

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

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| **Code assigned:** | **2021.003A** |  |
| **Short title:** Rename genus *Gammalipothrixvirus* to *Captovirus* and move it to a new family *Ungulaviridae* (*Ligamenvirales*) | | |
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**Author(s) and email address(es)**

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**List the ICTV Study Group(s) that have seen this proposal**

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| Archaeal Viruses Subcommittee, Tokiviricetes Study Group |

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

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| All members of the Tokiviricetes SG have approved this proposal. |

**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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| 2021.003A.R.Ungulaviridae.xlsx |

**Abstract**

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| To resolve the polyphyly of the family *Lipothrixviridae*, I propose renaming genus *Gammalipothrixvirus* to *Captovirus* and moving it to a new family *Ungulaviridae*. Furthermore, species *Acidianus filamentous virus 1* is proposed to be renamed to *Captovirus AFV1*. |

**Text of proposal**

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| |  | | --- | | Family *Lipothrixviridae* includes enveloped filamentous dsDNA viruses infecting hyperthermophilic archaea of the order Sulfolobales and together with non-enveloped filamentous viruses of the family *Rudiviridae* forms the order *Ligamenvirales* [1]. *Lipothrixviridae* currently includes four genera: *Alphalipothrixvirus*, *Betalipothrixvirus,* *Gammalipothrixvirus* and *Deltalipothrixvirus* (<https://talk.ictvonline.org/taxonomy/>). The similarity between lipothrixvirids is unequivocal at the structural level [2-5], but is rather remote when sequences alone are compared. Consistently, Genome Relationship Applied to Virus Taxonomy (GRAViTy) analysis, which has been designed to recognize family level groups [6], has suggested that members of the genus *Gammalipothrixvirus* are not monophyletic with viruses from the other three genera and form a separate group (Figure 1) [7]. Furthermore, in phylogenomic analyses using VICTOR, gammalipothrixvirus AFV1 consistently forms a sister group to members of the family *Rudiviridae*, rendering the family *Lipothrixviridae* polyphyletic[2,8] (Figure 2). To rectify this discrepancy, I propose renaming genus *Gammalipothrixvirus* to *Captovirus* (from Latin *capto*, meaning “to grab”, referring to the characteristic claw-like structures decorating the termini of the AFV1 virion which grab onto pili of the host cells [Figure 3]) and moving it to a new family *Ungulaviridae* (from Latin *ungula* for *claw*, referring to the claw-like structures decorating the termini of the AFV1 virion) within the existing order *Ligamenvirales*. Finally, to conform to the binomial species nomenclature, species *Acidianus filamentous virus 1* is proposed to be renamed to *Captovirus AFV1.* | |

**Supporting evidence**

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**Figure 1.** Heat map and dendrogram showing the genome relationships of archaeal viruses and other related viruses using pairwise composite generalized Jaccard (CGJ) distances. Branches and labels were colour coded by their hosts - *Podoviridae*: blue; other bacterial: purple; archaeal: red; dual host (archaea and bacteria): yellow (*Sphaerolipoviridae*); eukaryotic: black. The order of taxa in the heat map followed the phylogeny of the dendrogram and was not therefore constrained by ICTV family assignments. Bootstrap support is shown above branches in the dendrogram (values of >70 % are shown). The figure is adapted from [7]. Blue arrowhead points to the family *Rudiviridae*, which splits the family *Lipothrixviridae* into two clades (green arrows).



**Figure 2.** Inferred phylogenomic tree of archaeal filamentous viruses of the class *Tokiviricetes*. The tree is based on whole-genome VICTOR analysis at the amino acid level [9]. The tree is rooted with tristromavirids, and the branch length is scaled in terms of the Genome BLAST Distance Phylogeny (GBDP) distance formula D6. The numbers above branches are GBDP pseudobootstrap support values from 100 replications. For each genome, the abbreviated virus name and RefSeq/GenBank accession number are indicated. The tree is divided into colored blocks according to the taxonomy of the compared viruses: *Lipothrixviridae*, green; *Rudiviridae*, grey; *Tristromaviridae*, blue.

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**Figure 3.** Electron micrographs of negatively stained virions of Acidianus filamentous virus 1. Scale bar, 100 nm.

**References**

1. Prangishvili D, Krupovic M. A new proposed taxon for double-stranded DNA viruses, the order "Ligamenvirales". Arch Virol. 2012; 157(4):791-5. doi: 10.1007/s00705-012-1229-7. PMID: 22270758
2. Wang F, Baquero DP, Beltran LC, Su Z, Osinski T, Zheng W, Prangishvili D, Krupovic M, Egelman EH. Structures of filamentous viruses infecting hyperthermophilic archaea explain DNA stabilization in extreme environments. Proc Natl Acad Sci U S A. 2020; 117(33):19643-19652. doi: 10.1073/pnas.2011125117. PMID: 32759221
3. Liu Y, Osinski T, Wang F, Krupovic M, Schouten S, Kasson P, Prangishvili D, Egelman EH. Structural conservation in a membrane-enveloped filamentous virus infecting a hyperthermophilic acidophile. Nat Commun. 2018; 9(1):3360. doi: 10.1038/s41467-018-05684-6. PMID: 30135568
4. Kasson P, DiMaio F, Yu X, Lucas-Staat S, Krupovic M, Schouten S, Prangishvili D, Egelman EH. Model for a novel membrane envelope in a filamentous hyperthermophilic virus. Elife. 2017; 6:e26268. doi: 10.7554/eLife.26268. PMID: 28639939
5. Baquero DP, Liu Y, Wang F, Egelman EH, Prangishvili D, Krupovic M. Structure and assembly of archaeal viruses. Adv Virus Res. 2020; 108:127-164. doi: 10.1016/bs.aivir.2020.09.004. PMID: 33837715
6. Aiewsakun P, Simmonds P. The genomic underpinnings of eukaryotic virus taxonomy: creating a sequence-based framework for family-level virus classification. Microbiome. 2018; 6(1):38. doi: 10.1186/s40168-018-0422-7. PMID: 29458427
7. Aiewsakun P, Adriaenssens EM, Lavigne R, Kropinski AM, Simmonds P. Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. J Gen Virol. 2018; 99(9):1331-1343. doi: 10.1099/jgv.0.001110. PMID: 30016225
8. Liu Y, Brandt D, Ishino S, Ishino Y, Koonin EV, Kalinowski J, Krupovic M, Prangishvili D. New archaeal viruses discovered by metagenomic analysis of viral communities in enrichment cultures. Environ Microbiol. 2019; 21(6):2002-2014. doi: 10.1111/1462-2920.14479. PMID: 30451355
9. Meier-Kolthoff JP, Göker M. VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics. 2017; 33(21):3396-3404. doi: 10.1093/bioinformatics/btx440. PMID: 29036289