

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Add 12 new species to the genus *Yuavirus*, Class *Caudoviricetes* |
| **Code assigned:**  | 2025.081B.Yuavirus\_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, The Ontario Veterinary College, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com | X |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany  | liliana.cristina.moraru@uol.de  |  |

**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:** |  15/06/2025 |

**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 |  |
| 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| W - Withdrawn |  |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** |
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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*: Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*: The genus *Yuavirus* currently consists of five species. Previous proposals related to this genus are 2012.008a-dB.A.v3.Yualikevirus and 2015.006aB.A.v2.Phage\_Genera\_ren.*Proposed* *taxonomic change(s):* To create 14 new species in the genus *Yuavirus**Justification*: The species are classified within the genus in accordance with the demarcation criteria for new genera and species [3]. |

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| * **Text of Taxonomy proposal:**
 |
| *Taxonomic rank(s) affected*: Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*: The genus *Yuavirus* currently consists of five species. Previous proposals related to this genus are 2012.008a-dB.A.v3.Yualikevirus and 2015.006aB.A.v2.Phage\_Genera\_ren.*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].*Justification*: The species are classified within the genus in accordance with the demarcation criteria for new genera and species [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** |
| Yuavirus\_12ns\_VIRIDIC\_heatmap.xlsx | VIRIDIC analysis of genus |
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| **Tables, Figures:**  |

**Table 1.** List of new species in the genus *Yuavirus*

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| **Accession No.** | **Phage name** | **Taxon** |
| PP596838.1 | Pseudomonas phage PC1 | *“Yuavirus PC1”* |
| PP661417.1 | Pseudomonas phage Bella | *“Yuavirus bella”* |
| PP661418.1 | Pseudomonas phage Jack | *“Yuavirus jack”* |
| PP944331.1 | Pseudomonas phage JM2 | *“Yuavirus JM2”* |
| PP408251.1 | Pseudomonas phage vB\_Pa-PAC4 | *“Yuavirus PAC4”* |
| PP408253.1 | Pseudomonas phage vB\_Pa-PAC6 | *“Yuavirus PAC6”* |
| MT118302.1 | Pseudomonas phage Epa38 | *“Yuavirus Epa38”* |
| MZ089734.1 | Pseudomonas phage PSA20, | *“Yuavirus PSA20”* |
| OR538761.1 | Pseudomonas phage PSP2 | *“Yuavirus PSP2”* |
| PQ144889.1 | Pseudomonas phage NEU2024 | *“Yuavirus NEU2024”* |
| OQ992553.1 | Pseudomonas phage Clover | *“Yuavirus clover”* |
| PP760143.1 | Pseudomonas phage vB\_Pae\_HLL23 | *“Yuavirus HLL23”* |

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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. Names which have been highlighted in gold correspond to existing species. Data values which are bordered in black correspond to strains. Abbreviations: Pseu = *Pseudomonas*; phg = phage. The complete VIRIDIC heatmap accompanies this proposal as Yuavirus\_VIRIDIC heatmap.xlsx