

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 (*Illiduovirus*) with three species in the Class *Caudoviricetes* |
| **Code assigned:**  | 2025.023B.Ac.v3.Illiduoavirus\_1ng\_3ns |

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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, The Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com |  |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany  | liliana.cristina.moraru@uol.de  |  |
| Andrew | Millard | Department of Genetics and Genome Biology,University of Leicester, UK | adm39@leicester.ac.uk | 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:** |  15/06/2025 |

**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| W - Withdrawn |  |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. |

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

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| **Response of proposer:**  |
| The abstract has been amended |

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| **Revision date:** | 29/08/2025 |

**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** |
| ***Illiduovirus***  | **Name derived from that of the first sequenced *Pseudomonas putida* jumbo phage**  |
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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):* To create a new genus, Illiduovirus, with three species of *Pseudomonas* phages*Justification*: The bacterial viruses described in this proposal are lytic myoviruses with genomes of approximately 200 kb. Analysis with ViPTree and VIRIDIC indicate that these viruses form a distinct genus that includes three new species based on the current ICTV demarcation criteria for these ranks. |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Genus, species  *Description of current taxonomy*:The bacterial viruses described in this proposal are currently unclassified*Proposed* *taxonomic change(s):* To create a new genus, Illiduovirus, with three species of jumbo *Pseudomonas* phages*Demarcation criteria:* Species demarcation criteria: Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates. These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].Genus demarcation criteria: An intergenomic similarity cut-off of 70%, a combination of average nucleotide identity and alignment fraction is used to determine genera demarcation. Members of the same genus have >70% intergenomic similarity and cluster tightly in marker gene phylogenies.*Justification*: The bacterial viruses described in this proposal are lytic myoviruses with genomes of approximately 200 kb. Analysis with ViPTree and VIRIDIC indicate that these viruses form a distinct genus that includes three new species based on the current ICTV demarcation criteria for these ranks [3].  |

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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. 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/ 3. 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: PMC8003253.4. 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: 121424236. 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: PMC6602494.7. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Res. 2021 Jul 2;49(W1):W293-W296. doi: 10.1093/nar/gkab301. PMID: 33885785; PMCID: PMC8265157.  |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
|  |  |
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| **Tables, Figures:**  |

**Table 1.** Characteristics of the phages described in the proposal

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Pseudomonas phage vB\_PpuM-Peetri | *Pseudomonas putida* PaW85 | Myovirus | Lytic | PP496444.1 | 200264 bp | 233 | 0 |
| Pseudomonas phage vB\_PpuM-Voja-6 | *Pseudomonas putida* PaW85 | Myovirus | Lytic | PP496442.1 | 200784 bp | 239 | 0 |
| Pseudomonas phage vB\_PpuM-Lauda | *Pseudomonas putida* PaW85 | Myovirus | Lytic | PP496443.1 | 201030 bp | 238 | 0 |

**Figure 1.** VIRIDIC heat map (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) heatmap for this group of phages. It computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: Pseu = *Pseudomonas*; phg = phage.

**Figure 2:** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phages of interest are indicated with **red arrowhead**.