

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

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| **Code assigned:** | **2022.004A** |  |
| **Short title:** Create 3 new families for classification of viruses infecting methanogenic archaea | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Archaeal Viruses Subcommittee |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 |  |
| 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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| 2022.004A.N.v1.Caudoviricetes\_3nf.xlsx |

**Abstract**

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| Here we propose to create three new families for classification of tailed viruses (class *Caudoviricetes*) infecting diverse methanogenic archaea from the classes Methanococci, Methanomicrobia and Methanobacteria. The viruses do not show appreciable sequence similarity to each other or to other classified viruses. |

**Text of proposal**

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| |  | | --- | | Viruses with helical tails and icosahedral capsids (tailed viruses), classified into the class *Caudoviricetes*, represent the most widespread, abundant and diverse group of viruses on our planet. Members of the *Caudoviricetes* infect organisms from both prokaryotic domains, Bacteria and Archaea. Until recently, only a handful of archaeal tailed viruses have been officially classified. In 2022, 12 and 2 families of archaeal tailed viruses (arTVs) respectively infecting halophilic and methanogenic hosts have been created. Since then, genomes of 3 additional arTVs infecting methanogenic archaea have been described and this proposal focuses on their classification.  The three viruses infect evolutionarily different lineages of methanogenic archaea and do not display appreciable similarity to each other or to the previously classified arTVs. Nevertheless, all three viruses encode all proteins typical of members of the class *Caudoviricetes*, including the HK97-fold major capsid protein, portal, large subunit of the terminase and various tail proteins, and hence are genuine members of this virus class. Below we describe the three viruses in more detail.  Methanocaldococcus fervens tailed virus 1 (MFTV1) was initially discovered as a provirus [1] in the genome of hyperthermophilic archaeon *Methanocaldococcus fervens* AG 86T, a strain isolated in Guaymas Basin, Gulf of California, at a depth of ~2000 m [5]. The provirus has been subsequently induced, producing particles with the siphovirus-like morphology (i.e., icosahedral head and long, non-contractile tails; Fig. 1A) [3]. The genome is linear dsDNA molecule of 31,202 bp and contains 44 open reading frames (Fig. 1B). MFTV1 does not show appreciable similarity to other characterized viruses at the nucleotide or protein level (except for the large subunit of the terminase and integrase proteins), although related proviruses have been described in the genomes of *Methanocaldococcus* and *Methanococcus* species [1].  Methanoculleus virus Blf4 infects *Methanoculleus bourgensis* E02.3, a methanogenic archaeon [4]. Both the virus and its host were isolated from a commercial biogas plant in Germany. The virions display a typical siphovirus-like morphology with an icosahedral head 60 nm in diameter and a long non-contractile tail of 125 nm in length. Blf4 appears to recognize the host by binding to a flagellum (Fig. 2A). The complete 37 kb dsDNA genome of Blf4 contains 63 open reading frames, all organized in the same transcriptional direction (Fig. 2B). Blf4 does not show appreciable similarity to other characterized viruses at the nucleotide or protein level (except for the large subunit of the terminase).  Methanobacterium virus C158 genome was sequenced from a microcosm enriched in *Methanobacterium* species [2]. The genome was assembled as a circular contig of 42,490 bp and contains 49 open reading frames (Fig. 3). Based on the gene content, the virus is likely to have a siphovirus-like morphology and such particles were indeed observed in the microcosm samples. The host was assigned using various bioinformatic tools as well as stable isotope probing (SIP) [2]. C158 does not show appreciable similarity to other characterized viruses at the nucleotide or protein level (Fig. 3), even though it does form a clade with other viruses of methanogenic archaea in the ViPTree analysis (see below).  ViPTree analysis places MFTV1, Blf4 and C158 into separate family-level groups when considering the same genetic distance (branch length of 0.05) separating all other families within archaeal *Caudoviricetes* (Fig. 4). Thus, we propose to create 3 new genera and 3 new families for the classification of these viruses, as summarized in Table 1.  **Etymology**  Methanocaldococcus fervens tailed virus 1:   * *Fervensviridae*, from Latin *fervens* for hot, referring to the high temperature of the hydrothermal vent from which the host carrying the provirus was isolated. * *Deepoceanvirus*, after deep ocean, a natural habitat of *M. fervens*. * *Deepoceanvirus guaymasense*, Latinized binomial species name with the epithet referring to Guaymas Basin, a region in the Gulf of California hosting the hydrothermal vent from which *M. fervens* was isolated.   Methanoculleus virus Blf4:   * *Pungoviridae*, from Latin *pungo* for prick, puncture, referring to the ability of the virus to lyse its *Methanoculleus* (from Latin meaning methane producing bag) host. * *Flagovirus*, after flagellum, a presumed receptor of the virus. * *Flagovirus limi*, Latin binomial species name with the epithet derived from Latin *limus* which can be translated as sludge, a material from which the virus and its host were isolated.   Methanobacterium virus C158:   * Genus and family names are inspired by green color, symbol of hope. * *Speroviridae*, from Latin *spero* for "I hope". * *Glazvirus*, from Breton *glaz* for green or blue-green. * *Glazvirus inraei,* Latinized binomial species name with the epithet referring to INRAE (l'Institut national de recherche pour l'agriculture, l'alimentation et l'environnement), a place where the virus was discovered.   **Demarcation**  For future members of the families, we propose using 95% sequence identity as a species demarcation criterion, to be consistent with the classification of other bacterial and archaeal viruses in the class *Caudoviricetes*. | |

**Supporting evidence**

**Table 1. Proposed taxonomy of viruses infecting methanogenic archaea.**

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| **Family** | **Genus** | **Species** | **Virus name** | **Genome length (bp)** | **Accession number** |
| *Fervensviridae* | *Deepoceanvirus* | *Deepoceanvirus guaymasense* | Methanocaldococcus fervens tailed virus 1 | 31202 | MT711370 |
| *Pungoviridae* | *Flagovirus* | *Flagovirus limi* | Methanoculleus virus Blf4 | 37078 | MZ171369 |
| *Speroviridae* | *Glazvirus* | *Glazvirus inraei* | Methanobacterium virus C158 | 42490 | OX365879 |

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**Figure 1.** Methanocaldococcus fervens tailed virus 1. A. Electron micrograph of the Methanocaldococcus fervens tailed virus 1 virion. The virions were negatively stained with 2% uranyl acetate. Scale bar, 20 nm. Reproduced from [3]. B. Genome map of MFTV1. Abbreviations: TerS and TerL, small and large subunits of the terminase, respectively; Pro, protease; HK97-MCP, HK97-fold major capsid protein; TMP, tape measure protein; MCM, minichromosome maintenance helicase.

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**Figure 2.** Methanoculleus virus Blf4. A. Electron micrograph of the Blf4 virions bound to a presumed flagellum (white arrows). The sample was negatively stained with uranyl acetate. Scale bar, 100 nm. Reproduced from [4]. B. Genome map of Blf4. Abbreviations: MTase, methyltransferase; TerL, large subunit of the terminase; GNAT ATase, GNAT superfamily acetyltransferase; HK97-MCP, HK97-fold major capsid protein; TMP, tape measure protein.

Timeline

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**Figure 3.** Genome map of Methanobacterium virus C158 and its comparison with other *Methanobacterium* viruses. Homologous regions based on tblastx comparison are connected through shadings with colors corresponding to % identity (the key is provided on the right). Abbreviations: MTase, methyltransferase; TerS and TerL, small and large subunits of the terminase, respectively; Pro, protease; HK97-MCP, HK97-fold major capsid protein; TMP, tape measure protein; type IIL RM, type IIL restriction-modification enzyme.

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**Figure 4.** Classification of new *Caudoviricetes* viruses infecting methanogenic archaea. The Viral Proteomic Tree (ViPTree) of archaeal tailed viruses. The tree is constructed using BIONJ based on all-versus-all genomic similarity matrix, and mid-point rooted. Branch lengths are log-scaled. The branch length for family-level demarcation is around 0.05. The three new families described in the proposal are highlighted with colored backgrounds.

**References**

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