

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | To create a new genus, *Malkevirus*, for *Streptococcus* prophages [Class: *Caudoviricetes*] | |
| **Code assigned:** | 2024.021B |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Tolstoy I | National Center for Biotechnology Information, MD, USA | tolstoy@ncbi.nlm.nih.gov |  |
| Moraru C | Carl von Ossietzky Universität Oldenburg, Germany | liliana.cristina.moraru@uol.de |  |
| Kropinski AM | University of Guelph, Ontario, Canada | Phage.Canada@gmail.com | **x** |

**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:** |
| The 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:** | 07/05/2024 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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| W - Withdrawn |  |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:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.021B.A.v1.Malkevirus\_ng.xlsx |

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

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| **Is any taxon name used here derived from that of a living person:** | | **Y** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
| *Malkevirus* | Horst Malke | 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 viruses classified in this proposal do not have a current taxonomic assignment.  *Proposed* *taxonomic change(s):*  We propose a new genus, named in honour of Professor Dr. Horst Malke, comprised of temperate siphoviruses infecting *Streptococcus* spp.  *Justification*:  The viruses fall into a genus based on current demarcation criteria. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Species, Genus  *Description of current taxonomy*: None of these phages have been classified.  *Proposed* *taxonomic change(s)*: We propose a new genus, named in honour of Professor Dr. Horst Malke, of *Streptococcus* temperate siphoprophages.  *Demarcation criteria:*  **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates. These values can be calculated by a number of tools, such as BLASTn [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree [10]. In the case of temperate phages such as these we have allowed some leeway on this cutoff.  *Justification*: These taxa fit within the demarcation criteria outlined above. |

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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: 33095870  2. 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. 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;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.  9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.  10. 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. |

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| **Tables, Figures:** |

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**Proposals Data:**

1. **Create a new genus,** ***Malkevirus* with five species**

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**Figure 1. A. VIRIDIC heat map Subfamily 2:** 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; Stre = *Streptococcus*. The **purple** arrowhead indicate the *Malkevirus.*

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

1. **Create a new genus, *Malkevirus* with five species**

**Origin of the name of this taxon:** This taxon is named in honour of German microbiologist, Professor Dr. Horst Malke (b. 1937, Altrehfeld, Germany). He received his PhD in microbiology from Ernst Moritz Arndt University (EMAU) Greifswald, Germany in 1965; and, his habilitation (Dr. rer. nat. habil.) in 1972. From 1973 ‐ 1983 he was the Head, Research Group for Streptococcal Genetics, Central Institute of Microbiology and Experimental Therapy (ZIMET) of the Academy of Sciences of the GDR, Jena, Germany. From 1984 ‐ 1991 he served as Head, Department of Molecular Genetics at ZIMET. Subsequently, he was the Director, Institute of Molecular Biology, Faculty of Biology and Pharmacy, Friedrich Schiller University in Jena, Germany. Upon retirement in 2002 he became a research professor at Oklahoma University Health Sciences Center (OUHSC) where he was an advisor on their Streptococcus pyogenes Genome sequencing project. Since the late 1990s he has been a Member of Akademie gemeinnütziger Wissenschaften zu Erfurt, Germany, German National Academy of Sciences Leopoldina; and, an Honorary Editor of the Journal of Basic Microbiology (Wiley‐VCH Verlag GmbH).



(picture copied from: <https://www.leopoldina.org/en/members/list-of-members/list-of-members/member/Member/show/horst-malke/>)

**Historical aspects:** Temperate siphoviral prophage phiARI0285-3 was discovered in*Streptococcus pneumoniae*.

**Genome summary:**

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| Phage name | INSDC | Size (kb) | Overall % DNA sequence identity (\*) |
| *Streptococcus* phage phiARI0285-3 | KT337347.1 | 39.5 | 100.0 |
| *Streptococcus* phage IPP67 | KY065503.1 | 33.6 | 67.4 |
| *Streptococcus* phage IPP45 | KY065485.1 | 37.4 | 63.6 |
| *Streptococcus* phage 23782 | FR671408.1 | 32.0 | 62.7 |
| *Streptococcus* phage 11865 | FR671409.1 | 32.6 | 61.0 |

**(\*) determined using VIRIDIC [3]**

**Specific references for these phages:**

Croucher NJ, Mostowy R, Wymant C, Turner P, Bentley SD, Fraser C. Horizontal DNA Transfer Mechanisms of Bacteria as Weapons of Intragenomic Conflict. PLoS Biol. 2016 Mar 2;14(3):e1002394. doi: 10.1371/journal.pbio.1002394. PMID: 26934590; PMCID: PMC4774983. [*Streptococcus* phage phiARI0285-3]

Brueggemann AB, Harrold CL, Rezaei Javan R, van Tonder AJ, McDonnell AJ, Edwards BA. Pneumococcal prophages are diverse, but not without structure or history. Sci Rep. 2017 Feb 20;7:42976. doi: 10.1038/srep42976. PMID: 28218261; PMCID: PMC5317160. [*Streptococcus* phage IPP45]

Croucher NJ, Harris SR, Fraser C, Quail MA, Burton J, van der Linden M, McGee L, von Gottberg A, Song JH, Ko KS, Pichon B, Baker S, Parry CM, Lambertsen LM, Shahinas D, Pillai DR, Mitchell TJ, Dougan G, Tomasz A, Klugman KP, Parkhill J, Hanage WP, Bentley SD. Rapid pneumococcal evolution in response to clinical interventions. Science. 2011 Jan 28;331(6016):430-4. doi: 10.1126/science.1198545. PMID: 21273480; PMCID: PMC3648787. [*Streptococcus* phage 11865]