

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, *Margaretvirus,* with seven species in a new subfamily, *Ceeteevirinae* (Class *Caudoviricetes*). |
| **Code assigned:**  | 2025.009B.Ac.v3.Ceeteevirinae\_1nsf\_1ng\_15ns |

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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  |  |
| Ipek  | Kurtböke | University of the Sunshine Coast - Faculty of Science, Health, Education and Engineering, Australia | ikurtbok@usc.edu.au |  |
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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> |
| Actinophages 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 | **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:** | August 19, 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** |
| **Margaretvirus** | **Name derived from one of the first phage of its type *- Gordonia* phage Margaret** |
| **Ceeteevirinae** | **Named after Actinobacteriophage Database Cluster CT** |
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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*: These are unclassified lytic siphoviruses which are related to *Aziravirus, Ponsvirus* and *Emalynvirus**Proposed* *taxonomic change(s):* Create a new genus (*Margaretvirus*) and cluster it with *Aziravirus, Ponsvirus* and *Emalynvirus* in a new subfamily, *Ceeteevirinae*.*Justification*: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in accord with the criteria for the establishment of new species, genera and subfamilies this group of viruses belong to a new subfamily which we have chosen to call *Ceeteevirinae* after Cluster CT in the Actinobacteriophage Database[8]. |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*:Subfamily, genus, species*Description of current taxonomy*:These are unclassified lytic siphoviruses which are related to the genera *Aziravirus, Ponsvirus* and *Emalynvirus**Proposed* *taxonomic change(s)*:Create a new genus (*Margaretvirus*) and cluster it with *Aziravirus, Ponsvirus* and *Emalynvirus* in a new subfamily, *Ceeteevirinae*.*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*: On the basis of VIRIDIC, ViPTree, CoreGenes and phylogenetic analyses and in accord with the criteria for the establishment of new species, genera and subfamilies this group of viruses belong to a new subfamily which we have chosen to call *Ceeteevirinae* after Cluster CT in the Actinobacteriophage Database [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: PMC10243930.11. 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** |
| 2025.009B.N.Ceeteevirinae\_1nsf\_1ng\_15ns2025.009B.N.v3.Ceeteevirinae\_VIRIDIC\_heatmap | Data for this proposal |
|  | VIRIDIC heatmap |

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| **Tables, Figures:**  |

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Table 1A. Characteristics of new species in the genus *Aziravirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Gordonia phage Fribs8 | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | OR553910.1 | 45985 bp | 67 | 0 |
| Gordonia phage Nibbles | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | OR253918.1 | 45601 bp | 67 | 0 |

Table 1B. Characteristics of new species in the genus *Ponsvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Gordonia phage MAnor | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | PQ184784.1 | 48,333 bp | 73 | 0 |
| Gordonia phage SummitAcademy | *Gordonia rubripertincta* Grub38 | Siphovirus | Lytic | OP297531.1 | 47,328 bp | 71 | 0 |
| Gordonia phage Elinal | *Gordonia rubripertincta* Grub38 | Siphovirus | Lytic | OR553897.1 | 48,336 bp | 76 | 0 |

Table 1C. Characteristics of new species in the genus *Emalynvirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Gordonia phage SweatNTears | Gordonia terrae 3612 | Siphovirus | Lytic | MK967383.1 | 45,917 bp | 71 | 0 |
| Gordonia phage BillDoor | Gordonia rubripertincta NRRL B-16540 | Siphovirus | Lytic | PP208920.1 | 44,875 bp | 69 | 0 |
| Gordonia phage Tolls | Gordonia terrae CAG3 | Siphovirus | Lytic | MW862988.1 | 44,786 bp | 67 | 0 |

Table 1D. Characteristics of species in the new genus *Margaretvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Gordonia phage Orla | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | MT889367.1 | 47,354 bp | 75 | 0 |
| Gordonia phage Yakult | *Gordonia terrae* 3612 | Siphovirus | Lytic | MK875791.1 | 47,197 bp | 74 | 0 |
| Gordonia phage Margaret | *Gordonia terrae* 3612 | Siphovirus | Lytic | MH271302.1 | 46,950 bp | 75 | 0 |
| Gordonia phage RanchParmCat | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | PQ868985.1 | 47,226 bp | 74 | 0 |
| Gordonia phage GiKK | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | OL455888.1 | 47,537 bp | 75 | 0 |
| Gordonia phage Button | *Gordonia rubripertincta* | Siphovirus | Lytic | ON970621.1 | 46,090 bp | 71 | 0 |
| Gordonia phage Jamzy | *Gordonia rubripertincta* | Siphovirus | Lytic | OR159649.1 | 47,245 bp | 76 | 0 |

**Figure 1.** Partial VIRIDIC heat map of a group of phages with the one under discussion. 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. The names in the first column which are highlighted in **green** correspond to currently recognized species. See the complete heatmap here (Ceeteevirinae VIRIDIC heatmap.xlsx)




**Figure 2.** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages belonging to the genus *Margaretvirus* are indicated with **red bar**.



**Figure 3.** Electron micrograph: Electron micrographs of negatively stained Gordonia phage Margarette (<https://phagesdb.org/phages/Margaret/>). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.



**Figure 4.** Phylogenetic tree constructed with large subunit terminase proteins from these and related phages using “One Click” phylogeny.fr at <http://phylogeny.lirmm.fr/phylo_cgi/simple_phylogeny.cgi> [11].

**CoreGenes 3.5 Analysis [7]**: revealed that the phages listed in Table 1 share 40 protein homologs, including terminase small subunit, terminase large subunit, portal protein, MuF-like minor capsid protein, scaffolding protein, major capsid protein, head-to-tail adaptor, head-to-tail stopper, tail terminator, major tail protein, two tail assembly chaperones, tape measure protein, three minor tail proteins, lysin A, L-Ala-D-Glu peptidase domain, MerR-like helix-turn-helix DNA binding protein, Holliday junction resolvase, RecA-like DNA recombinase, Cas4 family exonuclease, DNA polymerase I, deoxycytidylate deaminase, lysin B, thymidylate synthase, dUTPase, polynucleotide kinase, DNA helicase, RecA-like DNA recombinase. This indicates that approximately 55.5% of the phage-encoded proteins are conserved.