

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2020.168B** |  |
| **Short title:** Create one new genus (*Betatristromavirus*) including one existing species (*Thermoproteus tenax virus 1*) and create one new species in the genus *Alphatristromavirus* (*Tristromaviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial and Archaeal Viruses Subcommittee, Archaeal viruses SG |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | July 2020 |
| Date of this revision (if different to above) |  |

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

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2020.168B.R.Tristromaviridae.xlsx |

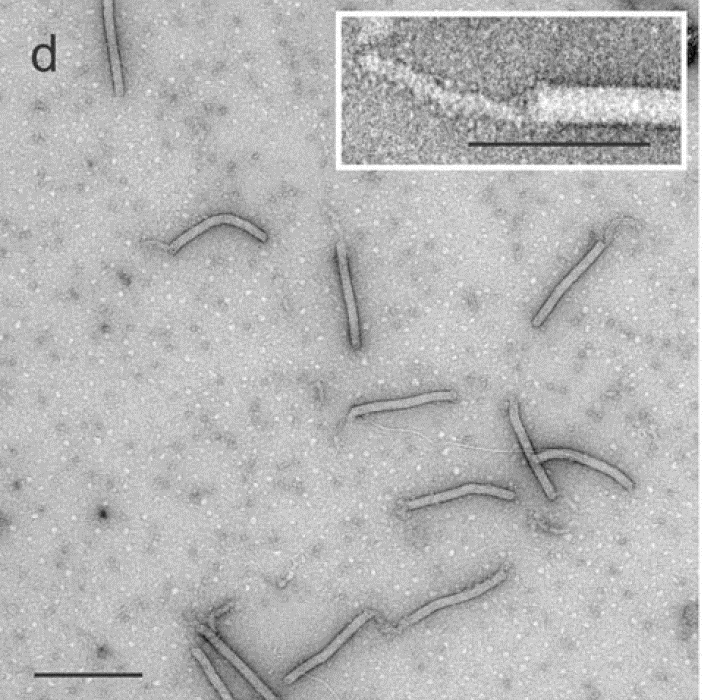
**Abstract**

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| We propose to classify Pyrobaculum filamentous virus 2 into a new species, *Alphatristromavirus PFV2*, within the genus *Alphatristromavirus*, in the family *Tristromaviridae*. Furthermore, we propose creating a new genus *Betatristromavirus* and moving species *Betatristromavirus TTV1* (renamed from *Thermoproteus tenax virus 1*) into this genus. Finally, we propose renaming species *Pyrobaculum filamentous virus 1* to *Alphatristromavirus PFV1*. |

**Text of proposal**

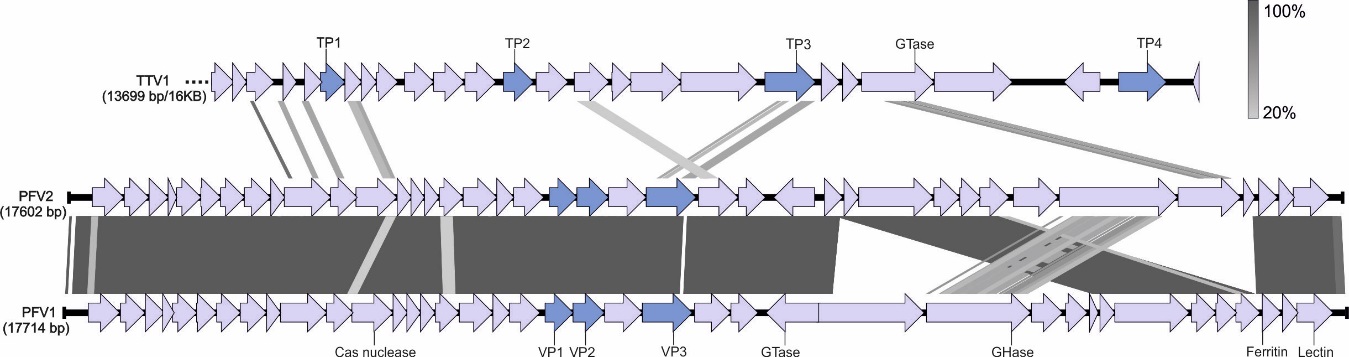
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| |  | | --- | | Family *Tristromaviridae* includes a single genus, *Alphatristromavirus*, with two species, *Pyrobaculum filamentous virus 1* (type species) and *Thermoproteus tenax virus 1* [1]. Recently, a new member of the family, Pyrobaculum filamentous virus 2 (PFV2), has been isolated from a hot spring water of the Campi Flegrei volcano in Pozzuoli, Italy [2]. Negatively stained virions of PFV2 are filamentous and flexible particles of about 450 ± 20 × 34 ± 4 nm in size with terminal filaments of up to 130 nm in length attached to one or both ends of the virions (Fig. 1), similar to what has been reported for PFV1 [3]. The virus infects *Pyrobaculum arsenaticum* 2GA and *Pyrobaculum oguniense* TE7.  The linear genome of PFV2 is 17,602 bp long and contains 39 ORFs, all except one located on the same strand. The coding region is flanked by 59 bp-long terminal inverted repeats. PFV2 genome is closely similar to that of PFV1 over 70% of its length. Two events account for the differences between PFV1 and PFV2: (i) a deletion spanning most of the PFV1 gene 27 (including codons 72–495) as well as the downstream genes 28–30, and (ii) insertion of a four-gene block between PFV1 genes 36 and 37 in PFV2 (Fig. 2). Thus, we propose creating a new species, *Alphatristromavirus PFV2*, in the genus *Alphatristromavirus* for classification of PFV2.  Species demarcation criteria for the *Alphatristromavirus* genus have not been previously proposed*,* due to scarcity of available representatives. We propose to use a 95% global genome identity as a species demarcation criterion, to be consistent with the thresholds used for other prokaryotic viruses.  Thermoproteus tenax virus 1 (TTV1), the only representative of the species *Thermoproteus tenax virus 1*, shares no detectable nucleotide sequence similarity with PFV1 or PFV2, with the distant similarities being restricted to a handful of proteins (Figure 2) and virion organization. Due to high sequence divergence of TTV1, we propose to (i) create a new genus, *Betatristromavirus*, (ii) rename the *Thermoproteus tenax virus 1* species to *Betatristromavirus TTV1* and (iii) move this species into the new genus.  Finally, for the sake of uniformity, we propose renaming species *Pyrobaculum filamentous virus 1* to *Alphatristromavirus PFV1*. | |

**Supporting evidence**

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**Figure 1. Electron micrograph of Pyrobaculum filamentous virus 2.** Sample was

negatively stained with 2% (wt/vol) uranyl acetate. Scale bars: 500 nm; in inset: 100 nm. The image is reproduced from [2].

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**Figure 2. Genome comparison of the three members of the *Tristromaviridae* family.** The open reading frames (ORFs) are represented by arrows that indicate the direction of transcription. The terminal inverted repeats (TIRs) are denoted by black bars at the ends of the genomes. Genes encoding the major structural proteins are shown in dark gray, whereas the four-gene block discussed in the text is shown in black. The functional annotations of the predicted ORFs are depicted above/below the corresponding ORFs. Homologous genes are connected by shading in grayscale based on the level of amino acid sequence identity. The dotted line represents the incompleteness of the TTV1 genome. GHase, glycoside hydrolase; GTase, glycosyltransferase; TP/VP, virion protein.

**References**

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2. Baquero DP, Contursi P, Piochi M, Bartolucci S, Liu Y, Cvirkaite-Krupovic V, Prangishvili D, Krupovic M. New virus isolates from Italian hydrothermal environments underscore the biogeographic pattern in archaeal virus communities. ISME J. 2020 Jul;14(7):1821-1833. doi: 10.1038/s41396-020-0653-z. PMID: 32322010
3. Rensen EI, Mochizuki T, Quemin E, Schouten S, Krupovic M, Prangishvili D. A virus of hyperthermophilic archaea with a unique architecture among DNA viruses. Proc Natl Acad Sci U S A. 2016 Mar 1;113(9):2478-83. doi: 10.1073/pnas.1518929113. PMID: 26884161