

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

<https://ictv.global/taxonomy/templates>**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create a new subfamily *Alphabravovirinae* containing two new genera, *Siouxcentervirus* and *Merionvirus* and the existing genus *Mapvirus* (*Caudoviricetes*) |
| **Code assigned:**  | 2025.001B.Alphabravovirinae\_1nsf\_2ng\_2ns |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Andrew M. | Kropinski | Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com | x |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany  | liliana.cristina.moraru@uol.de  |  |
| Ipek  | Kurtböke | University of the Sunshine Coast - Faculty of Science, Health, Education and Engineering, Australia | ikurtbok@usc.edu.au |  |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **x** |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** <https://ictv.global/sc> |
| Actinophages Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  015/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:**  |
| *Brief description of current situation:* *Proposed changes:* *Justification:*  |

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| **Text of General Proposal:**  |
| *Background:* *Proposed* *changes:* *Justification:*  |

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| **References:** |
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

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

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **x** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| ***Alphabravovirinae*** | **Named after Actinobacteriophage Database Cluster AB** |
| ***Siouxcentervirus*** | **Named after the city where the first example of this type of virus was isolated** |
| ***Merionvirus*** | **Named after the region of the city where the first example of this type of virus was isolated** |
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| **Permission for use of names derived from a living person:**  |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached**  |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*:Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class Caudoviricetes *Description of current taxonomy*: The genus *Mapvirus* was originally established under the name Ff47virus in 2015 (proposal [2015.004a-dB.A.v2.Ff47virus](https://ictv.global/ictv/proposals/2015.004a-dB.A.v2.Ff47virus.pdf)) and renamed in 2018 (proposal 2018.007B.A.v4.rename137gen6sp). The genus is currently comprised of two species. The other viruses described in these proposal are unclassified lytic siphoviruses which are related to phages of the genus *Mapvirus**Proposed* *taxonomic change(s):* Create two new genera (*Siouxcentervirus, Merionvirus*) and assign these genera and *Mapvirus* to a new subfamily, *Alphabravovirinae*.*Justification*: This proposal is in accord with our definition of a subfamily |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*:Realm Duplodnaviria, kingdom Heunggongvirae, phylum Uroviricota, class Caudoviricetes *Description of current taxonomy*: The genus *Mapvirus* was originally established under the name Ff47virus in 2015 (proposal [2015.004a-dB.A.v2.Ff47virus](https://ictv.global/ictv/proposals/2015.004a-dB.A.v2.Ff47virus.pdf)) and renamed in 2018 (proposal 2018.007B.A.v4.rename137gen6sp). The genus is currently comprised of two species. The other viruses described in these proposal are unclassified lytic siphoviruses which are related to phages of the genus *Mapvirus**Proposed* *taxonomic change(s):* Create two new genera (*Siouxcentervirus, Merionvirus*) and assign these genera and *Mapvirus* to a new subfamily, *Alphabravovirinae*.*Demarcation criteria:* The Bacterial and Archaeal Virus Subcommittee established 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species [8]. Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny [8].*Justification*: This proposal is in accord with our definition of a subfamily  |

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| **References:**  |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 330958702. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.3. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. https://www.genome.jp/viptree/ 5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423 6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.7. Davis P, Seto D, Mahadevan P. CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses. 2022 Nov 16;14(11):2534. doi: 10.3390/v14112534. PMID: 36423143; PMCID: PMC9693508.8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, Gascuel O. NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Res. 2019 Jul 2;47(W1):W260-W265. doi: 10.1093/nar/gkz303. PMID: 31028399; PMCID: PMC6602494.9. Letunic I, Bork P. Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. Bioinformatics. 2007 Jan 1;23(1):127-8. doi: 10.1093/bioinformatics/btl529. Epub 2006 Oct 18. PMID: 17050570.10. Zhou T, Xu K, Zhao F, Liu W, Li L, Hua Z, Zhou X. itol.toolkit accelerates working with iTOL (Interactive Tree of Life) by an automated generation of annotation files. Bioinformatics. 2023 Jun 1;39(6):btad339. doi: 10.1093/bioinformatics/btad339. PMID: 37225402; PMCID: PMC10243930.  |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| **Alphabravovirinae** | **Data for this proposal** |
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| **Tables, Figures:**  |

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Table 1A. Characteristics of new species in the genus *Siouxcentervirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Mycobacterium phage JacoRen57 | *Mycobacterium smegmatis* mc2 155 | Siphovirus | Lytic | MK279840.1 | 52411 bp | 73 | o |

Table 1B. Characteristics of new species in the genus *Merionvirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Mycobacterium phage NoShow | *Mycobacterium smegmatis* mc#155 | Siphovirus | Lytic | ON108645.1 | 52825 bp | 80 | 0 |

**Figure 1.** VIRIDIC heat map of a group of phages with the one under discussion. VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. The names in the first column which are highlighted in **green** correspond to currently recognized species.





**Figure 2.** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phages belonging to the subfamily are indicated with **red bar**.

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**Figure 3.** Electron micrograph: Electron micrographs of negatively stained *Mycobacterium* phage NoShow (<https://phagesdb.org/phages/NoShow/>). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

**CoreGenes 3.5 Analysis [6]**: revealed that the phages listed in Table 1 share 35 protein homologs, including DNA helicase, thymidylate kinase dUTPase, thymidylate synthase, DNA polymerase, DNA helicase, 3 minor tail proteins, tape measure protein, major tail protein, tail terminator, head-to-tail stopper, major capsid protein, head-to-tail adaptor,

scaffolding protein, portal protein, terminase large subunit, terminase small subunit. This indicates that approximately 50.7% of the phage-encoded proteins are conserved.