

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 subfamily, *Durvirinae,* with three genera (Class *Caudoviricetes*). |
| **Code assigned:**  | 2025.016B.Durvirinae\_1nsf\_2ng\_6ns |

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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:**  |
| 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 |  |
| 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| W - Withdrawn |  |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** |
| *Durvirinae* | Name derived from The Actinobacteriophage Database Cluster (DR) |
| *Mossrosevirus* | Named after Gordonia phage MossRose |
| *Ligmavirus* | Named after Gordonia phage Ligma |
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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 bacterial viruses described in this proposal are currently unclassified. These lytic siphoviruses are peripherally related to the genus *Sourvirus* (Taxonomy Protocol 2018.122B.A.v1.Sourvirus)*Proposed* *taxonomic change(s):*Create a new subfamily (“*Durvirinae”*) with *Sourvirus* and two new proposed genera, “*Mossrosevirus”* and *“Ligmavirus”* based upon The Actinobacteriophage Database Cluster DR phages.*Justification*: This proposal is in accord with our definition of a subfamily |

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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. These lytic siphoviruses are peripherally related to the genus *Sourvirus* (Taxonomy Protocol 2018.122B.A.v1.Sourvirus)*Proposed* *taxonomic change(s):*Create a new subfamily (“*Durvirinae”*) with *Sourvirus* and two new proposed genera, “*Mossrosevirus”* and *“Ligmavirus”* based upon The Actinobacteriophage Database Cluster DR phages.*Demarcation criteria:* Sub-family demarcation criteria: Robust clustering in the core genome phylogenetic tree with a suggested minimum shared core gene content of 25%. Members of the same subfamily typically share >25% nucleotide identity across the genome length. 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. Species demarcation criteria: A demarcation value of 95% intergenomic similarity was used to define different species according to intergenomic similarity. Members of the same species have >95% intergenomic similarity.*Justification*: This proposal is in accord with our definition of a subfamily  |

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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** |
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| **Tables, Figures:**  |

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**Figure 1.** 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.





**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 this subfamily are indicated with **red bar**.

**Table 1.** Characteristics of new species in the genus *Ligmavirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Gordonia* phage Ligma | *Gordonia terrae* NRRL B-16283 | Siphovirus | Lytic | OM105886.1 | 61714 bp | 87 | 0 |
| *Gordonia* phage Mariokart | *Gordonia terrae NRRL B-16283* | Siphovirus | Lytic | MT657335.1 | 60762 bp | 83 | 0 |

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**Figure 3.** Electron micrograph: Electron micrographs of negatively stained Gordonia phage Ligma (<https://phagesdb.org/phages/Ligma/>). 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.

**Table 2.** Characteristics of species in the genus *Mossrosevirus*

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Gordonia* phage NHagos | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | MN369758.1 | 59580 bp | 82 | 0 |
| *Gordonia* phage MossRose | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | OR253912.1 | 61072 bp | 84 | 0 |
| *Gordonia* phage CaiB | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | ON108644.1 | 61620 bp | 85 | 0 |
| *Gordonia* phage MakoManhole | *Gordonia rubripertincta* NRRL B-16540 | Siphovirus | Lytic | PQ184807.1 | 61592 bp | 83 | 0 |

Genomes are Circularly Permuted

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**Figure 3.** Electron micrograph: Electron micrographs of negatively stained Gordonia phage CaiB (<https://phagesdb.org/phages/CaiB/>). 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.

**CoreGenes 3.5 Analysis [7]**: revealed that the phages listed in Table 1, 2 and *Gordonia* phage Sour share 49 protein homologs, including ParB-like nuclease domain protein, terminase large subunit, RuvC-like resolvase, portal protein, major capsid proteins (hexamer and pentamer), head-to-tail adaptor, major tail protein, tape measure protein, 3 minor tail proteins, lysin B, exonuclease, DNA primase/polymerase/helicase, DNA polymerase and DNA binding protein. This indicates that approximately 59.0% of the phage-encoded proteins are conserved.