

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 (*Peetremavirus*) of *Mycobacterium* phages with eight species (Class *Caudoviricetes*). |
| **Code assigned:**  | 2025.048B.Ac.v3.Mycobacterium\_phages\_1ng\_8ns |

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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 |  |

**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 | **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| W - Withdrawn |  |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 section. |

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

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| **Response of proposer:**  |
| Since submission of the original Taxonomy Proposal a series of related phages were deposited in GenBank. The revised proposal includes these. |

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| **Revision date:** | August 18, 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** |
| ***Peetremavirus*** | **Name derived from first isolate phage of its type *Mycobacterium* phage P3MA** |
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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 and species*Description of current taxonomy*: None. Mycobacterium phage P3MA is defined in the Actinobacteriophage Database as a singleton. The prophages have not been included in the database as of writing (18/08/2025)*Proposed* *taxonomic change(s):* Create one new genus *Peetremavirus*with eight species*Justification*: Phage P3MA was isolated on *Mycobacterium abscessus* 330 while the other proposed members of this genus were identified in the genomes of a variety of *M. abscessus* isolates. All of these temperate siphoviruses conform to the criteria which we have established for creation of a genera and associated species. |

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| * **Text of Taxonomy proposal:**
 |
| *Taxonomic rank(s) affected*: genus and species*Description of current taxonomy*: None. Mycobacterium phage P3MA is defined in the Actinobacteriophage Database as a singleton. The prophages have not been included in the database as of writing (18/08/2025).*Proposed* *taxonomic change(s)*: Create one new genus “*Peetremavirus”*with eight 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*: Phage P3MA was isolated on *Mycobacterium abscessus* 330 while the other proposed members of this genus were identified in the genomes of a variety of *M. abscessus* isolates. All of these temperate siphoviruses conform to the criteria which we have established for creation of a genera and associated species.  |

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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** |
| **2025,0488.N.Mycobacterium\_phage\_1ng\_7ns** | **Data for this proposal** |
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| **Tables, Figures:**  |

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**Figure 1.** VIRIDIC heatmap 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. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; pphg = prophage; Gord = *Gordonia*; Tsuk = *Tsukamurella*; Myco = *Mycobacterium*.

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

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Mycobacterium phage P3MA | *Mycobacterium abscessus* 330 | Siphovirus | Temperate | PV089522.1 | 41151 bp | 63 | 0 |
| Mycobacterium phage prophi62-1 | *Mycobacterium abscessus* GD62 | Siphovirus | Temperate | MW584194.1 | 39,188 bp | 58 | 0 |
| Mycobacterium phage phiGD34-2 | *Mycobacterium abscessus* GD41 | Siphovirus | Temperate | MW314853.1 | 40,005 bp | 63 | 0 |
| Mycobacterium phage prophiGD21-1 | *Mycobacterium abscessus* GD21 | Siphovirus | Temperate | MW584205.1 | 40,775 bp | 62 | 0 |
| Mycobacterium phage prophiGD11-2 | *Mycobacterium abscessus* GD11 | Siphovirus | Temperate | MW584151.1 | 39,951 bp | 62 | 0 |
| Mycobacterium phage prophiGD16-1 | *Mycobacterium abscessus* GD16 | Siphovirus | Temperate | MW584149.1 | 40,056 bp | 58 | 0 |
| Mycobacterium phage prophiGD43A-2 | *Mycobacterium abscessus* GD43A | Siphovirus | Temperate | MW584198.1 | 40,147 bp | 60 | 0 |
| Mycobacterium phage phiGD89-1 | *Mycobacterium abscessus* GD89 | Siphovirus | Temperate | MW314851.1 | 40,450 bp | 63 | 0 |