

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 genus (*Lingdingyangvirus*) with 22 species (Caudoviricetes) |
| **Code assigned:** | 2025.037B.Lingdingyangvirus\_1ng\_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** |
| xAnimal 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:** |
| 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:** | 15/05/2025 |

**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| W - Withdrawn |  |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** |
| *Lingdingyangvirus* | Most of these *Bacteroides* phages were identified in the Shenzhen Institute of Synthetic Biology, Guangdong, China. We have chosen to name these taxa after one of the critical estuary of that province. Lingdingyang Bay is the critical estuary in the Pearl River Delta, flanked by Hong Kong, Macau, and Guangdong. Its name derives from the literary phrase "零丁洋" (Lingding Ocean) in the patriotic poem by Wen Tianxiang, symbolizing historical and cultural significance beyond mere geography. |
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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 and species  *Description of current taxonomy*: there is no taxonomy for these lytic phages isolated against *Bacteroides thetaiotaomicron* from sewage  *Proposed* *taxonomic change(s):* Add new genus and 22 new species  *Justification*: In keeping with the criteria that we have established for creation of a genus [8] these 22 phages are significantly different from one another to be considered separate species; and, significantly similar to each other to be considered part of the same genus (*Lingdingyangvirus*) |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: genus and species  *Description of current taxonomy*: there is no current taxonomy for these lyti*c* phages isolated against *Bacteroides thetaiotaomicron* from sewage  *Proposed* *taxonomic change(s)*: Add new genus and 22 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 [8]  *Justification*: These viruses conform to the criteria that we have established [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. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| Karilavirus\_VIRIDIC\_heatmap.pdf | **VIRIDIC intergenomic similarity data** |
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| **Tables, Figures:** |

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**Table 1.** Table of members of the genus *Lingdingyangvirus*

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| **Accession No.** | **Phage name** | **Taxon** |
| OP172709.1 | Bacteroides phage BT61P1 | *Lingdingyangvirus BT61P1* |
| MT074143.1 | Bacteroides phage HNL05 | *Lingdingyangvirus HNL05* |
| OP172708.1 | Bacteroides phage BT47P1 | *Lingdingyangvirus BT47P1* |
| OP172723.1 | Bacteroides phage BT638P5 | *Lingdingyangvirus BT638P5* |
| MT074158.1 | Bacteroides phage SJC22 | *Lingdingyangvirus SJC22* |
| MT074151.1 | Bacteroides phage SJC13 | *Lingdingyangvirus SJC13* |
| MT074150.1 | Bacteroides phage SJC12 | *Lingdingyangvirus SJC12* |
| MT074134.1 | Bacteroides phage ARB14 | *Lingdingyangvirus ARB14* |
| MT074148.1 | Bacteroides phage SJC10 | *Lingdingyangvirus SJC10* |
| MT074160.1 | Bacteroides phage SJC25 | *Lingdingyangvirus SJC25* |
| OP172713.1 | Bacteroides phage BT401P3 | *Lingdingyangvirus BT401P3* |
| OP172730.1 | Bacteroides phage BT709P1 | *Lingdingyangvirus BT709P1* |
| OP172725.1 | Bacteroides phage BT638P7 | *Lingdingyangvirus BT638P7* |
| OP172719.1 | Bacteroides phage BT638P1 | *Lingdingyangvirus BT638P1* |
| OP172720.1 | Bacteroides phage BT638P2 | *Lingdingyangvirus BT638P2* |
| OP172726.1 | Bacteroides phage BT638P8 | *Lingdingyangvirus BT638P8* |
| OP172724.1 | Bacteroides phage BT638P6 | *Lingdingyangvirus BT638P6* |
| OP172721.1 | Bacteroides phage BT638P3 | *Lingdingyangvirus BT638P3* |
| OP172727.1 | Bacteroides phage BT681P2 | *Lingdingyangvirus BT681P2* |
| OP172729.1 | Bacteroides phage BT681P4 | *Lingdingyangvirus BT681P4* |
| OP172714.1 | Bacteroides phage BT498P1 | *Lingdingyangvirus BT498P1* |
| OP172718.1 | Bacteroides phage BT566P2 | *Lingdingyangvirus BT566P2* |

A screenshot of a computer screen

AI-generated content may be incorrect.

**Figure 1.** Partial VIRIDIC heat map 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 Lingdingyangvirus \_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) famous Phage Proteomic Tree [5]. The taxon under discussion is indicated with a **red bar**. Abbreviations: phg = phage; Bact = *Bacteroides*