

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 *Dravavirinae* with three new genera (*Hualiencityvirus*, *Rodicavirus* and *Tongtianvirus*) and five species (Class: *Caudoviricetes*) |
| **Code assigned:** | 2025.014B.Ac.v3.Dravavirinae\_1nsf\_3ng\_5ns | |

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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 |
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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> |
| 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| W - Withdrawn |  |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:** |
| Corrected |

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| **Revision date:** |  |

**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** |
| *Dravavirinae* | Named after the Drava River flowing through the city of Maribor in Slovenia where many of these phages were isolated |
| *Hualiencityvirus* | Named after the city in Tiawan where the first virus of its type was isolated |
| *Rodicavirus* | Named in honour of Rodica in the community of Domžale, Slovenia |
| *Tongtianvirus* | Named after the city in China where the first virus of its type 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*:  Subfamily, genus, species  *Description of current taxonomy*:  The lytic siphophages isolated against *Bacteroides, Parabacteroides, Elizabethkingia* and *Alistipes* (Order *Bacteroidales*) described in this proposal are currently unclassified.  *Proposed* *taxonomic change(s):*  Create three new genera, “*Hualiencityvirus*”, “*Tongtianvirus*” and “*Rodicavirus*” consisting of five new species and assign them to a new subfamily, “*Dravavirinae”*  *Justification*:  These five viruses are lytic, possess a siphophage morphology and have ca. 44.5 kb genomes. On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in keeping with our definitions for what constitute a subfamily, we propose to create “*Dravavirinae*” with three genera “*Hualiencityvirus*”, “*Tongtianvirus*” and “*Rodicavirus*” |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Subfamily, genus, species  *Description of current taxonomy*:  The lytic siphophages isolated against *Bacteroides, Parabacteroides, Elizabethkingia* and *Alistipes* (Order *Bacteroidales*) described in this proposal are currently unclassified.  *Proposed* *taxonomic change(s):*  Create three new genera, “*Hualiencityvirus*”, “*Tongtianvirus*” and “*Rodicavirus*” consisting of five new species and assign them to a new subfamily, “*Dravavirinae”*  *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*: These five viruses are lytic, possess a siphophage morphology and have ca. 44.5 kb genomes. On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in keeping with our definitions for what constitute a subfamily, we propose to create “*Dravavirinae*” with three genera “*Hualiencityvirus*”, “*Tongtianvirus*” and “*Rodicavirus*” |

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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. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797; PMCID: PMC2447785. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| **Dravavirinae\_1nsf\_3ng\_5ns** | **Data file for this proposal** |
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| **Tables, Figures:** |

<Start here>**Table 1.** Phages which belong to this subfamily

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| **Accession No.** | **Phage name** | **Species** | **Host taxon** |
| OK632025.1 | Elizabethkingia phage TCUEAP2 | *Hualiencityvirus TCUEAP2* | *Elizabethkingia anophelis* |
|  |  |  |  |
| OP172640.1 | Alistipes phage AS73P1 | *Tongtianvirus AS73P1* | *Alistipes shahii* |
|  |  |  |  |
| OP172815.1 | Parabacteroides phage PD491P1 | *Rodicavirus PD491P1* | *Parabacteroides distasonis* |
| MN929097.1 | Parabacteroides phage PDS1 | *Rodicavirus PDS1* | *Parabacteroides distasonis* |
| OR296437.1 | Bacteroides phage C1\_85S2P | *Rodicavirus C185S2P* | *Bacteroides uniformis* |

**Specific references:**

Pekkle Lam HY, Peng SY, Paramita P, Wu WJ, Chen LK, Chao HJ, Lai MJ, Chang KC. Biological and genomic characterization of two newly isolated *Elizabethkingia anophelis* bacteriophages. J Microbiol Immunol Infect. 2022 Aug;55(4):634-642. doi: 10.1016/j.jmii.2022.05.004. Epub 2022 Jun 6. PMID: 35717525. [Elizabethkingia phage TCUEAP2]

Hedžet S, Rupnik M, Accetto T. Broad host range may be a key to long-term persistence of bacteriophages infecting intestinal Bacteroidaceae species. Sci Rep. 2022 Dec 6;12(1):21098. doi: 10.1038/s41598-022-25636-x. PMID: 36473906; PMCID: PMC9727126. [Bacteroides phage C1\_85S2P]

A screen shot of a computer

AI-generated content may be incorrect.

**Figure 1.** 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 Bact = *Bacteroides;* Para = *Parabacteroides*; Eliz = *Elizabethkingia*; Alis = *Alistipes*.

**A screenshot of a computer

AI-generated content may be incorrect.**

**Figure 2.** Phylogenetic tree constructed with the major capsid proteins from these and related phages using “One Click” phylogeny.fr at <http://phylogeny.lirmm.fr/phylo_cgi/simple_phylogeny.cgi> [11]

**CoreGenes 5 Analysis [7]**: revealed that the phages listed in Table 1 share 36 protein homologs, which included the large subunit terminase, tail tape-measure protein, major capsid protein, portal protein, tail fibre protein, Holliday junction resolvase, exonuclease, RNA polymerase sigma factor, HNH endonuclease, NinB protein, DNA polymerase and nucleoside triphosphate pyrophosphohydrolase. This indicates that approximately 62% of the phage-encoded proteins are conserved.