

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one new genus (*Fenglinvirus*) with one species (Class *Caudoviricetes*). |
| **Code assigned:** | 2025.019B.Ac.v3.Fenglinvirus\_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:** | 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 | **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| W - Withdrawn |  |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. ViPTree annotation - arrow does not point at anything!  Is there two BalMu-1 prophages, copy 1 and copy 2 in the genome? Can the authors indicate which one is the exemplar and update the Excel module with the "Exemplar virus name" to indicate the correct phage. |

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

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| **Response of proposer:** |
| Corrected |

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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 |  | 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** |
| Fenglinvirus | Named after the address of Key Laboratory of Synthetic Biology,  Institute of Plant Physiology and Ecology, Shanghai Institutes for  Biological Sciences, Chinese Academy of Sciences, 300 Fenglin Road, Shanghai, Shanghai 200032, China |
| Fenglinvirus BalMu1 | Derived from the name of Bacillus phage BalMu-1 |
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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*:  Genus, species  *Description of current taxonomy*:  The bacterial viruses described in this proposal are currently unclassified  *Proposed* *taxonomic change(s):*  Create one new genus “*Fenglinvirus”* and one new species  *Justification*:  *Bacillus alcalophilus* CGMCC 1.3604 possesses two Mu-like transposable prophages now identified in GenBank as Bacillus phage BalMu-1 copy 1 (KP063902; 39873 bp; and NC\_030945.1; Exemplar) and Bacillus phage BalMu-1 copy 2 (KP063903; 39861 bp). We have chosen the first mentioned as the exemplar. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus, species  *Description of current taxonomy*:  The bacterial viruses described in this proposal are currently unclassified  *Proposed* *taxonomic change(s):*  Create one new genus “*Fenglinvirus”* and one new species  *Demarcation criteria:*  The Bacterial and Archaeal Virus Subcommittee established 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species [3].  *Justification*:  *Bacillus alcalophilus* CGMCC 1.3604 possesses two Mu-like transposable prophages now identified in GenBank as Bacillus phage BalMu-1 copy 1 (KP063902; 39873 bp; and NC\_030945.1; Exemplar) and Bacillus phage BalMu-1 copy 2 (KP063903; 39861 bp). Phage BalMu-1 copy 1 conforms to the criteria laid out above allowing us to create a new genus with a single species. |

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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. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| **2025.019B.Fenglinvirus\_1ng\_1ns** | **Excel spreadsheet for this proposal** |
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| **Tables, Figures:** |

<Start here>

*Bacillus alcalophilus* CGMCC 1.3604 possesses two Mu-like transposable prophages now identified in GenBank as Bacillus phage BalMu-1 copy 1 (KP063902; 39873 bp; and NC\_030945.1; Exemplar) and Bacillus phage BalMu-1 copy 2 (KP063903; 39861 bp).

Table 1. Characteristics of the prophage described in the proposal

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| **Prophage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Bacillus* phage BalMu-1 | *Bacillus alcalophilus* | Myovirus | Temperate | KP063902.1 | 39873 bp | 56 | 0 |

A screen shot of a chart

AI-generated content may be incorrect.Figure 1. VIRIDIC heat map of a group of phages with the one under discussion indicated with a red arrowhead. 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; Baci = *Bacillus*; Sino = *Sinorhizobium*; Rhiz = *Rhizobium*; Sten = *Stenotrophomonas*; Rhod = *Rhodobacter*; Rhodv = *Rhodovulum*; Micr = *Microcystis*; Lept = *Leptolyngbya*

A close-up of a letter

AI-generated content may be incorrect.  
A screenshot of a computer

AI-generated content may be incorrect.

Figure 2. ViPTree analysis: ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The taxon under discussion is indicated with a red arrowhead. Abbreviations: phg = phage; Baci = *Bacillus*; Sino = *Sinorhizobium*; Rhiz = *Rhizobium*; Sten = *Stenotrophomonas*; Rhod = *Rhodobacter*; Rhodv = *Rhodovulum*; Micr = *Microcystis*; Lept = *Leptolyngbya*