

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create one new genus *Comeauvirus* with two new species (Class: *Caudoviricetes*). |
| **Code assigned:**  | 2025.012B.Comeauvirus\_1ng\_2ns |

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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  |  |
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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:**  |
| 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:** |  015/06/2025 |

**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| W - Withdrawn |  |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** |
| Comeauvirus | Named in honour of André M Comeau who sequenced this virus |
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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**  |
| Comeauvirus | André M Comeau | x |
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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 bacterial viruses described in this proposal are currently unclassified*Proposed* *taxonomic change(s):* Create a new genus “*Comeauvirus*” and two new species*Justification*: It represents the clustering of unique *Vibrio* phages |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes* *Description of current taxonomy*: The bacterial viruses described in this proposal are currently unclassified*Proposed* *taxonomic change(s):* Create a new genus “*Comeauvirus*” and two 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*: This are unique, currently unclassified viruses against *Vibrio*  |

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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** |
| Comeauvirus\_LoA.pdf | Letter of acceptance of Andre Comeau |
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| **Tables, Figures:**  |

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**Origin of the name of this taxon:** This genus is named in honour of André M. Comeau (b. 1975, Moncton NB, Canada). He received his PhD from the University of British Columbia (Vancouver, BC, Canada) where he studied the ecology of vibriophages, one of which (VpV262) became the third marine phage ever to be sequenced. He completed a first post-doctorate in France (CNRS, Toulouse), partially funded by a Les Treilles Foundation scientific prize, studying T4 phage genomics, PeSLs and phage-antibiotic synergy (PAS) with Henry M. Krisch. While there, he also collaborated with phage researchers from the G.Eliava Institute and sequenced the first phage of Iodobacteria. A second post-doctorate at Université Laval (Québec QC) led to further diverse phage characterization and sequencing with Hans-W. Ackermann and Sylvain Moineau. He currently holds a senior scientist position as the manager of Dalhousie University's Integrated Microbiome Resource (Halifax, NS, Canada).

Table 1. Characteristics of the phages described in the proposal

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| **Prophage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Vibrio* phage vB\_VchM-138 | *Vibrio cholerae* | Myovirus | lytic | JQ177064.1 | 44485 bp | 67 | 0 |
| *Vibrio* phage CP-T1 | *Vibrio cholerae* ElTor | Myovirus | lytic | JQ177061.1 | 44492 bp | 70 | 0 |

[Vibrio phage CP-T1]Figure 1. VIRIDIC heat map of a group of phages with the one under discussion indicated with a red arrowhead. 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; Vibr = *Vibrio*




Figure 2. ViPTree analysis: ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The taxon under discussion is indicated with a red arrowhead. Abbreviations: phg = phage; Vibr = *Vibrio*



Figure 3. Electron micrographs of negatively stained Vibriophage 138. (derived from The Félix d'Hérelle Reference Center for Bacterial Viruses, H.-W. Ackermann)



Figure 4. André M. Comeau (photo provided by the honouree).