



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

<b>Code assigned:</b>	<b>2016.064a-jB</b>	(to be completed by ICTV officers)
<b>Short title: Create genus <i>Alphatristromavirus</i> within the new family <i>Tristromaviridae</i> and remove genus <i>Alphalipothrixvirus</i> from the family <i>Lipothrixviridae</i>.</b> (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (modules 1 and 11 are required)	2 X    3 X    4 <input type="checkbox"/> 5 X 6 <input type="checkbox"/> 7 X    8 X    9 <input type="checkbox"/> 10 <input type="checkbox"/>	

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**List the ICTV study group(s) that have seen this proposal:**

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Archaeal Viruses Study Group

**ICTV Study Group comments (if any) and response of the proposer:**

Date first submitted to ICTV:

July, 2016

Date of this revision (if different to above):

**ICTV-EC comments and response of the proposer:**

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MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	<b>2016.064aB</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<i>Alphatristromavirus (new)</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>Tristromaviridae (new)</i>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Pyrobaculum filamentous virus 1</i>	Pyrobaculum filamentous virus 1 (PFV1)	KU307456

<p><b>Reasons to justify the creation and assignment of the new species:</b></p> <ul style="list-style-type: none"> <li>Explain how the proposed species differ(s) from all existing species.             <ul style="list-style-type: none"> <li>If species demarcation criteria (see module 3) have previously been defined for the genus, <b>explain how the new species meet these criteria.</b></li> <li>If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.</li> </ul> </li> <li>Further material in support of this proposal may be presented in the Appendix, Module 11</li> </ul>
<p>Based on the unique virion organization and genome content Pyrobaculum filamentous virus 1 cannot be assigned into any of the currently existing virus families (see Module 11 – Appendix: Figures 1, 2, and 3).</p>

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	<b>2016.064bB</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
Subfamily:		Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no family is specified, enter “ <b>unassigned</b> ” in the family box
Family:	<i>Tristromaviridae (new)</i>	
Order:		

naming a new genus

Code	<b>2016.064cB</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Alphatristromavirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2016.064dB</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<i>Pyrobaculum filamentous virus 1</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
2		

**Reasons to justify the creation of a new genus:**

Additional material in support of this proposal may be presented in the Appendix, Module 11

We propose classifying *Pyrobaculum filamentous virus 1* as the first representative of a new genus on the basis of its unique morphological features, gene content and genome organization (see Module 11 – Appendix: Figures 1, 2, and 3). PFV1 has a virion organization, which differs considerably from those reported for other archaeal viruses. The virion,  $400 \pm 20 \times 32 \pm 3$  nm, contains an envelope and an inner core consisting of two structural units: a rod-shaped helical nucleocapsid, formed of two 14 kDa major virion proteins, and a nucleocapsid-encompassing protein sheath composed of a single major virion protein of 18 kDa. The sheath layer is sandwiched between the nucleocapsid and the envelope, akin to the matrix protein layer found in certain eukaryotic viruses. The linear dsDNA genome of PFV1 is 17,714 bp in length, includes 60 bp-long terminal inverted repeats, and contains 39 predicted ORFs, most of which do not show similarities to sequences in public databases.

The only virus related to PFV1 is Thermoproteus tenax virus 1 (TTV1), which has been historically (in the pre-genomic era) classified into the genus *Alphalipothrixvirus* within the family *Lipothrixviridae*. However, more detailed examination of the TTV1 gene content and virion organization shows that it is unrelated to other lipothrixviruses, beyond the overall morphology. We propose to unite evolutionarily related TTV1 and PFV1 within the same genus (see Module 7

and 8).

**Origin of the new genus name:**

From Greek *tria* for three and *stroma* for a layer

**Reasons to justify the choice of type species:**

Pyrobaculum filamentous virus 1 is the most extensively characterized member of the genus.

**Species demarcation criteria in the new genus:**

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Species demarcation within this genus is based on the differences in the host range and gene content. There are too few representatives at the moment to provide more detailed demarcation criteria.

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code **2016.064eB** (assigned by ICTV officers)

**To create a new family containing the subfamilies and/or genera listed below within the Order:**

If there is no Order, write “**unassigned**” here.

If the Order has yet to be created (in Module 6) please write “**(new)**” after the proposed name.

Code **2016.064fB** (assigned by ICTV officers)

**To name the new family: *Tristromaviridae***

assigning subfamilies, genera and unassigned species to a new family

Code (assigned by ICTV officers)

**To assign the following subfamilies (if any) to the new family:**

You may list several subfamilies here. For each subfamily, please state whether it is new or existing.

- If the subfamily is new, it must be created in Module 4
- If the subfamily already exists, please complete Module 7 to ‘MOVE’ it from its existing family

Code **2016.064gB** (assigned by ICTV officers)

**To assign the following genera to the new family:**

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to ‘MOVE’ it from that family

***Alphatristromavirus***

The new family will also contain any other new species created and assigned to it (Module 3) and any

that are being moved from elsewhere (Module 7). Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):

*None*

**Reasons to justify the creation of the new family:**

[Additional material in support of this proposal may be presented in the Appendix, Module 11](#)

We propose classifying *Pyrobaculum filamentous virus 1* as the first representative of a new family on the basis of its unique morphological features, exceptional gene content and genome organization (see Module 11 – Appendix: Figures 1, 2, and 3). The virion of *Pyrobaculum filamentous virus 1* has a type of virion organization, not previously reported in DNA viruses. The virion,  $400 \pm 20 \times 32 \pm 3$  nm, contains an envelope and an inner core consisting of two structural units: a rod-shaped helical nucleocapsid, formed of two 14 kDa major virion proteins, and a nucleocapsid-encompassing protein sheath composed of a single major virion protein of 18 kDa. The linear dsDNA of *Pyrobaculum filamentous virus 1* carries 17,714 bp, including 60 bp-long terminal inverted repeats, and contains 39 predicted ORFs, most of which do not show similarities to sequences in public databases.

**Origin of the new family name:**

From Greek *tria* for three and *stroma* for a layer

MODULE 7: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	<b>2016.064hB</b>	(assigned by ICTV officers)
<b>To move the following taxon (or taxa) from their present position:</b>		
<b>Species: <i>Thermoproteus tenax virus 1</i></b>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Alphalipothrixvirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Lipothrixviridae</i>	
Order:	<i>Ligamenvirales</i>	
Code	<b>2016.064iB</b>	(assigned by ICTV officers)
<b>To re-assign the taxon (or taxa) listed in Part (a) as follows:</b>		
Genus:	<i>Alphatristromavirus (new)</i>	Fill in all that apply. • If the higher taxon has yet to be created write “(new)” after its proposed name and complete relevant module to create it. If no genus is specified, enter “unassigned” in the genus box.
Subfamily:		
Family:	<i>Tristromaviridae (new)</i>	
Order:		

**Reasons to justify the re-assignment:**

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

Although the *Thermoproteus tenax virus 1* (TTV1) (Janekovic *et al.*, 1983) – [genome sequence accession nr. X14855] has been historically classified into the family *Lipothrixviridae* (genus *Alphalipothrixvirus*) based on the overall morphology and the presence of the external envelope (King *et al.*, 2012), more detailed analyses on its virion organization and genome sequence show that it does not share any homologous gene with the rest of the members of this virus family (genera *Beta-*, *Gamma-*, *Deltalipothrixvirus*). Even the major virion proteins of TTV1 are unrelated to those of other members of the *Lipothrixviridae* and their virion organizations are markedly different. These observations question the validity of the classification of TTV1 within the same taxon, the *Lipothrixviridae*, with other enveloped filamentous viruses of archaea (genera *Betalipothrixviridae*, *Deltalipothrixviridae*, and *Gammalipothrixviridae*). The members of the three latter genera clearly share an origin with each other as well as with the members the family *Rudiviridae* and thus have been unified in the order *Ligamenvirales* (Prangishvili,

Krupovic, 2012). In order to avoid moving *Betalipothrixviridae*, *Detalipothrixviridae*, and *Gammalipothrixviridae* to a new family, which would necessitate modifications at the level of the order *Ligamenvirales*, it is more practical to move TTV1 — the sole member of the genus *Alphalipothrixvirus* — to a new virus family.

Comparison of TTV1 with the Pyrobaculum filamentous virus 1 (PFV1) (Rensen *et al.*, 2016), the first member of the new genus *Alphatristromavirus* of the new family *Tristromaviridae*, clearly shows that the two viruses are evolutionarily related. They share the three-layered virion organization - both virions contain an envelope and an inner core consisting of two structural units: a rod-shaped helical nucleocapsid, consisting of two major virion proteins, and a nucleocapsid-encompassing protein sheath composed of a single major virion protein of 18 kDa (Module 11 - Appendix: Figures 1 and 2). Moreover, the two viruses share 9 homologous genes (23 % of the PFV1 gene content), including a gene for one structural protein (Module 9 - Appendix: Figure 3). Both viruses are lytic and infect members of the hyperthermophilic archaeal order *Thermoproteales* (TTV1 infects members of the genus *Thermoproteus*, and PFV1 infects members of the genus *Pyrobaculum*). Thus, in all likelihood, TTV1 and PFV1 have evolved from a common ancestor and could be placed in the same genus (*Alphatristromavirus*) and the same family (*Tristromaviridae*).

MODULE 8: **REMOVE (ABOLISH)**

Use this module if an existing taxon needs to be completely removed (abolished). Use module 9 if there is simply a change of name.

removing (abolishing a taxon)

Code	<b>2016.064jB</b>	(assigned by ICTV officers)
<b>To remove the following taxon (or taxa) from their present position:</b>		
<b>Abolish genus <i>Alphalipothrixvirus</i></b>		
<b>The present taxonomic position of these taxon/taxa:</b>		
Genus:	<i>Alphalipothrixvirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Lipothrixviridae</i>	
Order:	<i>Ligamenvirales</i>	

**Reasons to justify the removal:**

Explain why the taxon (or taxa) should be removed

Further material in support of this proposal may be presented in the Appendix, Module 11

The only species in the genus *Alphalipothrixvirus*, the *Thermoproteus tenax virus 1*, is being moved to the new genus *Alphatristromavirus* of the family *Tristromaviridae*. Thus, no species will be left in the genus *Alphalipothrixvirus*.



MODULE 11: **APPENDIX**: supporting material

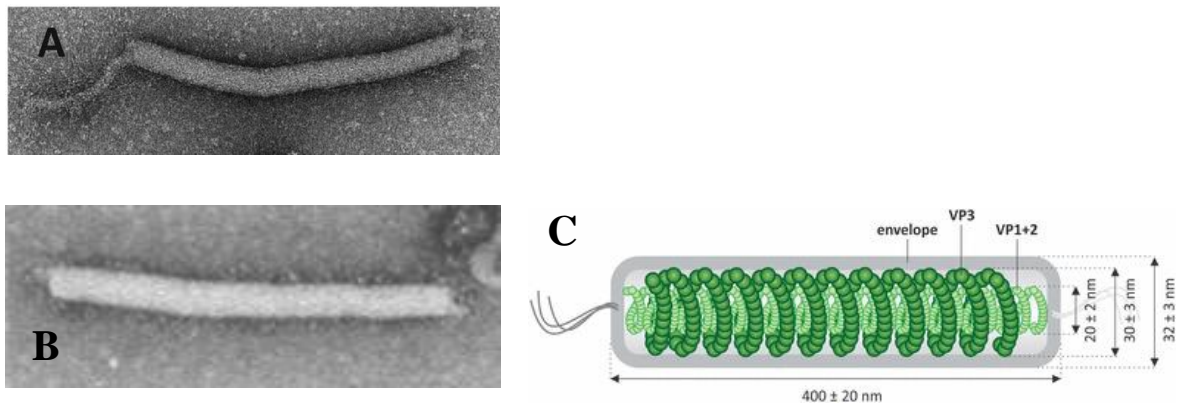


Figure 1. Electron micrographs of virions of PFV1 (A) and TTV1 (B), negatively stained with 2% uranyl acetate, and schematic of their structure with the position of three capsid proteins indicated (C).

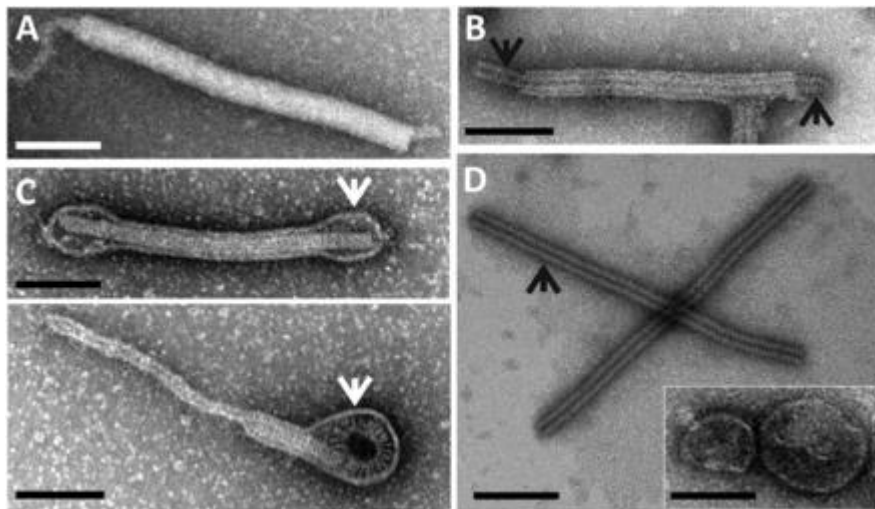


Figure 2. Transmission electron micrographs of native and disrupted PFV1 virions. (A) Native virion. (B) Virion disrupted in the course of purification. (C) Virions treated with Tween-20; white arrows indicate an envelope. (D) Structural entities resulting from virions treated with Triton X-100. Black arrows in B and D indicate a helical nucleocapsid. Negative stain with 2% uranyl acetate. (Scale bars: 100 nm.)

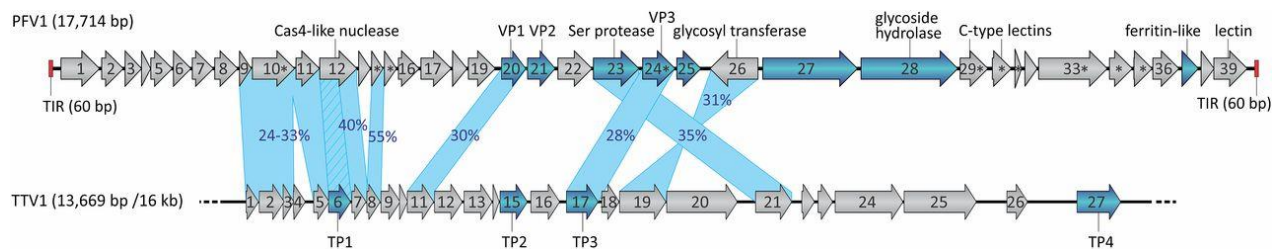


Figure 3. A genome map of PFV1 compared with the partial genome map of the virus TTV1. ORFs are indicated by arrows, which indicate the direction of transcription. Genes encoding the structural proteins are shown in blue; those encoding predicted membrane proteins are indicated by asterisks. Terminal inverted repeats (TIR) are depicted by red rectangles. The incompleteness of the TTV1 genome is illustrated by the broken line. The genes shared by PFV1 and TTV1 are connected by blue shading, and the identity between the corresponding proteins is indicated. The relationship between the *cas4* gene of PFV1 and the *TP1* gene of TTV1 is indicated by hatched shading.

## References:

Janekovic, D., S. Wunderl, I. Holz, W. Zillig, A. Gierl, and H. Neumann (1983) TTV1, TTV2 and TTV3, a family of viruses of the extremely thermophilic, anaerobic sulfur reducing archaeabacterium *Thermoproteus tenax*. *Mol. Gen. Genet.* 192: 39-45.

King, A.M., M. J. Adams, E. B. Carstens, and E. J. Lefkowitz (eds.) (2012) *Virus Taxonomy: Classification and Nomenclature of Viruses: Ninth Report of the International Committee on Taxonomy of Viruses*. Elsevier, London-Waltham-San Diego.

Prangishvili D., and M. Krupovic (2012) A new proposed taxon for double-stranded DNA viruses, the order "Ligamenvirales". *Arch.Virol.* 157: 791-795.

Rensen E., T. Mochizuki, E. Quemin, S. Schouten, M. Krupovic, and D. Prangishvili (2016) Novel virus of hyperthermophilic archaea with a unique architecture among DNA viruses. *Proc. Natl. Acad. Sci. USA* 113: 2478-2483.

## Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.