

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new subfamily, *Frobishervirinae* with one existing genus, *Samwavirus*, and one new genus, *Branvirus* (Class: *Caudoviricetes*) |
| **Code assigned:** | 2025.020B.Ac.v3.Frobishervirinae\_1nsf\_1ng\_1ns | |

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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 |  |

**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> |
| Caudoviricetes 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:** | 15/06/2025 |

**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 | **x** |
| 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| W - Withdrawn |  |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:** |
| Please improve the quality of the abstract, there is a lack of phylogenetic tree (not necessary but would improve the proposal). |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| Phylogenetic tree not possible so Clinker alignment added. |

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| **Revision date:** | August 19, 2025 |

**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 | **x** | 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** |
| *Frobishervirinae* | Named in honour of Martin Frobisher, Jr for his work on Corynebacterium phages and education |
| *Branvirus* | The taxon name is derived from the name of bacteriophage, Corynebacterium phage Bran |
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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*:  Subfamily, genus, species  *Description of current taxonomy*:  The genus *Samwavirus* was created via Taxonomy Proposal 2019.027B and contains five species. *Corynebacterium* phage Bran is currently unclassified.  *Proposed* *taxonomic change(s):*  Create a new subfamily “*Frobishervirinae”* containing one new genus “*Branvirus*” with a single species. Move the existing genus *Samwavirus* into the subfamily “*Frobishervirinae”*  *Justification*: VIRIDIC and Clinker analyses reveal that there is sufficient evidence to create a subfamily for Branvirus and *Samwavirus* [8] |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  The genus *Samwavirus* was created via Taxonomy Proposal 2019.027B and contains five species. Corynebacterium phage Bran is currently unclassified.  *Proposed* *taxonomic change(s):*  Create a new subfamily “*Frobishervirinae”* containing one new genus “*Branvirus*” with a single species. Move the existing genus *Samwavirus* into the subfamily “*Frobishervirinae”*  *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*:  VIRIDIC and Clinker analyses reveal that there is sufficient evidence to create a subfamily for Branvirus and *Samwavirus* [8] |

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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: 33095870  2. 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  11. van den Belt M, Gilchrist C, Booth TJ, Chooi YH, Medema MH, Alanjary M. CAGECAT: The CompArative GEne Cluster Analysis Toolbox for rapid search and visualisation of homologous gene clusters. BMC Bioinformatics. 2023 May 3;24(1):181. |

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

<Start here>**Table 1.** Properties of phage Bran

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Corynebacterium phage Bran | *Corynebacterium xerosis* ATCC 373 | Siphovirus | Temperate | MK977714.1 | 44484 bp | 69 | 1 |
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Corynebacterium phage Bran was isolated from Birmingham (AL, USA) soil by Kelly Kim in 2018, as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. This temperate siphovirus was assigned to Cluster EP by the Actinobacteriophage Database. Its genome possesses 17 nt 3'-cohesive termini (CCCCAGCGCCTCGGGTA).

Close-up of a microscope image of bacteria

AI-generated content may be incorrect.

**Figure 1.** Electron micrograph: Electron micrographs of negatively stained Corynebacterium phage Bran (<https://phagesdb.org/phages/Bran/>). 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.

A screenshot of a computer

AI-generated content may be incorrect.

**Figure 2.** VIRIDIC heatmap of this group of phages. 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. Abbreviations: phg = phage Cory = *Corynebacterium;* Past = *Pasteurella*.

A diagram of a graph

AI-generated content may be incorrect.

**Figure 3.** Clinker alignment of the genomes of *Corynebacterium* phages Bran (Top) and Dina (Bottom) [11] reveals that these mosaic genomes possess highly conserved 5’ termini (morphogenesis genes and highly variable 3’ ends.

**CoreGenes 5 Analysis [7]**: revealed that the phages defined by *Branvirus* and *Samwavirus* share 29 protein homologs, which include large subunit terminase, portal protein, head maturation protease, major capsid protein, head-tail connector protein, head-to-tail adaptor, head-to-tail stopper, head closure, major tail protein, two tail assembly chaperones, tail tape measure protein, and holin. This indicates that approximately 48% of the phage-encoded proteins are conserved.

This taxon is named in honour of Martin Frobisher, Jr. D.Sc. who received his SB degree from Johns Hopkins University in Hygiene in 1922 and then went on to get a D.Sc. in bacteriology. In his career her was Chief, Bacteriology Laboratories, The Communicable Disease Center, United States Public Health Service; Associate Professor of Bacteriology, Emory University; Lecturer in Bacteriology, Johns Hopkins University. He is noted for his work on *Corynebacterium diphtheriae* and its phages and being the author of *Fundamentals of Bacteriology* and *Fundamentals of Microbiology*. From 1937-1948 he was the Editor-in-chief of the American Journal of Hygiene.