

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:**  | Create two new genera of *Rhodococcus* phages (Class: *Caudoviricetes*). |
| **Code assigned:**  | 2025.067B.Ac.v3.Rhodococcus\_phages\_2ng\_2ns |

|  |
| --- |
| **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**

|  |
| --- |
| **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 - |  |

|  |
| --- |
| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** <https://ictv.global/sc> |
| Actinophages Study Group |

|  |
| --- |
| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

|  |  |
| --- | --- |
| **Submission date:** |  015/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

|  |  |
| --- | --- |
| **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| W - Withdrawn |  |

|  |
| --- |
| **Comments from the Executive Committee:** |
| Please improve the quality of the abstract. |

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

|  |
| --- |
| **Response of proposer:**  |
| The text of the abstract has been amended |

|  |  |
| --- | --- |
| **Revision date:** | 01/09/2025 |

**Part 3:** **TAXONOMIC PROPOSAL**

<https://ictv.global/taxonomy/templates>

|  |
| --- |
| **Taxonomic changes proposed:**  |
| Establish new taxon | **x** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

|  |
| --- |
| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| *Docdeeseptimavirus* | Name derived from first isolate phage of its type Rhodococcus phage ReqiDocB7 |
| *Eetrevirus* | Name derived from first isolate phage of its type Rhodococcus phage E3 |

|  |
| --- |
| **Permission for use of names derived from a living person:**  |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached**  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

|  |
| --- |
| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: genus and species*Description of current taxonomy*: The viruses described in this proposal are currently unclassified. They are defined in the Actinobacteriophage Database as singletons*Proposed* *taxonomic change(s):* Create two new genera, “*Docdeeseptimavirus”* and *“Eetrevirus”* each with a single species*Justification*: Rhodococcus phages Reqi DocB7 and E3 show little similarity to other phages in the extant nucleotide sequence databases when examined using BLASTN. Based on this, we propose that each represents a new species and genus.  |

|  |
| --- |
| * **Text of Taxonomy proposal:**
 |
| *Taxonomic rank(s) affected*: genus and species*Description of current taxonomy*: The viruses described in this proposal are currently unclassified. They are defined in the Actinobacteriophage Database as singletons*Proposed* *taxonomic change(s)*: Create two new genera, “*Docdeeseptimavirus”* and *“Eetrevirus”* each with a single 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*: Rhodococcus phages Reqi DocB7 and E3 show little similarity to other phages in the extant nucleotide sequence databases when examined using BLASTN. Based on this, we propose that each represents a new species and genus.  |

|  |
| --- |
| **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.  |

|  |
| --- |
| **Accompanying files:**  |
| **Filename** | **Description of contents** |
|  |  |
|  |  |

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

<Start here>

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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Rhodococcus phage Reqi DocB7 | *Rhodococcus equi* HDP1C | Siphovirus | Temperate | GU580940.1 | 75772 bp | 105 | 0 |
|  |  |  |  |  |  |  |  |
| Rhodococcus phage E3 | *Rhodococcus equi* NCIMB 10027 | Myovirus | Lytic | HM114277.1 | 142563 bp | 220 | 0 |
|  |  |  |  |  |  |  |  |

**Specific references:** [Rhodococcus phage ReqiDocB7] ; Salifu SP, Valero-Rello A, Campbell SA, Inglis NF, Scortti M, Foley S, Vázquez-Boland JA. Genome and proteome analysis of phage E3 infecting the soil-borne actinomycete Rhodococcus equi. Environ Microbiol Rep. 2013 Feb;5(1):170-8. doi: 10.1111/1758-2229.12028. Epub 2013 Jan 16. PMID: 23757146. [Rhodococcus phage E3]