*** We propose the creation of one new order, *Grandevirales,* comprising two new families, *Lakviridae* and *Epsomviridae,* three sub-families *(Quingentivirinae, Quadringentisvirinae* and *Sescentorumvirinae),* and four genera *(Vetruanivirus, Hatfieldvirus, Amboselivirus* and *Wendovervirus).* We also propose the creation of eight novel species within these genera.

***Justification:*** We investigated the evolutionary relationships of 23 megaphage genomes with sizes greater than 400 kb and propose a taxonomy for their classification. Analysis of their putative proteins revealed that Lak phages formed a deeply branching monophyletic clade within the class *Caudoviricetes* that contained no other genomes, and hence justifies the creation of a new order *Grandevirales.* One of the interesting features of this clade is that all current members are characterised by an alternative genetic code, where the TAG stop codon is repurposed to an amino acid.

*Submitted:* 04/06/2023; *Revised:* 07/10/2024

**TABLE 25 -** *Grandevirales*, 18 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | order | *Grandevirales* | | |
| New taxon | family | *Lakviridae* | | |
| New taxon | subfamily | *Quingentivirinae* | | |
| New taxon | genus | *Vetruanivirus* | | |
| New taxon | species | *Vetruanivirus primi* | Prevotella phage Lak-A1 | MK250015 |
| New taxon | species | *Vetruanivirus secundi* | Prevotella phage Lak-A2 | MK250019 |
| New taxon | species | *Vetruanivirus dhakaense* | Prevotella phage Lak-C1 | MK250029 |
| New taxon | species | *Vetruanivirus porcinprimi* | uncultured phage RVC AP1_GC26 | OR769218 |
| New taxon | species | *Vetruanivirus porcinsecundi* | uncultured phage RVC AP3_GC26 | OR769219 |
| New taxon | genus | *Amboselivirus* | | |
| New taxon | species | *Amboselivirus simi* | Prevotella phage Lak-B1 | MK250020 |
| New taxon | subfamily | *Quadringentisvirinae* | | |
| New taxon | genus | *Hatfieldvirus* | | |
| New taxon | species | *Hatfieldvirus porci* | uncultured phage RVC_JS4_GC31 | OR769222 |
| New taxon | family | *Epsomviridae* | | |
| New taxon | subfamily | *Sescentorumvirinae* | | |
| New taxon | genus | *Wendovervirus* | | |
| New taxon | species | *Wendovervirus sonii* | uncultured phage HB1 | OR769223 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.014B.A.v2.Grandevirales_1no_2nf_3nsf_4ng_8ns.xlsx

## 2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns

**Title:** To update the family *Grimontviridae* through the addition of three genera (Class: *Caudoviricetes)*

**Authors:** Dechesne A, Moraru C, Parra B, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The C3 of podoviruses are a very rare morphotype possessing elongated capsids, the "type virus" of which is *Escherichia* phage phiEco32. The family *Grimontviridae* currently consists of five genera: *Crifsvirus,* Dalianvirus, Libingvirus, *Moazamivirus* and *Privateervirus.*

***Proposed taxonomic change(s):***
Create a new single species genus *Trabzonvirus*
Create a new single species genus *Lundtoftevirus*
Transfer the genus *Lahexavirus* to this family

***Justification:***
The family is represented by a cohesive and monophyletic group in the main predicted proteome-

based clustering tools (VirClust, ViPTree, and vConTACT2). Members of the family share 12 core proteins.

*Submitted:* 06/05/2024; *Revised:* 30/09/2024

**TABLE 26 -** *Grimontviridae*, 4 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Trabzonvirus* | | |
| New taxon | species | *Trabzonvirus APT65* | Aeromonas phage APT65 | OP491958 |
| New taxon | genus | *Lundtoftevirus* | | |
| New taxon | species | *Lundtoftevirus Lu221* | IncN phage Lu221 | OQ829281 |

**TABLE 27 -** *Grimontviridae*, 1 move taxon*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Lahexavirus* | *Grimontviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.015B.A.v2.Grimontviridae_2ng_1mg_2ns.xlsx

## 2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns

**Title:** Create a new family, *Hodgkinviridae,* for a group of lytic *Microbacterium* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The genera *Momentomorivirus, Ouhwahvirus* and *Meganvirus* exist as floating genera in the class *Caudoviricetes*

***Proposed taxonomic change(s):***
To create a new single-species genus, *Fuzzbustervirus*
To add a single new species to the genus *Kozievirus*
To split the genus *Momentomorivirus* in two, creating *Margaeryvirus*
To add a single new species to the genus *Meganvirus*
To add two species to the genus *Quhwahvirus*
To create a new family, *Hodgkinviridae,* for these genera and *Metamorphovirus*

***Justification:***
Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Microbacterium* siphoviruses which share ≥12.2% DNA sequence similarity and 14 common proteins.

*Submitted:* 27/05/2024; *Revised:* 30/09/2024

**TABLE 28 -** *Hodgkinviridae*, 8 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|

| | | | | |
|---|---|---|---|---|
| New taxon | family | *Hodgkinviridae* | | |
| New taxon | species | *Kozievirus MO526* | Microbacterium phage MO526 | OR941552 |
| New taxon | species | *Meganvirus nichole72* | Microbacterium phage Nicole72 | OR159674 |
| New taxon | species | *Quhwahvirus pulchra* | Microbacterium phage Pulchra | MW601217 |
| New taxon | species | *Quhwahvirus littlefortune* | Microbacterium phage LittleFortune | OR475280 |
| New taxon | genus | *Fuzzbustervirus* | | |
| New taxon | species | *Fuzzbustervirus fuzzbuster* | Microbacterium phage FuzzBuster | MN062720 |
| New taxon | genus | *Margaeryvirus* | | |

**TABLE 29 -** *Hodgkinviridae*, 5 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Kozievirus* | *Hodgkinviridae* |
| Move taxon | genus | *Meganvirus* | *Hodgkinviridae* |
| Move taxon | genus | *Quhwahvirus* | *Hodgkinviridae* |
| Move taxon | genus | *Metamorphoovirus* | *Hodgkinviridae* |
| Move taxon | genus | *Mementomorivirus* | *Hodgkinviridae* |

**TABLE 30 -** *Hodgkinviridae*, 2 move; rename taxa*

| Operation | Rank | New taxon name | New parent taxon | Old taxon name |
|---|---|---|---|---|
| Move; rename taxon | species | *Margaeryvirus margaery* | *Hodgkinviridae* | *Mementomorivirus margaery* |
| Move; rename taxon | species | *Margaeryvirus terij* | *Hodgkinviridae* | *Mementomorivirus terij* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.016B.A.v2.Hodgkinviridae_1nf_2ng_4mg_5ns.xlsx

## 2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns

**Title:** Create a new family, *Jeanschmidtviridae* for a group of *Caulobacter* and *Brevundimonas* phages (Class: *Caudoviricetes)*

**Authors:** Millard A, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The taxa *Colossusvirus, Bertelyvirus*, *Shapirovirus* and *Poindextervirus* are floating genera in the class *Caudoviricetes*

***Proposed taxonomic change(s):***
To create a new genus, *Kikimoravirus,* with two species
To create a new genus, *Marchewkavirus,* with three species
To create a single-species genus, *Bajunvirus*
Abolish the subfamily *Dolichocephalovirinae*
To create a new family, *Jeanschmidtviridae,* for these genera and *Colossusvirus, Bertelyvirus*, *Shapirovirus* and *Poindextervirus.*

***Justification:***

The proposed members share ≥10.3% DNA sequence similarity and share 38 protein homologs.

*Submitted:* 10/06/2024; *Revised:* 30/09/2024

**TABLE 31 -** *Jeanschmidtviridae*, 10 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Jeanschmidtviridae* | | |
| New taxon | genus | *Kikimoravirus* | | |
| New taxon | species | *Kikimoravirus kikimora* | Brevundimonas phage vB_BpoS-Kikimora | ON529857 |
| New taxon | species | *Kikimoravirus gurke* | Brevundimonas phage vB_BpoS-Gurke | ON529850 |
| New taxon | genus | *Marchewkavirus* | | |
| New taxon | species | *Marchewkavirus marchewka* | Brevundimonas phage vB_BpoS-Marchewka | ON529851 |
| New taxon | species | *Marchewkavirus kabachok* | Brevundimonas phage vB_BpoS-Kabachok | ON529852 |
| New taxon | species | *Marchewkavirus domovoi* | Brevundimonas phage vB_BpoS-Domovoi | ON529855 |
| New taxon | genus | *Bajunvirus* | | |
| New taxon | species | *Bajunvirus bajun* | Brevundimonas phage vB_BpoS-Bajun | ON529858 |

**TABLE 32 -** *Jeanschmidtviridae*, 4 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Colossusvirus* | *Jeanschmidtviridae* |
| Move taxon | genus | *Bertelyvirus* | *Jeanschmidtviridae* |
| Move taxon | genus | *Shapirovirus* | *Jeanschmidtviridae* |
| Move taxon | genus | *Poindextervirus* | *Jeanschmidtviridae* |

**TABLE 33 -** *Jeanschmidtviridae*, 1 abolish taxon*

| Operation | Rank | Abolished taxon name |
|---|---|---|
| Abolish taxon | subfamily | *Dolichocephalovirinae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.017B.A.v2.Jeanschmidtviridae_1nf_3ng_4mg_6ns.xlsx

## 2024.018B.A.v1.Kronosvirus_1ng_3ns

**Title:** Create one new genus *(Kronosvirus)* with three species *(Caudoviricetes).*

**Authors:** Ely B (ely@sc.edu)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
*Caulobacter* bacteriophage Kronos is a unique siphovirus with a 50nm icosahedral head and a long (150nm) flexible tail. Aside from two phages, there are no close matches of its genome sequence to any other bacteriophage in the GenBank database. We described the phage and deposited its genome sequence in GenBank [14]. Additional phage that are closely related to Kronos can be grouped into three distinct species based on the ICTV criteria.

***Justification:***
The creation of the genus *Kronosvirus* complies with current demarcation criteria [10]

*Submitted:* 27/05/2024; *Revised:* -

**TABLE 34 -** *Kronosvirus*, 4 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | genus | *Kronosvirus* | | |
| New taxon | species | *Kronosvirus pelion* | Caulobacter phage Kronos | MH884648 |
| New taxon | species | *Kronosvirus pomeria* | Caulobacter phage TMCBR2 | OQ269668 |
| New taxon | species | *Kronosvirus elgin* | Caulobacter phage TMCBR4 | OQ330850 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.018B.A.v1.Kronosvirus_1ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.018B.A.v1.Kronosvirus_1ng_3ns.xlsx

### 2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns

**Title:** Create a new family, *Kruegerviridae,* for a group of *Gordonia* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
*Vanleevirus* currently exists as a floating genus in the class *Caudoviricetes*

***Proposed taxonomic change(s):***
To create a new genus *Cafassovirus* with four species
To create a new family, *Kruegerviridae,* for the *Cafassovirus* and *Vanleevirus.*

***Justification:***
By VIRIDIC analysis members of these two genera share ≥18.8% DNA sequence similarity and also share 46 protein homologs. The genera *Vanleevirus* and *Cafassovirus* form a deep-branching clade using tBLASTX distances, commensurate with the establishment of a new family of bacterial viruses.

*Submitted:* 28/05/2024; *Revised:* 30/09/2024

**TABLE 35 -** *Kruegerviridae*, 6 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Kruegerviridae* | | |
| New taxon | genus | *Cafassovirus* | | |

| | | | | |
|---|---|---|---|---|
| New taxon | species | *Cafassovirus cafasso* | Gordonia phage Cafasso | MZ322021 |
| New taxon | species | *Cafassovirus morgana* | Gordonia phage Morgana | PP537962 |
| New taxon | species | *Cafassovirus aleemily* | Gordonia phage Aleemily | ON970578 |
| New taxon | species | *Cafassovirus obladi* | Gordonia phage ObLaDi | OP297535 |

**TABLE 36 -** *Kruegerviridae*, 1 move taxon*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | genus | *Vanleevirus* | *Kruegerviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.019B.A.v2.Kruegerviridae_1nf_1ng_1mg_4ns.xlsx

### 2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns

**Title:** Create a new family, *Lindbergviridae,* for PB1-like phages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
PB1-like phages have been classified into the following genera: *Kylevirus, Tabernariusvirus, Bcepfunavirus, Pbunavirus, Wifcevirus*, *Myosmarvirus* and *Carpasinavirus.* All these are myoviruses infecting members of the Betaproteobacteria and Gammaproteobacteria.

***Proposed taxonomic change(s):***
To create ten new species in the genus *Pbunavirus*
To create one new species in the genus *Myosmarvirus*
To add six new species to the genus *Wifcevirus*
To add one new species to the genus *Carpasinavirus*
To create a new single species genus *Gladiolivirus*
To create a new single species genus *Irusalimvirus*
To create a new single species genus *Plutovirus*
To create a new family, *Lindbergviridae,* for the above-mentioned taxa as well as *Kylevirus, Tabernariusvirus,* and *Bcepfunavirus.*

***Justification:***
All our genomic and proteomic analyses reveal that the previously established genera *Kylevirus* (2020.086B.A.v1.R.Kylevirus), *Tabernariusvirus* ( (2018.099B.A.v1.A.v1.Tabernariusvirus), *Bcepfunavirus* ( (2020.116B.A.v1.R.Pbunavirus), *Pbunavirus, Wifcevirus, Myosmarvirus* and *Carpasinavirus* together with the three new genera listed above belong to a new family which we have named in honour of Alf A. Lindberg. The bacteriophages share 12 common proteins.

*Submitted:* 27/04/2024; *Revised:* 30/09/2024

**TABLE 37 -** *Lindbergviridae*, 25 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Lindbergviridae* | | |
| New taxon | species | *Pbunavirus SG1* | Pseudomonas phage SG1 | OQ594965 |
| New taxon | species | *Pbunavirus pv109* | Pseudomonas phage 109 | OQ831730 |

| | | | | |
|---|---|---|---|---|
| New taxon | species | *Pbunavirus FBPa14* | Pseudomonas phage vB_PaeM_FBPa14 | ON375839 |
| New taxon | species | *Pbunavirus wadjak13* | Pseudomonas phage Kara-mokiny kep-wari Wadjak_13 | OP310979 |
| New taxon | species | *Pbunavirus TH15* | Pseudomonas phage TH15 | MW406974 |
| New taxon | species | *Pbunavirus PSA09* | Pseudomonas phage PSA09 | MZ089730 |
| New taxon | species | *Pbunavirus ph0031* | Pseudomonas phage PhL_UNISO_PA-DSM_ph0031 | MW526258 |
| New taxon | species | *Pbunavirus PSA25* | Pseudomonas phage PSA25 | MZ089736 |
| New taxon | species | *Pbunavirus FBPa35* | Pseudomonas phage vB_PaeM_FBPa35 | ON857938 |
| New taxon | species | *Pbunavirus victoria* | Pseudomonas phage Victoria | OR805296 |
| New taxon | species | *Myosmarvirus SMP* | Serratia phage SMP | OP490597 |
| New taxon | species | *Wifcevirus SP13* | Escherichia phage vB_EcoM_SP13 | OP352608 |
| New taxon | species | *Wifcevirus AV128* | Escherichia phage AV128 | OR352958 |
| New taxon | species | *Wifcevirus Ro157lw* | Escherichia phage vB_EcoM-Ro157lw | MH051335 |
| New taxon | species | *Wifcevirus EC150* | Escherichia phage EC150 | ON210137 |
| New taxon | species | *Wifcevirus mansfield* | Escherichia phage Mansfield | MK903282 |
| New taxon | species | *Wifcevirus ECO71P1* | Escherichia phage ECO71P1 | OP172789 |
| New taxon | species | *Carpasinavirus FoX6* | Xanthomonas phage FoX6 | MT161386 |
| New taxon | genus | *Gladiolivirus* | | |
| New taxon | species | *Gladiolivirus maja* | Burkholderia phage Maja | MT708549 |
| New taxon | genus | *Irusalimvirus* | | |
| New taxon | species | *Irusalimvirus BCSR52* | Burkholderia phage BCSR52 | MW460246 |
| New taxon | genus | *Plutovirus* | | |
| New taxon | species | *Plutovirus pluto* | Luteibacter phage vB_LflM-Pluto | ON529861 |

**TABLE 38 -** *Lindbergviridae*, 7 move taxa*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | genus | *Kylevirus* | *Lindbergviridae* |
| Move taxon | genus | *Tabernariusvirus* | *Lindbergviridae* |
| Move taxon | genus | *Bcepfunavirus* | *Lindbergviridae* |
| Move taxon | genus | *Pbunavirus* | *Lindbergviridae* |
| Move taxon | genus | *Myosmarvirus* | *Lindbergviridae* |
| Move taxon | genus | *Wifcevirus* | *Lindbergviridae* |
| Move taxon | genus | *Carpasinavirus* | *Lindbergviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.020B.A.v2.Lindbergviridae_1nf_3ng_7mg_21ns.xlsx

## 2024.021B.A.v1.Malkevirus_1ng_5ns

**Title:** To create a new genus, *Malkevirus,* for *Streptococcus* prophages [Class: *Caudoviricetes*]

**Authors:** Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
We propose a new genus, named in honour of Professor Dr. Horst Malke, comprised of temperate siphoviruses infecting *Streptococcus* spp.

***Justification:***
The viruses fall into a genus based on current demarcation criteria.

*Submitted:* 07/05/2024; *Revised:* -

**TABLE 39 -** *Malkevirus*, 6 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Malkevirus* | | |
| New taxon | species | *Malkevirus ARI02853* | Streptococcus phage phiARI0285-3 | KT337347 |
| New taxon | species | *Malkevirus IPP67* | Streptococcus phage IPP67 | KY065503 |
| New taxon | species | *Malkevirus IPP45* | Streptococcus phage IPP45 | KY065485 |
| New taxon | species | *Malkevirus mv23782* | Streptococcus phage 23782 | FR671408 |
| New taxon | species | *Malkevirus mv11865* | Streptococcus phage 11865 | FR671409 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.021B.A.v1.Malkevirus_1ng_5ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.021B.A.v1.Malkevirus_1ng_5ns.xlsx

## 2024.022B.A.v1.Markadamsvirinae_1ng_1ns

**Title:** Create a new genus *(Kononvirus)* with a single species to the *Markadamsvirinae* subfamily *(Caudoviricetes: Demerecviridae)*

**Authors:** Wójcicki M (michal.wojcicki@ibprs.pl), Shymialevich D, Średnicka P, Gientka I, Błażejak S, Sokołowska B

***Summary:***
***Taxonomic rank(s) affected:***
Proposal to create a new genus *(Kononvirus)* with a single species (tailed phages from *Caudoviricetes* class, *Demerecviridae* family and *Markadamsvirinae* subfamily).

***Description of current taxonomy:***
In 2022, significant changes to the taxonomy of bacterial viruses were introduced: the paraphyletic morphological families *Podoviridae, Siphoviridae,* and *Myoviridae* as well as the order *Caudovirales* were abolished, which is replaced by the class *Caudoviricetes* to group all tailed bacterial and archaeal viruses with icosahedral capsids and a double-stranded DNA genome. Moreover, a binomial system of nomenclature for species was established.
Currently, the *Demerecviridae* family includes three subfamilies *(Ermolyevavirinae, Markadamsvirinae* and *Mccorquodalevirinae)* and six separate genera *(Keyvirus, Novosibvirus, Pogseptimavirus, Priunavirus, Shenzhenvirus* and *Sugarlandvirus)* not classified at the subfamily level. The *Markadamsvirinae* subfamily currently includes two genera: *Epseptimavirus* and *Tequintavirus.*

***Proposed taxonomic change(s):***
We performed genomic analysis of newly isolated Enterobacter phage KKP_3711. Genome and protein analyses suggest that this bacteriophage belongs to the *Markadamsvirinae* subfamily. Still, the differences are too great to assign it to one of the two genera within this subfamily. Therefore, we propose to create a new genus, *Kononvirus,* with one species **-** *Kononvirus* KKP_3711.

***Justification:***
Based on DNA and protein similarity this is a cohesive genus.

*Submitted:* 16/06/2024; *Revised:* -

**TABLE 40 -** *Markadamsvirinae*, 2 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Kononvirus* | | |
| New taxon | species | *Kononvirus KKP3711* | Enterobacter siphophage KKP_3711 | PP579741 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.022B.A.v1.Markadamsvirinae_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.022B.A.v1.Markadamsvirinae_1ng_1ns.xlsx

## 2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns

**Title:** To create a new subfamily, *Mcshanvirinae,* for *Streptococcus* prophages [Class: *Caudoviricetes*]

**Authors:** Tolstoy I, Moraru C, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
We propose a new subfamily, named in honour of Professor W. Michael McShan, of *Streptococcus* temperate siphoviruses containing three newly established genera: *Adrianbuildvirus, Medawarvirus* and *Phadecavirus.*

***Justification:***
The proposed taxa conform to the demarcation criteria employed by the ICTV Bacterial Viruses Subcommittee.

*Submitted:* 06/05/2024; *Revised:* -

**TABLE 41 -** *Mcshanvirinae*, 29 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | subfamily | *Mcshanvirinae* | | |
| New taxon | genus | *Adrianbuildvirus* | | |
| New taxon | species | *Adrianbuildvirus SpSL1* | Streptococcus phage SpSL1 | KM882824 |
| New taxon | species | *Adrianbuildvirus IPP5* | Streptococcus phage IPP5 | KY065449 |
| New taxon | species | *Adrianbuildvirus IPP44* | Streptococcus phage IPP44 | KY065484 |
| New taxon | species | *Adrianbuildvirus IPP42* | Streptococcus phage IPP42 | KY065482 |
| New taxon | species | *Adrianbuildvirus IPP51* | Streptococcus phage IPP51 | KY065489 |
| New taxon | species | *Adrianbuildvirus ARI0923* | Streptococcus phage phiARI0923 | KT337370 |
| New taxon | species | *Adrianbuildvirus IPP41* | Streptococcus phage IPP41 | KY065481 |
| New taxon | species | *Adrianbuildvirus IPP43* | Streptococcus phage IPP43 | KY065483 |

| | | | | |
|---|---|---|---|---|
| New taxon | genus | *Medawarvirus* | | |
| New taxon | species | *Medawarvirus IPP12* | Streptococcus phage IPP12 | KY065454 |
| New taxon | species | *Medawarvirus IPP22* | Streptococcus phage IPP22 | KY065463 |
| New taxon | species | *Medawarvirus IPP18* | Streptococcus phage IPP18 | KY065459 |
| New taxon | species | *Medawarvirus IPP57* | Streptococcus phage IPP57 | KY065494 |
| New taxon | species | *Medawarvirus IPP20* | Streptococcus phage IPP20 | KY065461 |
| New taxon | species | *Medawarvirus IPP21* | Streptococcus phage IPP21 | KY065462 |
| New taxon | species | *Medawarvirus IPP30* | Streptococcus phage IPP30 | KY065471 |
| New taxon | species | *Medawarvirus IPP11* | Streptococcus phage IPP11 | KY065453 |
| New taxon | species | *Medawarvirus IPP29* | Streptococcus phage IPP29 | KY065470 |
| New taxon | species | *Medawarvirus IPP19* | Streptococcus phage IPP19 | KY065460 |
| New taxon | species | *Medawarvirus ARI01312* | Streptococcus phage phiARI0131-2 | KT337342 |
| New taxon | species | *Medawarvirus IPP63* | Streptococcus phage IPP63 | KY065499 |
| New taxon | species | *Medawarvirus IPP17* | Streptococcus phage IPP17 | KY065458 |
| New taxon | species | *Medawarvirus IPP28* | Streptococcus phage IPP28 | KY065469 |
| New taxon | genus | *Phadecavirus* | | |
| New taxon | species | *Phadecavirus PH10* | Streptococcus phage PH10 | FN391954 |
| New taxon | species | *Phadecavirus pv23TH* | Streptococcus phage 23TH | MT900487 |
| New taxon | species | *Phadecavirus olisA1* | Streptococcus phage OlisA1 | OL774868 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.023B.A.v1.Mcshanvirinae_1nsf_3ng_25ns.xlsx

## 2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns

**Title:** Create a new family, *Mktvariviridae,* for PhiEco32-like phages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The genera *Kuravirus, Nieuwekanaalvirus,* and *Suseptimavirus* are currently classified within the subfamily *Gordonclarkvirinae,* class *Caudoviricetes*

***Proposed taxonomic change(s):***
Create eight new species in the genus *Kuravirus*
Create two new species in the genus *Suseptimavirus*
Create a new family, *Mktvariviridae*

***Justification:***
Species classified to the genera *Kuravirus, Nieuwekanaalvirus,* and *Suseptimavirus* within the subfamily *Gordonclarkvirinae* share 12 core proteins and form a deep branching clade in ViPTree tBLASTx distance analysis.

*Submitted:* 06/05/2024; *Revised:* 30/09/2024

**TABLE 42 -** *Mktvariviridae*, 11 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Mktvariviridae* | | |
| New taxon | species | *Kuravirus myPSH1131* | Escherichia phage myPSH1131 | MG983840 |

| | | | | |
|---|---|---|---|---|
| New taxon | species | *Kuravirus myPSH2311* | Escherichia phage myPSH2311 | MG976803 |
| New taxon | species | *Kuravirus XT18* | Escherichia phage vB-EcoP-XT18 | OR757434 |
| New taxon | species | *Kuravirus LAMP* | Escherichia phage LAMP | MG673519 |
| New taxon | species | *Kuravirus SDYTW1F1223* | Escherichia phage SDYTW1-F1-2-2_3 | OR296290 |
| New taxon | species | *Kuravirus pECN12032Af1* | Escherichia phage pEC-N1203-2Af.1 | OQ540978 |
| New taxon | species | *Kuravirus YF01* | Escherichia phage vB_EcoP_YF01 | OQ025076 |
| New taxon | species | *Kuravirus SR02* | Escherichia phage SR02 | OQ870566 |
| New taxon | species | *Suseptimavirus PAS59* | Escherichia phage vB_EcoP_PAS59 | OQ921332 |
| New taxon | species | *Suseptimavirus sv4E8* | Escherichia phage 4E8 | OQ689734 |

**TABLE 43 -** *Mktvariviridae*, 1 move taxon*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | subfamily | *Gordonclarkvirinae* | *Mktvariviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.024B.A.v2.Mktvariviridae_1nf_1msf_10ns.xlsx

### 2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns

**Title:** Create a new family, *Obscuriviridae* (Class: *Caudoviricetes)*

**Authors:** Bartlau N (nina.bartlau@univie.ac.at), Moraru C, Wichels A, Holmfeldt K, Amann RI

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

***Description of current taxonomy:***
The viruses described in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
A new family, *Obscuriviridae,* is proposed, comprising two new genera, *Omtjevirus* and *Cebaduodecimvirus.*

***Justification:***
The *Obscuriviridae* family was delineated with two genera. The *genus Omtjevirus* has *Omtjevirus Omtje* as a species and the genus *Cebaduodecimvirus* has *Cebaduodecimvirus phi12duo* and *Cebaduodecimvirus phi12auna* as species. The proposed taxonomic assignments are based on six different methods including nucleotide-, protein-, amino acid-, and core protein-based analysis.

*Submitted:* 21/06/2024; *Revised:* 30/09/2024

**TABLE 44 -** *Obscuriviridae*, 6 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Obscuriviridae* | | |
| New taxon | genus | *Omtjevirus* | | |

| | | | | |
|---|---|---|---|---|
| New taxon | species | *Omtjevirus Omtje* | Cellulophaga phage Omtje_1 | MT732445 |
| New taxon | genus | *Cebaduodecimvirus* | | |
| New taxon | species | *Cebaduodecimvirus phi12duo* | Cellulophaga phage phi12:2 | KC821606 |
| New taxon | species | *Cebaduodecimvirus phi12auna* | Cellulophaga phage phi12a:1 | KC821623 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.025B.A.v2.Obscuriviridae_1nf_2ng_3ns.xlsx

## 2024.026B.A.v1.Pantevenvirales_1no_3mf

**Title:** Create one new order *Pantevenvirales (Duplodnaviria)*

**Authors:** Adriaenssens EM (Evelien.adriaenssens@quadram.ac.uk), Cook R, Millard AD, Turner D

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

***Description of current taxonomy:*** The families *Straboviridae, Kyanoviridae* and *Ackermannviridae* are unassigned at the order rank within the class *Caudoviricetes.*

***Proposed taxonomic change(s):*** The order *Pantevenvirales* is created for these families.

***Justification:*** The families *Straboviridae, Kyanoviridae* and *Ackermannviridae* form a monophyletic cluster in proteome-based analyses. Members of these families share a number of core orthologous genes.

*Submitted:* 21/06/2024; *Revised:* -

**TABLE 45 -** *Pantevenvirales*, 3 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | family | *Straboviridae* | *Pantevenvirales* |
| Move taxon | family | *Kyanoviridae* | *Pantevenvirales* |
| Move taxon | family | *Ackermannviridae* | *Pantevenvirales* |

**TABLE 46 -** *Pantevenvirales*, 1 new taxon*

| Operation | Rank | New taxon name |
|---|---|---|
| New taxon | order | *Pantevenvirales* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.026B.A.v1.Pantevenvirales_1no_3mf.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.026B.A.v1.Pantevenvirales_1no_3mf.xlsx

## 2024.028B.A.v1.Philemonvirus_1ns

**Title:** To create one (1) new species in the genus *Bifilivirus,* family *Paulinoviridae*

**Authors:** Deptula P (deptula@food.ku.dk), Sha Y, Potipimpanon S, Vogensen FK, Nielsen DS, Knezevic P

***Summary:***

***Taxonomic rank(s) affected:*** This is a proposal for creating a new species within the genus *Bifilivirus.*

***Description of current taxonomy:***

***Proposed taxonomic change(s):*** Addition of a new species *Bifilivirus philemonii*

***Justification:***
Filamentous phage Philemon was isolated from raw milk Emmental cheese on a dairy-associated strain of *Propionibacterium freudenreichii* PB4. The obtained TEM confirmed filamentous morphology. Philemon forms plaques on three *P. freudenreichii* strains in our collection, including the strain TL18, which was used for characterization of phage B5 (though no plaquing was reported for phage B5) {11889111}. The phage genome was sequenced with Illumina platform after formation of complementary strand with MDA technique. The genome is 5802 nt long, with 63 G+C %mol. Comparison with the only other representative of genus *Bifilivirus,* Propionibacterium virus B5 (NC_003460.1) revealed that the genome of Philemon is 92.8% identical to the genome of the Propionibacterium virus B5, thus fulfilling the criteria for creation of a separate species. The similarity of morphogenesis protein and CoaB confirms that Philemon belongs to the genus *Bifilivirus*. We propose the name of the species – *Bifivilus philemonii.*

*Submitted:* 23/04/2024; *Revised:* -

**TABLE 47 -** *Philemonvirus*, 1 new taxon*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | species | *Bifilivirus philemonii* | Propionibacterium phage Philemon | PP693361 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.028B.A.v1.Philemonvirus_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.028B.A.v1.Philemonvirus_1ns.xlsx

## 2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns

**Title:** Create seven new genera for *Rhodococcus* siphoviruses [Class: *Caudoviricetes]*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
We propose the creation of seven new taxa for unique *Rhodococcus* siphoviruses: *Edwardsroadvirus, Wodongavirus, Reqipinevirus, Melbournevirus, Trogglehumpervirus, Mboduovirus, Reynauldvirus*

***Justification:***
The taxa proposed conform to demarcation criteria specified by the ICTV bacterial viruses subcommittee.

*Submitted:* 09/05/2024; *Revised:* -

**TABLE 48** – *Rhodococcus* siphoviruses, 14 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Edwardsroadvirus* | | |
| New taxon | species | *Edwardsroadvirus RRH1* | Rhodococcus phage RRH1 | JN116822 |
| New taxon | genus | *Wodongavirus* | | |
| New taxon | species | *Wodongavirus REQ3* | Rhodococcus phage REQ3 | JN116824 |
| New taxon | genus | *Reqipinevirus* | | |
| New taxon | species | *Reqipinevirus reqipine5* | Rhodococcus phage ReqiPine5 | GU580943 |
| New taxon | genus | *Melbournevirus* | | |
| New taxon | species | *Melbournevirus REQ2* | Rhodococcus phage REQ2 | JN116823 |
| New taxon | genus | *Trogglehumpervirus* | | |
| New taxon | species | *Trogglehumpervirus trogglehumper* | Rhodococcus phage Trogglehumper | OQ709222 |
| New taxon | genus | *Mboduovirus* | | |
| New taxon | species | *Mboduovirus mbo2* | Rhodococcus phage Mbo2 | ON191531 |
| New taxon | genus | *Reynauldvirus* | | |
| New taxon | species | *Reynauldvirus reynauld* | Rhodococcus phage Reynauld | OR159659 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.029B.A.v1.Rhodococcus_siphoviruses_7ng_7ns.xlsx

## 2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns

**Title:** Create a new family, *Trautnerviridae,* subfamily *Polsinellivirinae* and two genera *(Rivavirus,* and *Splendidrerdvirus)* [class *Caudoviricetes*]

**Authors:** Cook R, Tavares P, Lurz R, Barylski J, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
The viruses classified in this proposal do not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
To create a new genus, *Rivavirus*, with three species
To create a new genus, *Spendidredvirus*, with two species
To create a new subfamily, *Polsinellivirinae*, with these two genera (*Rivavirus* and *Spendidredvirus*)
To create a new single-species genus, *Prospektnaukivirus*
To create a new family, *Trautnerviridae,* for these taxa

***Justification:*** *Bacillus* phage SPP1 was isolated in 1966; sequenced in 1997 (corrected in 2018); and, has been the subject of numerous morphological and physiologically studies; yet has remained unclassified. In this proposal it has been assigned to a new genus, *Rivavirus,* together with phage SplendidRed *(Splendidredvirus),* form a new subfamily, *Polsinellivirinae.* The members of this taxon are siphoviruses which have genomes of 42.8 – 46.3 kb (43.7 - 44.6 mol% G+C) and encode 74-77 proteins and no tRNAs. As a result of detailed genomic, proteomic and phylogenetic analyses using VIRIDIC, ViPTree, VirClust we further propose to create a new family named *Trautnerviridae* named in honour of Thomas A. Trautner.

*Submitted:* 25/05/2024; *Revised:* 30/09/2024

**TABLE 49 -** *Trautnerviridae*, 11 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Trautnerviridae* | | |
| New taxon | subfamily | *Polsinellivirinae* | | |
| New taxon | genus | *Rivavirus* | | |
| New taxon | species | *Rivavirus SPP1* | Bacillus phage SPP1 | X97918 |
| New taxon | species | *Rivavirus rv000TH010* | Bacillus phage 000TH010 | MN176219 |
| New taxon | species | *Rivavirus rv049ML001* | Bacillus phage 049ML001 | MN176227 |
| New taxon | genus | *Splendidredvirus* | | |
| New taxon | species | *Splendidredvirus splendidred* | Bacillus phage vB_BspS_SplendidRed | MN013088 |
| New taxon | species | *Splendidredvirus ray17* | Bacillus phage Ray17 | MH752385 |
| New taxon | genus | *Prospektnaukivirus* | | |
| New taxon | species | *Prospektnaukivirus sam112* | Bacillus phage vB_BcM_Sam112 | MN604230 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.030B.A.v2.Trautnerviridae_1nf_1nsf_3ng_6ns.xlsx

## 2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg

**Title:** Create a new family, *Sarkviridae* for the Jersey-like siphophages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
*Jerseyvirus, Cornellvirus and Kagunavirus* in the *subfamily Guernseyvirinae;* and, amongst the *Serratia* phages *Seretavirus* and *Otakuvirus*

***Proposed taxonomic change(s):***
To create a new family *Sarkviridae*

***Justification:***
Genomic, proteomic and phylogenetic data indicate that this group of phages is a family. In addition, Taxonomy Proposal 2023.068B.A.v1.Caudoviricetes_Serratia_3ng suggested a higher level relationship between the *Otakuvirus* and the *Guernseyvirinae.*

*Submitted:* 04/06/2024; *Revised:* 30/09/2024

**TABLE 50 -** *Sarkviridae*, 3 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | subfamily | *Guernseyvirinae* | *Sarkviridae* |
| Move taxon | genus | *Seretavirus* | *Sarkviridae* |
| Move taxon | genus | *Otakuvirus* | *Sarkviridae* |

**TABLE 51 -** *Sarkviridae*, 1 new taxon*

| Operation | Rank | New taxon name |
|---|---|---|
| New taxon | family | *Sarkviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.031B.A.v2.Sarkviridae_1nf_1msf_2mg.xlsx

## 2024.032B.A.v1.Sepahanvirus_1ng_2ns

**Title:** Create a new genus, *Seraphanvirus,* containing two species *(Caudoviricetes)*

**Authors:** Ganjoor MS, Bouzari M (bouzari@sci.ui.ac.ir), Soleimani-Delfan A

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

***Description of current taxonomy:***
These phages are currently unclassified.

***Proposed taxonomic change(s):***
To create a new genus, *Sepahanvirus,* within the class *Caudoviricetes* comprising two species, vB_Yru_GN1 and YerA41.

***Justification:***
Phages vB_Yru_GN1 and phage YerA41 exhibit nucleotide sequence similarity that falls within the demarcation threshold for the creation of a new genus.

*Submitted:* 09/12/2023; *Revised:* -

**TABLE 52 -** *Sepahanvirus*, 3 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Sepahanvirus* | | |
| New taxon | species | *Sepahanvirus vB_Yru_GN1* | Yersinia phage vB_Yru_GN1 | LC779065 |
| New taxon | species | *Sepahanvirus GN1* | Yersinia phage YerA41 | MW570730 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.032B.A.v1.Sepahanvirus_1ng_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.032B.A.v1.Sepahanvirus_1ng_2ns.xlsx

## 2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns

**Title:** Create a new family *(Mazoviaviridae)* and a new genus *(Dabrowskivirus)* with a single species *(Caudoviricetes* class)

**Authors:** Shymialevich D, Wójcicki M (michal.wojcicki@ibprs.pl), Sokołowska B

***Summary:***
***Taxonomic rank(s) affected:***
Proposal to create a new family *(Mazoviaviridae)* and a new genus *(Dabrowskivirus)* with a single species *(Caudoviricetes* class).

***Description of current taxonomy:***
In 2022, significant changes to the taxonomy of bacterial viruses were introduced: the paraphyletic morphological families *Podoviridae, Siphoviridae,* and *Myoviridae* as well as the order *Caudovirales* were abolished, which is replaced by the class *Caudoviricetes* to group all tailed bacterial and archaeal viruses with icosahedral capsids and a double-stranded DNA genome. Moreover, a binomial system of nomenclature for species was established. Based on the morphology and the comparative analysis of its predicted proteins, Alicyclobacillus myophage vB_Aac_IAFB_3916 was assigned to viruses with complex structures *(Caudoviricetes* class).

***Proposed taxonomic change(s):***
Analyses of the phylogenetic relationship of Alicyclobacillus myophage vB_Aac_IAFB_3916 prevented its unambiguous assignment to a specific family and genus. The weak similarity with other phage genomes deposited in the databases suggests that the isolated bacteriophage may be a representative of a new genus and new family of tailed bacteriophages.

***Justification:***
The genome of newly isolated Alicyclobacillus myophage vB_Aac_IAFB_3916 possesses no DNA homologs. At the protein level, this virus is unique. Therefore, we propose the creation of a new species *(Dabrowskivirus KKP3916),* genus *(Dabrowskivirus)* and family *(Mazoviaviridae)* for viruses of this type.

*Submitted:* 09/06/2024; *Revised:* 09/10/2024

**TABLE 53 -** *Mazoviaviridae*, 3 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Mazoviaviridae* | | |
| New taxon | genus | *Dabrowskivirus* | | |
| New taxon | species | *Dabrowskivirus KKP3916* | Alicyclobacillus myophage vB_Aac_IAFB_3916 | OQ846916 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.033B.Uc.v2.Mazoviaviridae_1nf_1ng_1ns.xlsx

## 2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns

**Title:** Create a new family, *Stackebrandtviridae,* for a group of *Gordonia* phages (Class: *Caudoviricetes)*

**Authors:** Kurtböke I, Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

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

***Description of current taxonomy:***
At present the following taxa exist as floating genera in the order *Caudoviricetes; Wizardvirus, Clownvirus, Vididuovirus, Dexdertvirus, Zitchvirus*, *Kroosvirus* and *Leonardvirus*

***Proposed taxonomic change(s):***
To create one new species in the genus *Wizardvirus*
To create a new subfamily, *Frickvirinae* with two genera *(Clownvirus* and *Wizardvirus)*

To add one new species to the genus *Vididuovirus*
To add one new species to the genus *Dexdertvirus*
To add four new species to the genus *Zitchvirus*
To add one new species to the genus *Leonardvirus*
To create a new subfamily, *Schenleyvirinae,* for the above four genera and *Kroosvirus.*
To create a new family, *Stackebrandtviridae,* for the above-mentioned taxa.

***Justification:***
Members of the Actinobacteriophage Database Cluster DC ((https://phagesdb.org/clusters/DC/) are temperate *Gordonia* phages for which we have created two genera. The related lytic viruses of Cluster DE (https://phagesdb.org/clusters/DE/) have resulted in five new genera.

*Submitted:* 15/06/2024; *Revised:* 30/09/2024

**TABLE 54 -** *Stackebrandtviridae*, 11 new taxa*

| **Operation** | **Rank** | **New taxon name** | **Exemplar** | **Accession** |
|---|---|---|---|---|
| New taxon | family | *Stackebrandtviridae* | | |
| New taxon | subfamily | *Frickvirinae* | | |
| New taxon | species | *Wizardvirus halo3* | Gordonia phage Halo3 | OR521081 |
| New taxon | subfamily | *Schenleyvirinae* | | |
| New taxon | species | *Vividuovirus sitar* | Gordonia phage Sitar | MH153809 |
| New taxon | species | *Dexdertvirus kwekel* | Gordonia phage Kwekel | OR521074 |
| New taxon | species | *Zitchvirus tardus* | Gordonia phage Tardus | ON392159 |
| New taxon | species | *Zitchvirus viaconlectus* | Gordonia phage ViaConlectus | OP068342 |
| New taxon | species | *Zitchvirus sampson* | Gordonia phage Sampson | ON456337 |
| New taxon | species | *Zitchvirus apunk* | Gordonia phage APunk | ON755186 |
| New taxon | species | *Leonardvirus phauci* | Gordonia phage Phauci | ON456349 |

**TABLE 55 -** *Stackebrandtviridae*, 8 move taxa*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | genus | *Clownvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Wizardvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Kroosvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Vividuovirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Dexdertvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Zitchvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Leonardvirus* | *Stackebrandtviridae* |
| Move taxon | genus | *Lilbeanievirus* | *Stackebrandtviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.034B.A.v2.Stackebrandtviridae_1nf_2nsf_8mg_8ns.xlsx

## 2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections

**Title:** Corrections to species names in the classes *Caudoviricetes* and *Fraserviricetes*

**Authors:** Turner D (dann2.turner@uwe.ac.uk)

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

***Description of current taxonomy:***
All of these species are currently classified within the latest release of the ICTV taxonomy

***Proposed taxonomic change(s):***
Rename species to conform to the binomial species epithet.
Correct spelling errors
Create genus to contain floating species in *Tevenvirinae*
*Change* to genus and constituent species in the genus *Roskildevirus* as "Roskilde virus" refers to Norovirus in Danish
Correction of misspelt genus names in binomial species epithets.

***Justification:***
To ensure that the naming of viruses is consistent with the guidelines for binomial species names, to remove any names that could cause confusion in native languages and to remove any genome records that do not represent coding complete sequences.

*Submitted:* 19/06/2024; *Revised:* 30/09/2024

**TABLE 56 -** *Caudoviricetes*, 96 rename taxa*. Table too large, see supplementary information sheet supp_info_tab_56

**TABLE 57 -** *Caudoviricetes*, 3 move; rename taxa*

| Operation | Rank | New taxon name | Old parent taxon | New parent taxon | Old taxon name |
|---|---|---|---|---|---|
| Move; rename taxon | species | *Centumtrigintavirus cv133* | *Tevenvirinae* | *Centumtrigintavirus* | *Acinetobacter virus 133* |
| Move; rename taxon | species | *Mosigvirus jaykay* | *Tequatrovirus* | *Mosigvirus* | *Tequatrovirus jaykay* |
| Move; rename taxon | species | *Mosigvirus efftwo* | *Tequatrovirus* | *Mosigvirus* | *Tequatrovirus efftwo* |

**TABLE 58 -** *Caudoviricetes*, 1 abolish taxon*

| Operation | Rank | Abolished taxon name |
|---|---|---|
| Abolish taxon | species | *Campylobacter virus IBB35* |

**TABLE 59 -** *Caudoviricetes*, 1 new taxon*

| Operation | Rank | New taxon name |
|---|---|---|
| New taxon | genus | *Centumtrigintavirus* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.036B.A.v2.Caudoviricetes_Faserviricetes_Name_Corrections.xlsx

## 2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns

**Title:** Create a new family, *Vandenendeviridae,* for a group of lytic *Pseudomonas* phages (Class: *Caudoviricetes)*

**Authors:** Moraru C, Tolstoy I, Kropinski AM (Phage.Canada@gmail.com)

***Summary:***

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

***Description of current taxonomy:***
Four genera are currently classified; *Baldwinvirus, Nankokuvirus, Otagovirus*, *Flaumdravirus* and *Pakpunavirus.*

***Proposed taxonomic change(s):***
To create seven new single-species genera: *Weillhallvirus, Omahavirus, Torinovirus, Yunamivirus, Ventosusvirus*, *Uavernvirus,* and *Chemalvirus*
To create a new genus, *Tartuvirus,* with four species
To create two new species in the genus *Kremarvirus*
To create a new family, *Vandenendviridae,* for these genera and *Balwinvirus, Kremarvirus, Nankokuvirus, Otagovirus, Flaumdravirus*, *Pakpunavirus* and *Shenlongvirus.*

***Justification:***
Using VIRIDIC, ViPTree, VIRCLUST and vConTACT v.3.0 we have established that this is a cohesive group of lytic *Pseudomonas* myoviruses which share ≥12.2% DNA sequence similarity and 15 core proteins. The new family is named in honour of Marius van de Ende of South Africa.

*Submitted:* 25/05/2024; *Revised:* 30/09/2024

**TABLE 60 -** *Vandenendeviridae*, 20 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Vandenendeviridae* | | |
| New taxon | genus | *Weillhallvirus* | | |
| New taxon | species | *Weillhallvirus wv16Q* | Pseudomonas phage 16Q | OR001909 |
| New taxon | genus | *Omahavirus* | | |
| New taxon | species | *Omahavirus UNOG1W1* | Pseudomonas phage UNO-G1W1 | PP551948 |
| New taxon | genus | *Torinovirus* | | |
| New taxon | species | *Torinovirus K7A1* | Pseudomonas phage phiK7A1 | MT740307 |
| New taxon | genus | *Yunamivirus* | | |
| New taxon | species | *Yunamivirus Y1MI* | Pseudomonas phage vB_PF_Y1-MI | OR500437 |
| New taxon | genus | *Ventosusvirus* | | |
| New taxon | species | *Ventosusvirus ventosus* | Pseudomonas phage ventosus | MG018930 |
| New taxon | genus | *Uavernvirus* | | |
| New taxon | species | *Uavernvirus uavern* | Pseudomonas phage UAVern | MZ605293 |
| New taxon | genus | *Tartuvirus* | | |
| New taxon | species | *Tartuvirus amme3* | Pseudomonas phage vB_PpuM-Amme-3 | PP496413 |
| New taxon | species | *Tartuvirus nopa* | Pseudomonas phage vB_PpuM-NoPa | PP496415 |
| New taxon | species | *Tartuvirus kopa4* | Pseudomonas phage vB_PpuM-KoPa-4 | PP496414 |
| New taxon | species | *Tartuvirus roomu2* | Pseudomonas phage vB_PpuM-Roomu-2 | PP496417 |
| New taxon | genus | *Chemalvirus* | | |
| New taxon | species | *Chemalvirus PseuGes254* | Pseudomonas phage PseuGes_254 | OR575930 |

**TABLE 61 -** *Vandenendeviridae*, 3 move taxa*

| **Operation** | **Rank** | **Taxon name** | **New parent taxon** |
|---|---|---|---|
| Move taxon | subfamily | *Skurskavirinae* | *Vandenendeviridae* |
| Move taxon | subfamily | *Gorskivirinae* | *Vandenendeviridae* |
| Move taxon | genus | *Nankokuvirus* | *Vandenendeviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.037B.A.v2.Vandenendeviridae_1nf_2msf_8ng_1mg_11ns.xlsx

## 2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms

**Title:** Create three new families *Mestraviridae, Asemoviridae,* and *Parnassusviridae,* and move the family *Autolykiviridae* into the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria)*

**Authors:** Bardy P, FoggPCM, Kalatzis PG, Middelboe M, Oksanen HM (hanna.oksanen@helsinki.fi)

***Summary:***
***Taxonomic rank(s) affected:***
The taxonomic ranks affected are the genus *Corticovirus* in the family *Corticoviridae,* the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria),* and the family *Autolykiviridae (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria).* In addition, some species are affected.

***Description of current taxonomy:***
Currently, the order *Vinavirales (Tectiviricetes, Preplamiviricota, Bamfordvirae, Varidnaviria)* contains one family *Corticoviridae* composed of one genus *Corticovirus* (2 species). The family *Autolykiviridae* belongs to the class *Tectiviricetes* but is not assigned to any order. The family *Autolykiviridae* is composed of two genera *Livvievirus* (2 *species)* and *Paulavirus* (3 species).

***Proposed taxonomic change(s):***
The genus *Corticovirus* (the family *Corticoviridae)* is renamed as the genus *Merivirus* and its two species are renamed accordingly. The *Vinavirales* order is rearranged so that the family *Autolykiviridae* is placed under the order along with the family *Corticoviridae.* Two new genera *Oliviavirus* and *Ameliavirus* are created in the family *Autolykiviridae.* Both genera consist of a single species *Oliviavirus viph1020o* and *Ameliavirus viph1008o* respectively*.* The genus of the virus species *Paulavirus viph1044o* is moved to the genus *Paulavirus* (the family *Autolykiviridae).* In addition, three new families *Mestraviridae, Asemoviridae,* and *Parnassusviridae* are created in the order *Vinavirales. Two* new genera *Anticleavirus* and *Polymedevirus* are created in the family *Mestraviridae.* One new species is created in each of the two genera: *Anticleavirus jorvik* and *Polymedevirus YY.* Two new genera *Elsinorevirus* and *Rumoivirus* are created in the family *Asemoviridae.* One new species is created in each of the two genera: *Elsinoreirus NO16* and *Rumoivirus VruC.* One new species *Corycianvirus MfV* is created in a new genus *Corycianvirus* in the family *Parnassusviridae.*

***Justification:***
The inclusion/creation of four families in the order *Vinavirales,* together with the family *Corticoviridae,* is based on the 9 signature genes shared by their members, which corresponds to approximately 50 % of their genome. This demonstrates their common evolutionary origin. Classification of *Paulavirus viph1044o* into the genus *Livvievirus* instead of *Paulavirus* was a mistake. To make the names of the family *Corticoviridae* and the genus *Corticovirus* based on a different word stem, the genus *Corticovirus* is renamed *Merivirus.*

*Submitted:* 20/06/2024; *Revised:* 30/09/2024

**TABLE 62 -** *Vinavirales*, 15 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Oliviavirus* | | |
| New taxon | genus | *Ameliavirus* | | |
| New taxon | family | *Mestraviridae* | | |
| New taxon | genus | *Anticleavirus* | | |
| New taxon | species | *Anticleavirus jorvik* | Rhodobacter phage Jorvik | OP588643 |
| New taxon | genus | *Polymedevirus* | | |
| New taxon | species | *Polymedevirus YY* | Marinomonas phage YY | MH105080 |
| New taxon | family | *Asemoviridae* | | |
| New taxon | genus | *Elsinorevirus* | | |
| New taxon | species | *Elsinorevirus NO16* | Vibrio phage fNo16 | MH730557 |
| New taxon | genus | *Rumoivirus* | | |
| New taxon | species | *Rumoivirus VruC* | Vibrio phage vB_VruC_PG21 | OM867525 |
| New taxon | family | *Parnassusviridae* | | |
| New taxon | genus | *Corycianvirus* | | |
| New taxon | species | *Corycianvirus MfV* | Marinomonas phage MfV | MW618650 |

**TABLE 63 -** *Vinavirales*, 4 move taxa*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | family | *Autolykiviridae* | *Vinavirales* |
| Move taxon | species | *Paulavirus viph1044o* | *Vinavirales* |
| Move taxon | species | *Oliviavirus viph1020o* | *Vinavirales* |
| Move taxon | species | *Ameliavirus viph1008o* | *Vinavirales* |

**TABLE 64 -** *Vinavirales*, 3 rename taxa*

| Operation | Rank | New taxon name | Previous taxon name |
|---|---|---|---|
| Rename taxon | genus | *Merivirus* | *Corticovirus* |
| Rename taxon | species | *Merivirus Cr39582* | *Corticovirus Cr39582* |
| Rename taxon | species | *Merivirus PM2* | *Corticovirus PM2* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.038B.A.v2.Vinavirales_3nf_1mf_7ng_5ns_3ms.xlsx

## 2024.039D.A.v1.Artimaviricota_np

**Title:** Create new phylum, *"Artimaviricota"* in the kingdom *Orthornavirae* (realm *Riboviria)* for classification of a hyperthermophilic RNA virus

**Authors:** Syun-ichi Urayama (urayama.shunichi.gn@u.tsukuba.ac.jp ), Akihito Fukudome, Eugene V. Koonin, Takuro Nunoura, Mart Krupovic (mart.krupovic@pasteur.fr )

***Summary:***
***Taxonomic rank(s) affected:*** *Riboviria, Orthornavirae*

***Description of current taxonomy:***
Realm *Riboviria* includes two kingdoms, *Orthornavirae* and *Pararnavirae,* which include highly diverse viruses that encode RNA dependent RNA polymerases (RdRP) and reverse transcriptases (RT), respectively. Kingdom *Orthornavirae* includes six phyla which were established based on

phylogenetic analysis of the RdRP and comparative analysis of the viral genomes and proteins.

***Proposed taxonomic change(s):***
We propose to create a new phylum in the kingdom *Orthornavirae* for classification of a group of RNA viruses discovered in hot springs that are characterized by unusual RdRPs.

***Justification:***
The RdRPs of HsRV1 and its relatives seem to deviate from the RdRP consensus farther than any of the other recently discovered putative phyla, with none of which they appear to be affiliated, and possess unusual structural features that appear to link them to viral RTs.

*Submitted:* 21/06/2024; *Revised:* -

**TABLE 65 -** *Artimaviricota*, 6 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | phylum | *Artimaviricota* | | |
| New taxon | class | *Furtirnaviricetes* | | |
| New taxon | order | *Divaquavirales* | | |
| New taxon | family | *Hakuzoviridae* | | |
| New taxon | genus | *Atsuirnavirus* | | |
| New taxon | species | *Atsuirnavirus caloris* | hot spring RNA virus 1 | RNA1: BTCN01000001,<br>RNA2: BTCN01000005 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Animal DNA viruses and Retroviruses (D) proposals/2024.039D.A.v1.Artimaviricota_np.docx
https://ictv.global/system/files/proposals/pending/Animal DNA viruses and Retroviruses (D) proposals/2024.039D.A.v1.Artimaviricota_np.xlsx

## 2024.040B.A.v1.Sharonstreetvirus_1ns

**Title:** Create a new species *Sharonstreetvirus xiamensis (Caudoviricetes)*

**Authors:** Liu H-T (15844493757@163.com)

**Summary:**

We isolated a new Aeromonas phage from aquaculture water of Xiamen named phiA034, and ViPTree analysis classified as a new species of an existing genus *Sharonstreetvirus, (Duplodnaviria Heunggongvirae, Uroviricota, Caudoviricetes*, *Casjensviridae).* Therefore, we propose a new species *Sharonstreetvirus xiamensis.* The genome of phiA034 is available under the accession number OP792756.

*Submitted:* 25/04/2024; *Revised:* -

**TABLE 66 -** *Sharonstreetvirus*, 1 new taxon*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | species | *Sharonstreetvirus xiamensis* | Aeromonas phage phiA034 | OP792756 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.040B.A.v1.Sharonstreetvirus_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.040B.A.v1.Sharonstreetvirus_1ns.xlsx

## 2024.041B.A.v1.Camvirus_2ns

**Title:** Create two new species **-** *Camvirus vanseggelen* and *Camvirus verabelle* [subfamily *Arquatrovirinae*, class *Caudoviricites].*

**Authors:** Kempff A (annabelkempff@gmail.com), van Neer V (vanneervera@gmail.com), Ongenae V (v.m.a.ongenae@biology.leidenuniv.nl), Rozen DE, Briegel A, Claessen D

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

***Description of current taxonomy:***
The genus *Camvirus* is classified within the subfamily *Arquatrovirinae,* class *Caudoviricetes*

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

***Justification:***
We have defined two new species, *Camvirus vanseggelen* and *Camvirus verabelle,* based upon phages isolated for host *Streptomyces coelicolor* from soil samples in the Netherlands at longitude N52°23’31” and latitude E4°34’49”. *Camvirus vanseggelen* contains a linear dsDNA genome of 50,426 bp (65,5% G+C) encoding 73 proteins. *Camvirus verabelle* contains a linear dsDNA genome of 49,832 bp (65,0% G+C) encoding 73 proteins. These new species can be included in the genus *Camvirus* together with *Streptomyces* phage Alsaber, *Streptomyces* phage Amela, *Streptomyces* phage phiCAM, *Streptomyces* phage Endor1, *Streptomyces* phage Endor2, *Streptomyces* phage Joe, *Streptomyces* phage Saftant and *Streptomyces* phage Sitrop.

*Submitted:* 02/04/2024; *Revised:* -

**TABLE 67 -** *Camvirus*, 2 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | species | *Camvirus vanseggelen* | Streptomyces phage Vanseggelen | OQ970438 |
| New taxon | species | *Camvirus verabelle* | Streptomyces phage Verabelle | OQ970439 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.041B.A.v1.Camvirus_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.041B.A.v1.Camvirus_2ns.xlsx

## 2024.042B.A.v1.Lacfervirus_1ng_1ns

**Title:** Create one new genus, *Lacfervirus,* in the class *Caudoviricetes*

**Authors:** Qiannan Wen, Xia Chen (chenxia8280@163.com)

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

***Description of current taxonomy:***
The virus classified in this proposal does not have a current taxonomic assignment.

***Proposed taxonomic change(s):***
We propose a new genus, *Lacfervirus,* comprised of a single species, *Lactobacillus* phage LFP01 in the class *Caudoviricetes.*

***Justification:***
The genome of *Lactobacillus* phage LFP01 has very low homology to all other bacteriophage sequences in the GenBank database. A complete genome sequence comparison using the BLASTn method revealed that the genome of *Lactobacillus* phage LFP01 had a maximum nucleotide identity of 92.83% and 55% coverage with *Lactobacillus* phage LF1. The low homology indicated that the newly sequenced bacteriophage likely represents a new genus with a single species..

*Submitted:* 05/06/2023; *Revised:* -

**TABLE 68 -** *Lacfervirus*, 2 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Lacfervirus* | | |
| New taxon | species | *Lacfervirus LFP01* | Lactobacillus virus LFP01 | OR048821 |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.042B.A.v1.Lacfervirus_1ng_1ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.042B.A.v1.Lacfervirus_1ng_1ns.xlsx

## 2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp

**Title:** Rename and split an existing genus of the family *Cystoviridae (Vidaverviricetes: Mindivirales),* rename seven virus species, create two new species and genera

**Authors:** Poranen MM (minna.poranen@helsinki.fi), Mäntynen S

***Summary:***
***Taxonomic rank(s) affected:*** The proposal affects species and genus ranks under the *Cystoviridae* family.

***Description of current taxonomy:*** The *Cystoviridae* family currently includes one *genus Cystovirus* and seven species, *Cystovirus phi6, Cystovirus phi8, Cystovirus phi12, Cystovirus phi13, Cystovirus phi2954, Cystovirus phiNN* and *Cystovirus phiYY. Cystoviridae* is the only family of the order *Mindivirales* and the class *Vidaverviricetes* that belongs to the phylum *Duplornaviricota (Orthornavirae, Riboviria)* together with classes *Resentoviricetes* and *Chrymotiviricetes.*

***Proposed taxonomic change(s):*** We propose a new name for the genus *Cystovirus* and its splitting into five genera*.* Due to the introduction of the new genera, we propose renaming of all the current species. In addition, we propose to create two new species and two additional new genera in the family *Cystoviridae.*

***Justification:*** Seven new dsRNA bacteriophage isolates have been identified and now proposed to be taxonomically classified to create two new species. Sequence comparisons of these viruses and previously classified dsRNA bacteriophages of the genus *Cystovirus* justify splitting of the *Cystovirus* genus and creation of all together seven genera under the *Cystoviridae.* The genus *Cystovirus* is renamed to distinguish the name stems of genus and family rank.

*Submitted:* 21/06/2024; *Revised:* 30/09/2024

**TABLE 69 -** *Cystoviridae*, 5 move; rename taxa*

| Operation | Rank | New taxon name | Old parent taxon | New parent taxon | Old taxon name |
|---|---|---|---|---|---|
| Move; rename taxon | species | *Alphacystovirus phi8* | *Cystovirus* | *Alphacystovirus* | *Cystovirus phi8* |
| Move; rename taxon | species | *Betacystovirus phi12* | *Cystovirus* | *Betacystovirus* | *Cystovirus phi12* |
| Move; rename taxon | species | *Gammacystovirus phi13* | *Cystovirus* | *Gammacystovirus* | *Cystovirus phi13* |
| Move; rename taxon | species | *Gammacystovirus phiYY* | *Cystovirus* | *Gammacystovirus* | *Cystovirus phiYY* |
| Move; rename taxon | species | *Deltacystovirus phi2954* | *Cystovirus* | *Deltacystovirus* | *Cystovirus phi2954* |

**TABLE 70 -** *Cystoviridae*, 4 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | genus | *Epsiloncystovirus* | | |
| New taxon | species | *Epsiloncystovirus phiNY* | Microvirgula phage phiNY | MW471133;<br>MW471134;<br>MW471135 |
| New taxon | genus | *Zetacystovirus* | | |
| New taxon | species | *Zetacystovirus CAP* | Acinetobacter phage CAP7 | MZ558516;<br>MZ558517;<br>MZ558518 |

**TABLE 71 -** *Cystoviridae*, 3 rename taxa*

| Operation | Rank | New taxon name | Previous taxon name |
|---|---|---|---|
| Rename taxon | genus | *Orthocystovirus* | *Cystovirus* |
| Rename taxon | species | *Orthocystovirus phi6* | *Cystovirus phi6* |
| Rename taxon | species | *Orthocystovirus phiNN* | *Cystovirus phiNN* |

**TABLE 72 -** *Cystoviridae*, 2 split taxa*

| Operation | Rank | Old taxon | New taxon 1 | New taxon 2 |
|---|---|---|---|---|
| Split taxon | genus | Cystovirus | Alphacystovirus | Betacystovirus |
| Split taxon | genus | Cystovirus | Gammacystovirus | Deltacystovirus |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.043B.A.v2.Cystoviridae_6ng_2nsp_1rng_7rnsp.xlsx

## 2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns

**Title:** Create one (1) new family *(Felixviridae),* including one (1) new subfamily *(Maevirinae),* three (3) genera (two new: *Nakavirus, Chronisvirus;* one existent*: Certevirus),* including two (2) new species *(Nakavirus sapi* and *Chronisvirus chronis).*

**Authors:** Nobrega F.L. (f.nobrega@soton.ac.uk), Rothschild-Rodriguez, D., Lambon, K.

***Summary:***
***Taxonomic rank(s) affected:***
*Viruses; Duplodnaviria; Heunggongvirae; Uroviricota; Caudoviricetes*

***Description of current taxonomy:***
Unclassified *Caudoviricetes.*

***Proposed taxonomic change(s):***
We propose a new family, *Felixviridae,* which includes at least one new subfamily, *Maevirinae,* and at least three genera, *Nakavirus* (new), *Chronisvirus* (new) and *Certevirus* (already existent). The *Nakavirus* and *Chronisvirus* genera include at least one newly proposed species each, *Nakavirus sapi* (for phages RothC and RothD), and *Chronisvirus chronis* (for phage vB_Kpn_Chronis), respectively.

***Justification:***
This family has not been taxonomically characterised, with only one previously cultured *Klebsiella* phage relative, vB_Kpn_Chronis, and a Protoea phage, PdC23. We isolated 53 phages as part of the Klebsiella Phage Collection, two of which, RothC and RothD were not able to be assigned to any existing viral families, leading us to propose a new family, *Felixviridae.* We additionally found this family of phages to be present in metagenomes coming from human stool, a proxy for the human gut microbiota, which are also currently unclassified, but previously identified by the Gut Phage Database (GPD). Genomic analyses provide sufficient evidence to suggest the *Felixviridae* family is currently composed of at least one subfamily, *Maevirinae,* comprising RothC, D and Chronis; at least three genera, *Nakavirus, Chronisvirus,* and previously existent *Certevirus.* The *Nakavirus* genus holds phages RothC and RothD. High similarity between RothC and RothD places them under the same species proposed to be *Nakavirus sapi.* The *Chronisvirus* genus holds the phage vB_Kpn_Chronis, forming the *Chronisvirus chronis* species.

*Submitted:* 19/06/2024; *Revised:* 27/06/2024

**TABLE 73 -** *Felixviridae*, 6 new taxa*

| Operation | Rank | New taxon name | Exemplar | Accession |
|---|---|---|---|---|
| New taxon | family | *Felixviridae* | | |
| New taxon | subfamily | *Maevirinae* | | |
| New taxon | genus | *Chronisvirus* | | |
| New taxon | species | *Chronisvirus chronis* | vB_Kpn_Chronis | MN013086 |
| New taxon | genus | *Nakavirus* | | |
| New taxon | species | *Nakavirus sapi* | Klebsiella phage RothC | PP934563 |

**TABLE 74 -** *Felixviridae*, 1 move taxon*

| Operation | Rank | Taxon name | New parent taxon |
|---|---|---|---|
| Move taxon | genus | *Certevirus* | *Felixviridae* |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.044B.A.v1.Felixviridae_1nf_1nsf_2ng_1mg_2ns.xlsx

## 2024.045B.A.v2.Autographivirales

**Title:** Promoting the family *Autographiviridae* to create one new order, *Autographivirales,* with four new families, four new subfamilies, 93 new genera and 607 new species *(Duplodnaviria, Caudoviricetes).*

**Authors:** Turner D (dann2.Turner@uwe.ac.uk), Carrillo D, Lood C, Ely B, Lehman SM, Dutilh B, Kropinski AM, Lavigne R, Adriaenssens EM, Millard AD

***Summary:***

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

Realm: *Duplodnaviria;* Kingdom: *Heunggongvirae;* Phylum: *Uroviricota;* Class: *Caudoviricetes*

***Description of current taxonomy:***

The family *Autographiviridae* was established under taxonomic proposal

***Proposed taxonomic change(s):***

We propose;
The establishment of a new order, *Autographivirales,* containing four new families.
The creation of four new subfamilies
The creation of 93 new genera
The creation of 610 new species
Abolition of 21 species

***Justification:***

The proposed order forms a single deep-branching clade in tBLASTx distance analysis, reflected in core gene maximum-likelihood phylogeny. The proposed families form monophyletic clusters in proteome-based analyses and each share a number of core orthologous genes.

*Submitted:* 21/06/2024; *Revised:* 30/09/2024

**TABLE 75 -** *Autographivirales*, 708 new taxa*. Table too large, see supplementary information sheet supp_info_tab_75

**TABLE 76 -** *Autographivirales*, 60 move taxa*. Table too large, see supplementary information sheet supp_info_tab_76

**TABLE 77 -** *Autographivirales*, 21 abolish taxa*

| Operation | Rank | Abolished taxon name |
|---|---|---|
| Abolish taxon | species | *Friunavirus SWHAb1* |
| Abolish taxon | species | *Friunavirus SWHAb3* |
| Abolish taxon | species | *Phikmvvirus NFS* |
| Abolish taxon | species | *Phikmvvirus PT2* |
| Abolish taxon | species | *Vectrevirus cee* |
| Abolish taxon | species | *Maculvirus OWB* |
| Abolish taxon | species | *Murciavirus CB5A* |
| Abolish taxon | species | *Kaohsiungvirus AS51* |
| Abolish taxon | species | *Cuernavacavirus RHEph09* |
| Abolish taxon | species | *Atuphduovirus atuph03* |
| Abolish taxon | species | *Przondovirus KpV766* |
| Abolish taxon | species | *Teseptimavirus YpsPG* |
| Abolish taxon | species | *Teseptimavirus YpPY* |
| Abolish taxon | species | *Helsettvirus fPS53* |
| Abolish taxon | species | *Teetrevirus T7M* |
| Abolish taxon | species | *Berlinvirus Yepe2* |
| Abolish taxon | species | *Berlinvirus Yepf* |
| Abolish taxon | species | *Kayfunavirus EcpYZU01* |
| Abolish taxon | species | *Pektosvirus PP81* |
| Abolish taxon | species | *Ghunavirus Psa17* |

|  |  |  |
|---|---|---|
| Abolish taxon | species | *Friunavirus AB3* |

**TABLE 78 -** *Autographivirales*, 14 move; rename taxa*

| Operation | Rank | New taxon name | New parent taxon | Old taxon name |
|---|---|---|---|---|
| Move; rename taxon | species | *Rodentiumvirus LL11* | *Autographivirales* | *Vectrevirus LL11* |
| Move; rename taxon | species | *Rodentiumvirus CrRp3* | *Autographivirales* | *Vectrevirus CrRp3* |
| Move; rename taxon | species | *Nerthusvirus achelous* | *Autographivirales* | *Uliginvirus achelous* |
| Move; rename taxon | species | *Nerthusvirus nerthus* | *Autographivirales* | *Uliginvirus nerthus* |
| Move; rename taxon | species | *Nerthusvirus alpheus* | *Autographivirales* | *Uliginvirus alpheus* |
| Move; rename taxon | species | *Njordvirus njord* | *Autographivirales* | *Uliginvirus njord* |
| Move; rename taxon | species | *Ebriosvirus ebrios* | *Autographivirales* | *Teseptimavirus ebrios* |
| Move; rename taxon | species | *Ebriosvirus IME15* | *Autographivirales* | *Teseptimavirus IME15* |
| Move; rename taxon | species | *Hennigervirus shl2* | *Autographivirales* | *Ghunavirus shl2* |
| Move; rename taxon | species | *Hennigervirus PPPL1* | *Autographivirales* | *Ghunavirus PPPL1* |
| Move; rename taxon | species | *Hennigervirus henninger* | *Autographivirales* | *Ghunavirus henninger* |
| Move; rename taxon | species | *Unosvirus UNOSLW1* | *Autographivirales* | *Pifdecavirus UNOSLW1* |
| Move; rename taxon | species | *Pfluvirus PFP1* | *Autographivirales* | *Pifdecavirus PFP1* |
| Move; rename taxon | species | *Pfluvirus pv22PfluR64PP* | *Autographivirales* | *Pifdecavirus pv22PfluR64PP* |

**TABLE 79 -** *Autographivirales*, 2 rename taxa*

| Operation | Rank | New taxon name | Previous taxon name |
|---|---|---|---|
| Rename taxon | species | *Ghunavirus gv17A* | *Ghunavirus 17A* |
| Rename taxon | species | *Warsawvirus wv3MF5* | *Warsawvirus 3MF5* |

**TABLE 80 -** *Autographivirales*, 1 promote taxon*

| Operation | New taxon name | Old rank | New rank |
|---|---|---|---|
| Promote taxon | *Autographivirales* | order | order |

*Source / full text:
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.045B.A.v2.Autographivirales.docx
https://ictv.global/system/files/proposals/pending/Bacterial%20viruses%20(B)%20proposals/2024.045B.A.v2.Autographivirales.xlsx