

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Add species to existing genera in the family *Chaseviridae* and create one new genus, *Qiaoyingvirus* (Class: *Caudoviricetes*) |
| **Code assigned:**  | 2025.011B.Ac.v3.Chaseviridae\_1ng\_12ns |

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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 |  |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany  | liliana.cristina.moraru@uol.de  |  |
| Hany | Anany | Guelph Research and Development Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada | hany.anany@agr.gc.cahanany@alumni.uoguelph.ca  | X |

**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:** <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:** |  15/05/2025 |

**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 | **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:** | 25/08/2025 |

**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** |
| *Qiaoyingvirus* | Named after the address (313 Qiaoying Street) of the Fisheries College, Jimei University, China where Aeromonas phage phiA050 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*:Genus, species*Description of current taxonomy*: The family *Chaseviridae* was created through Taxonomy Proposal 2019.047B. The family currently consists of two subfamilies (*Cleopatravirinae* and *Nefertitivirinae*) and 13 genera.*Proposed* *taxonomic change(s):* Add new species to the genera *Fifivirus, Loessnervirus, Carltongylesvirus Longwangvirus* and *Shantouvirus*; and create a new genus “*Qiaoyingvirus”* *Justification*: Species included in the family *Chaseviridae* are myoviruses which infect members of the genera *Escherichia, Erwinia, Pectobacterium, Shewanella* and *Aeromonas*. Common proteins include a RNA polymerase, DNA polymerase, primase and exonuclease. This proposal adds new species to several existing genera and creates one new genus. These genomes satisfy the existing demarcation criteria for the creation of new species and genera. |

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| * **Text of Taxonomy proposal:**
 |
| *Taxonomic rank(s) affected*:Genus, species*Description of current taxonomy*: The family *Chaseviridae* was created through Taxonomy Proposal 2019.047B. The family currently consists of two subfamilies (*Cleopatravirinae* and *Nefertitivirinae*) and 13 genera.*Proposed* *taxonomic change(s):* Add new species to the genera *Fifivirus, Loessnervirus, Carltongylesvirus Longwangvirus* and *Shantouvirus*; and create a new genus “*Qiaoyingvirus”* *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*: Species included in the family *Chaseviridae* are myoviruses which infect members of the genera *Escherichia, Erwinia, Pectobacterium, Shewanella* and *Aeromonas*. Common proteins include a RNA polymerase, DNA polymerase, primase and exonuclease. This proposal adds new species to several existing genera and creates one new genus. These genomes satisfy the existing demarcation criteria for the creation of new species and genera [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: 330958702. 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** |
| Chaseviridae\_VIRIDIC\_heatmap.xlsx | Data for this proposal |
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| **Tables, Figures:**  |

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Table 1A. Addition of three new phages to the genus *Fifivirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Erwinia phage EaPF7 | *Erwinia amylovora 4/82* | Myovirus | Lytic | PQ431420.1 | 54,114 bp | 85 | 1(\*) |
| Erwinia phage Aioli | *Erwinia amylovora* | Myovirus | Lytic | OQ818694.1 | 53,903 bp | 77 | 1(\*) |
| Erwinia phage pEa\_SNUABM\_27 | *Erwinia amylovora* | Myovirus | Lytic | MW349138.1 | 53,014 bp | 77 | 1 |

(\*) discovered using tRNAscan-SE2 (<https://lowelab.ucsc.edu/tRNAscan-SE/>)

Table 1B. Addition of two new phages to the genus *Loessnervirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Erwinia phage Papaline | *Erwinia amylovora* | Myovirus | Lytic | OQ818704.1 | 54,761 bp | 83 | 0 |
| Erwinia phage Fougasse | *Erwinia amylovora* | Myovirrus | Lytic | OQ818698.1 | 54,213 bp | 79 | 0 |

Table 1C. Addition of four new phages to the genus *Carltongylesvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Escherichia phage Ecp\_YSF | *Escherichia coli* | Myovirus | Lytic | OR327751.1 | 53,268 bp | 102(\*\*) | 1 |
| Staphylococcus phage Pel53 (\*) | *Staphylococcus hyicus* | Myovirus | Lytic | PP952070.1 | 53,660 bp | 78 | 1 |
| Escherichia phage FXie-2024a | *Escherichia coli* | Myovirus | Lytic | PP107930.1 | 53,383 bp | 83 | 0 |
| Escherichia phage vB\_EcoM\_JL1 | *Escherichia coli* | Myovirus | Lytic | OR791690.1 | 55,571 bp | 76 | 0 |
| Escherichia phage EcoM1 | *Escherichia coli* | Myovirus | Lytic | PQ818760.1 | 52,452 bp | 75 | 0 |

(\*) Not included because the host is incorrect; (\*\*) potential overannotation

Table 1D. Addition of one new phage to the genus *Longwangvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Aeromonas phage vB\_AhydM-H1 | *Aeromonas hydrophila* A331 | Myovirus | Lytic | OR795024.1 | 52614 bp | 72 | 1 |

Table 1E. Addition of one new phage to the genus *Shantouvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Aeromonas phage LA93P1 | *Aeromonas dhakensis* A24.1T | Myovirus | Lytic | PV258714.1 | 52196 bp | 68 | 0 |

Table 1F. Characteristics of a phage belonging to the proposed new genus “*Qiaoyingvirus”*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Aeromonas phage phiA050 | *Aeromonas hydrophila* A050 | Myovirus | Lytic | PP763568.1 | 53322 bp | 20(\*) | 0 |

**(\*) significantly underannotated**

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**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. In the third column if the genus is highlighted in gold it indicates that this is a new species. Abbreviations: Prot = *Proteus*; Erwi = *Erwinia*; Pant = *Pantoea*; phg = phage. A full heatmap of intergenomic similarity for all genera and species within the family *Chaseviridae* is available as supplementary material.