

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 (*Jianjiangvirinae*) with two genera and 22 species (Class *Caudoviricetes*) |
| **Code assigned:** | 2025.027B.Ac.v3.Jianjiangvirinae\_1nsf\_2ng\_22ns | |

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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 |  |
| Juntao | Shen | Center for Synthetic Microbiome,  Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences, China | jt.shen1@siat.ac.cn |  |

**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:** |
| We have included additional text in the abstract |

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| **Revision date:** | 01/09/2025 |

**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** |
| *Jianjiangvirinae* | All of these *Bacteroides* phages were identified in the Shenzhen Institute of Synthetic Biology, Guangdong, China. We have chosen to name these taxa after the main rivers of that province |
| *Luojiangvirus* | Named after a tributary of Jian(jiang) River – the Luojiang River |
| *Caojiangvirus* | Named after a tributary of the Jian(jiang) River – Caojiang (River) |
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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*:  There is no taxonomy for these lytic phages isolated against *Bacteroides caccae* and *Bacteroides ovatus* from sewage  *Proposed* *taxonomic change(s):*  Add two new genera (*Luojiangvirus* and *Caojiangvirus*) and 22 new species to a new subfamily  *Justification*:  In accord with the established demarcation criteria for delineating a new subfamily, genus and species [3] these *Bacteroides* phages, isolated in China, fall into two new genera (*Luojiangvirus* and *Caojiangvirus*) in a new subfamily which we have chosen to call *Pearlrivervirinae*. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Subfamily, genus, species  *Description of current taxonomy*:  There is no current taxonomy for these lyti*c* phages isolated against *Bacteroides caccae* and *Bacteroides ovatus* from sewage  *Proposed* *taxonomic change(s)*:  Add two new genera (*Luojiangvirus* and *Caojiangvirus*) and 22 new species to a new subfamily  *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*: In accord with our definition of what constitutes a new subfamily, genus and species [3] these *Bacteroides* phages, isolated in China, fall into two new genera (*Luojiangvirus* and *Caojiangvirus*) in a new subfamily which we have chosen to call *Jianjiangvirinae*. |

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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** |
| Jianjiangvirinae\_1nsf\_2ng\_22ns.xlsx | Data for this proposal |
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| **Tables, Figures:** |

<Start here>**Table 1.** Table of members of the subfamily *Jianjiangvirinae*

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| **Accession No.** | **Phage name** | **Taxon** |
| *OP172651.1* | *Bacteroides phage BC679P5* | *Luojiangvirus BC679P5* |
| *OP172644.1* | *Bacteroides phage BC669P1* | *Luojiangvirus BC669P1* |
| *OP172645.1* | *Bacteroides phage BC669P2* | *Luojiangvirus BC669P2* |
| *OP172647.1* | *Bacteroides phage BC679P1* | *Luojiangvirus BC679P1* |
| *OP172648.1* | *Bacteroides phage BC679P2* | *Luojiangvirus BC679P2* |
| *OP172646.1* | *Bacteroides phage BC669P3* | *Luojiangvirus BC669P3* |
| *OP172649.1* | *Bacteroides phage BC679P3* | *Luojiangvirus BC679P3* |
| *OP172699.1* | *Bacteroides phage BO668P2* | *Caojiangvirus BO668P2* |
| *OP172684.1* | *Bacteroides phage BK687P4* | *Caojiangvirus BK687P4* |
| *OP172682.1* | *Bacteroides phage BK687P2* | *Caojiangvirus BK687P2* |
| *OP172683.1* | *Bacteroides phage BK687P3* | *Caojiangvirus BK687P3* |
| *OP172691.1* | *Bacteroides phage BK745P1* | *Caojiangvirus BK745P1* |
| *OP172693.1* | *Bacteroides phage BK745P4* | *Caojiangvirus BK745P4* |
| *OP172643.1* | *Bacteroides phage BC422P2* | *Caojiangvirus BC422P2* |
| *OP172681.1* | *Bacteroides phage BK687P1* | *Caojiangvirus BK687P1* |
| *OP172685.1* | *Bacteroides phage BK687P5* | *Caojiangvirus BK687P5* |
| *OP172692.1* | *Bacteroides phage BK745P3* | *Caojiangvirus BK745P3* |
| *OP172688.1* | *Bacteroides phage BK735P2* | *Caojiangvirus BK735P2* |
| *OP172689.1* | *Bacteroides phage BK735P3* | *Caojiangvirus BK735P3* |
| *OP172698.1* | *Bacteroides phage BO668P1* | *Caojiangvirus BO668P1* |
| *OP172687.1* | *Bacteroides phage BK735P1* | *Caojiangvirus BK735P1* |
| *OP172690.1* | *Bacteroides phage BK735P4* | *Caojiangvirus BK735P4* |

A screenshot of a computer screen

AI-generated content may be incorrect.

**Figure 1.** Partial 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: Bact = *Bacteroides*; phg = phage. The complete VIRIDIC heatmap accompanies this proposal as Jianjiangvirinae\_VIRIDIC heatmap.xlsx.

A close-up of a document

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) Phage Proteomic Tree [5]. The taxon under discussion is indicated with a **red bar**. Abbreviations: phg = phage; Bact = *Bacteroides*

**CoreGenes 5 Analysis [7]**: revealed that the phages listed in Table 1 share 29 protein homologs, all listed as hypothetical proteins except for the terminase, large subunit. This indicates that approximately 62% of the phage-encoded proteins are conserved.