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

Main Text

Contents

2024.001A.Uc.v2.N.v1.Apasviridae_newfam

Title: Create one new family in the order *Magrovirales* (class *Caudoviricetes)*

Authors: Prabhu A (apoorva.prabhu@uq.edu.au), Rinke C

Summary:
Taxonomic rank(s) affected: Magrovirus group A (order *Magrovirales;* class *Caudoviricetes)*

Description of current taxonomy: Recently, the order *Magrovirales* has been created for viruses associated with Marine Group II Archaea (order *Poseidoniales),* belonging to the class *Caudoviricetes.* Within *Magrovirales,* the family *Aoguangviridae,* representing the group "Magrovirus B" has been created.

Proposed taxonomic change(s): Here we propose creating the new family *'Apasviridae',* representing the group "Magrovirus A", with one new genus *'Agnivirus',* which includes the species *'Agnivirus brisbanense'.*

Please note, that the genus Savitrvirus and the species '*Savitrvirus brisbanense*', which are included in the text and the figures of this proposal, are not officially proposed at this point because complete genomes are currently not available for this virus group.

Justification: Most of the recovered magroviruses belonging to group A have not been deposited into public databases, i.e. GenBank. Hence, we propose the classification of viruses based on the demarcation criteria previously established for classification of archaeal tailed viruses (arTVs) infecting halophilic and methanogenic archaea [1].

Submitted: 24/07/2023; *Revised:* 07/10/2024

TABLE 1 - *Apasviridae*, 3 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Apasviridae*		
New taxon	genus	*Agnivirus*		
New taxon	species	*Agnivirus brisbanense*	Magrovirus_A_01	OR863078

*Source / full text:

https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.001A.Uc.v2.Apasiiviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.001A.Uc.v2.Apasiiviridae_newfam.xlsx

2024.002A.N.v1.Adrikaivirales_neworder_2newfam

Title: Create one new family in the order *Magrovirales* (class *Caudoviricetes)* and one new order, *'Adrikavirales'* within the class *Caudoviricetes*

Authors: Prabhu A (apoorva.prabhu@uq.edu.au), Rinke C

Summary:
Taxonomic rank(s) affected: Magrovirus group E (unofficially assigned to the order *Magrovirales;* class *Caudoviricetes)* and a new order within the class *Caudoviricetes*

Description of current taxonomy: Recently, the order *Magrovirales* has been created for viruses associated with Marine Group II Archaea (order *Poseidoniales*), belonging to the class *Caudoviricetes.* Within *Magrovirales,* the family *Aoguangviridae,* representing the group "Magrovirus B" has been created.

Proposed taxonomic change(s): Here we propose creating a new family *'Krittikaviridae',* representing the group "Magrovirus E", with one new genus *'Velanvirus',* which will include the species *'Velanvirus brisbanense'.* In addition, we identified a virus associated with *Poseidoniales*, which belongs to a novel order within the class *Caudoviricetes.* The new order is proposed to be named *'Adrikavirales'* and include a new family *'Satyavativiridae'.* The genus and species representative for this order is *'Vyasavirus'* and *'Vyasavirus brisbanense',* respectively.

Justification: Most of the currently available magroviruses assigned to group E are not of high quality and do not have GenBank entries. Furthermore, Poseidoniales associated viruses assigned to an order other than *Magrovirales* have not been described. Hence, we propose the classification of viruses based on the demarcation criteria previously established for classification of archaeal tailed viruses (arTVs) infecting halophilic and methanogenic archaea [1].

Submitted: 18/03/2024; *Revised:* 07/10/2024

TABLE 2 - *Adrikavirales*, 7 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Krittikaviridae*		
New taxon	genus	*Velanvirus*		
New taxon	species	*Velanvirus brisbanense*	Magrovirus_E_01	PP497039
New taxon	order	*Adrikavirales*		
New taxon	family	*Satyavativiridae*		
New taxon	genus	*Vyasavirus*		
New taxon	species	*Vyasavirus brisbanense*	Poseidoniales virus P01	PP497040

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.002A.Uc.v2,Adrikaivirales_neworder_2newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.002A.Uc.v2,Adrikaivirales_neworder_2newfam.xlsx

2024.003A.N.v1.Nipumfusiviridae_newfam

Title: Create 1 new family 'Nipumfusiviridae' with 4 genera and 10 species for archaeal viruses

Authors: Yimin Ni (Nemo.ni@outlook.com), Tianqi Xu, Shuling Yan, Lanming Chen, Yongjie Wang

Summary:

We propose a new family for Nitrosopumilaceae virus NYM1 and its relatives, the 'Nipumfusiviridae' ('Ni' and 'pum' for having sequence features similar to archaea from the family *Nitrosopumilaceae* and for being the deduced host; 'fusi' after the Latin word meaning spindles for the possible morphology). The four proposed genera are named 'Yangshanfusivirus', 'Terrafusivirus', 'Marefusivirus', and 'Baiafusivirus' after their original sampling sites, and species names are given based on the sampling locations. To be classified within this proposed family, the new members should share a minimum of 30% of average amino acid identity (AAI) with the virus genomes classified within 'Nipumfusiviridae' and share a minimum set of homologous proteins including the MCP, and the ATPase.

Submitted: 20/05/2024; *Revised:* -

TABLE 3 - *Nipumfusiviridae*, 15 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Nipumfusiviridae*		
New taxon	genus	*Marefusivirus*		
New taxon	species	*Marefusivirus pacificense*	Nitrosopumilaceae spindle-shaped virus NMP1	BK067782
New taxon	species	*Marefusivirus helgoense*	Nitrosopumilaceae spindle-shaped virus NMH1	BK067784
New taxon	species	*Marefusivirus jervisense*	Nitrosopumilaceae spindle-shaped virus NMJ1	BK067785
New taxon	species	*Marefusivirus columbiaense*	Nitrosopumilaceae spindle-shaped virus NMC1	BK067789
New taxon	species	*Marefusivirus montereyense*	Nitrosopumilaceae spindle-shaped virus NMM1	BK067790
New taxon	genus	*Terrafusivirus*		
New taxon	species	*Terrafusivirus michiganense*	Nitrosopumilaceae spindle-shaped virus NTM1	BK067788
New taxon	species	*Terrafusivirus tennesseense*	Nitrosopumilaceae spindle-shaped virus NTT1	BK067791
New taxon	genus	*Baiafusivirus*		
New taxon	species	*Baiafusivirus delawarense*	Nitrosopumilaceae spindle-shaped virus NBD1	BK067787
New taxon	species	*Baiafusivirus chesapeakense*	Nitrosopumilaceae spindle-shaped virus NBC1	BK067786
New taxon	genus	*Yangshanfusivirus*		
New taxon	species	*Yangshanfusivirus mimetica*	Nitrosopumilaceae spindle-shaped virus NYM1	BK067792

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

2024.004A.N.v1.Thalassapleoviridae_newphylum

Title: Create a phylum within kingdom *'Trapavirae'* (realm *Monodnaviria)* for classification of hyperthermophilic archaeal viruses with pleomorphic virions

Authors: Baquero DP, Bignon EA, Krupovic M (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected: *Monodnaviria, Trapavirae*

Description of current taxonomy: Monodnavirian kingdom *Trapavirae* currently comprises a single family, *Pleolipoviridae,* which includes haloarchaeal viruses with enveloped pleomorphic virions and single-stranded (ss) or double-stranded (ds)DNA genomes.

Proposed taxonomic change(s): Here we propose to classify viruses infecting hyperthermophilic marine archaea, distantly related to pleolipovirids, into a new family, "Thalassapleoviridae", and include it into a new phylum within the kingdom *Trapavirae.*

Justification: Whole-genome phylogenomic analysis and maximum likelihood phylogenetic analysis based on the membrane fusion protein characteristic of members of the kingdom *Trapavirae* show that members of the proposed family "Thalassapleoviridae" form a monophyletic group separate from the haloarchaeal pleolipovirids and currently unclassified related viruses of methanogenic archaea.

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

TABLE 4 - *Thalassapleoviridae*, 12 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	phylum	*Calorviricota*		
New taxon	class	*Caminiviricetes*		
New taxon	order	*Ageovirales*		
New taxon	family	*Thalassapleoviridae*		
New taxon	genus	*Avenivirus*		
New taxon	genus	*Aprofuvirus*		
New taxon	genus	*Geogavirus*		
New taxon	species	*Avenivirus atlanticense*	Archaeoglobus veneficus pleomorphic virus 1	BK065155
New taxon	species	*Aprofuvirus guaymasense*	Archaeoglobus profundus pleomorphic virus 1	BK065154
New taxon	species	*Geogavirus atlanticense*	Geoglobus acetivorans pleomorphic virus 1	BK065156
New taxon	species	*Geogavirus guaymasense*	Geoglobus ahangari pleomorphic virus 1	BK065157
New taxon	species	*Geogavirus pacificense*	Thalassapleovirus 2	BK065158

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.004A.A.v1.Thalassapleoviridae_newphylum_v1.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.004A.A.v1.Thalassapleoviridae_newphylum_v1.xlsx

2024.005A.N.v1.Bathyarchaeia_4newfam

Title: Create four new families for Bathyarchaeia viruses

Authors: Duan CH, Liu Y, Liu Y, Liu LR, Cai MW, Zhang R, Zeng QL, Koonin V E, Krupovic M, Li M (limeng848@szu.edu.cn)

Summary:

Bathyarchaeia is an archaeal class widespread in marine and freshwater sediments. Here we propose four new families for viruses identified by metagenomics and associated with host of the Bathyarchaeia class. The families "Fuxiviridae" and "Kunpengviridae" include head-tailed viruses of the class *Caudoviricetes* in the realm *Duplodnaviria.* The family "Chiyouviridae" consists of filamentous viruses of the archaea-specific realm *Adnaviria.* The fourth putative family, "Huangdiviridae," with only one representative genome, includes an archaea-specific spindle-shaped virus; the spindle-shaped viruses have not yet been classified at higher taxonomy ranks.

Submitted: 20/06/2024; *Revised:* 04/09/2024

TABLE 5 - *Bathyarchaeia*, 12 new taxa*

Operation	Rank	New taxon name	Exemplar	Accession
New taxon	family	*Fuxiviridae*		
New taxon	family	*Kunpengviridae*		
New taxon	family	*Chiyouviridae*		
New taxon	family	*Huangdiviridae*		
New taxon	genus	*Taijivirus*		
New taxon	genus	*Dafengvirus*		
New taxon	genus	*Wargodvirus*		
New taxon	genus	*Xuanyuanvirus*		
New taxon	species	*Taijivirus yinyang*	Bathyarchaeia bifangarchaeales Fuxivirus 1	PP467601
New taxon	species	*Dafengvirus linsing*	Bathyarchaeia jinwuousiales Kupengvirus 1	PP467599
New taxon	species	*Wargodvirus xiongnu*	Bathyarchaeia bifangarchaeales Chiyouvirus 1	PP467602
New taxon	species	*Xuanyuanvirus yandi*	Bathyarchaeia baizomonadales Huangdivirus 1	QMYA01000001

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.005A.A.v2.Bathyarchaeia_4newfam.docx
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2024.006A.N.v1.Usuviridae_newfam

Title: Create new family, ‘Usuviridae’, with two genera in the order *Methanobavirales* (class *Caudoviricetes)*

Authors: Diana P. Baquero, Sofia Medvedeva, Guillaume Borrel, SimonettaGribaldo, Mart Krupovic (mart.krupovic@pasteur.fr)

Summary:
Taxonomic rank(s) affected:
Duplodnaviria, Heunggongvirae, Uroviricota, Caudoviricetes, Methanobavirales

Description of current taxonomy:
Order *Methanobavirales* (class *Caudoviricetes)* currently includes 5 families of viruses infecting methanogenic archaea.

Proposed taxonomic change(s):
Create a new family, ‘Usuviridae’ with two genera for classification of viruses infecting human and animal gut associated methanogenic archaea, and include this family into the existing order *Methanobavirales.*

Justification:
Whole-proteome-based phylogenomic analysis using VipTree placed MSTV1-like viruses in a distinct clade, outside of the recently established families of tailed viruses associated with methanogenic archaea or other archaeal hosts.

Submitted: 21/06/2024; *Revised:* 11/09/2024

TABLE 6 - *Usuviridae*, 5 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Accession**
New taxon	family	*Usuviridae*		
New taxon	genus	*Manusuvirus*		
New taxon	genus	*Hewusuvirus*		
New taxon	species	*Manusuvirus methanobrevibacteri*	Methanobrevibacter smithii tailed virus 1	PP537965
New taxon	species	*Hewusuvirus methanobrevibacteri*	Methanobrevibacter gottschalkii virus vir075	BK068243

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.006A.Uc.v2.Usuviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.006A.Uc.v2.Usuviridae_newfam.xlsx

2024.007A.N.v1.Eurekaviridae_newfam

Title: Create a new family, “Eurekaviridae” of spindle-shaped archaeal virus

Authors: Coves M, Krupovic M, Bize A (ariane.bize@inrae.fr)

Summary:
Taxonomic rank(s) affected:
We suggest creating a new family, a new genus and a new species for classification of a spindle-shaped archaeal virus predicted to infect *Methanosarcina* species.

Description of current taxonomy:
Three families of small spindle-shaped archaeal viruses are currently defined: *Fuselloviridae, Halspiviridae and Thaspiviridae.* In addition, several spindle-shaped viruses are still unclassified. No spindle-shaped viruses infecting a methanogen has been classified so far.

Proposed taxonomic change(s):
We suggest creating a new family (“Eurekaviridae”), a new genus (“Hesperidvirus“) and a new species (“Hesperidvirus aureum”) to classify a newly sequenced uncultured virus, *Methanosarcina* spindle-shaped virus 1 (MetSSV1).

Justification:
MetSSV1 genome has been obtained through metavirome co-assembly, from samples collected in mesophilic anaerobic digestion batch microcosms fed with biowaste. This genome is complete and circular. It encodes several copies of the major coat proteins similar to those of previously characterized spindle-shaped viruses. However, it does not show significant genomic similarity to other archaeal spindle-shaped viruses, which justifies the creation of a new family.

Submitted: 26/06/2024; *Revised:* 02/10/2024

TABLE 7 - *Eurekaviridae*, 3 new taxa*

Operation	**Rank**	**New taxon name**	**Exemplar**	**Exemplar**
New taxon	family	*Eurekaviridae*		
New taxon	genus	*Hesperidvirus*		
New taxon	species	*Hesperidvirus aureum*	Methanosarcina spindle-shaped virus 1	PQ167755

*Source / full text:
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.007A.Uc.v2.Eurekaviridae_newfam.docx
https://ictv.global/system/files/proposals/pending/Archaeal%20viruses%20(A)%20proposals/2024.007A.Uc.v2.Eurekaviridae_newfam.xlsx