

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 *Wallmarkvirinae* with three new genera, *Machiasvirus* *Lentusvirus*, and *Madawaskavirus* in the Class *Caudoviricetes* |
| **Code assigned:**  | 2025.079B.Ac.v3.Wallmarkvirinae\_1nsf\_3ng\_9ns |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
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| Andrew D. | Millard | Department of Genetics and Genome Biology,University of Leicester, UK | adm39@leicester.ac.uk | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **x** |
| xAnimal 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> |
| 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:** |  15/06/2025 |

**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| W - Withdrawn |  |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 and correct typos throughout the document. Any further references available?Lacks phylogenetic tree of subfamily and constituent genera, core genes analysis is present |

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

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| **Response of proposer:**  |
| The abstract has been revised to include additional detail. The references used are appropriate for this proposal. |

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| **Revision date:** | 19/08/2025 |

**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** |
| *Wallmarkvirinae* | Named in honour of Swedish clinical microbiologist and pioneering phage worker Gösta Wallmark MD (State Bacteriological Laboratory, Stockholm, Sweden) |
| *Machiasvirus* | Named after *Staphylococcus* phage Machias |
| *Lentusvirus* | Named after the species of *Staphylococcus* that this phage infects |
| *Madawaskavirus* | Named after *Staphylococcus* phage Madawaska |

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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 *Description of current taxonomy*: The bacterial viruses described in this proposal are currently unclassified*Proposed* *taxonomic change(s):* To create a new subfamily “*Wallmarkvirinae”* with three new genera, “*Machiasvirus”, “Lentusvirus”* and “*Madawaskavirus”* of jumbo *Staphylococcus* myophages*Justification*: This proposal covers a clade of bacterial viruses with genomes of greater than 250 kb that infect *Staphylococcus* spp. Comparative analysis at the nucleotide level indicates that this clade of phages exhibit a minimum of 54% inter-genomic similarity. At the protein level, these bacteriophages 163 proteins. This indicates that approximately 60.8% of the phage-encoded proteins are conserved. In accordance with the demarcation criteria, we propose one new subfamily that includes three new genera and nine new species. |

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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*Proposed* *taxonomic change(s):* To create a new subfamily “*Wallmarkvirinae”* with three new genera, “*Machiasvirus”, “Lentusvirus”* and “*Madawaskavirus”* of jumbo *Staphylococcus* myophages*Demarcation criteria:* Subfamily 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 includes bacterial viruses with genomes of greater than 250 kb that infect *Staphylococcus* spp. Comparative analysis at the nucleotide level indicates that this clade of phages exhibit a minimum of 54% inter-genomic similarity (Figure 1). At the protein level, these bacteriophages 163 proteins (Table 1). This indicates that approximately 60.8% of the phage-encoded proteins are conserved. In accordance with the demarcation criteria [3], we propose one new subfamily that includes three new genera and nine new 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. 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/ 3. 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: PMC8003253.4. 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: 121424236. 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: PMC6602494.7. Letunic I, Bork P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. Nucleic Acids Res. 2021 Jul 2;49(W1):W293-W296. doi: 10.1093/nar/gkab301. PMID: 33885785; PMCID: PMC8265157.  |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| **Wallmarkvirinae\_1nsf\_3ng\_9ns** | **Data for this proposal** |
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| **Tables, Figures:**  |

**Table 1A.** Characteristics of the phages described in the proposal (*Machiasvirus*)

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Staphylococcus phage AH12 | *Staphylococcus aureus* | Myovirus | Lytic | OR455461.1 | 264661 bp | 281 | 1(\*) |
| Staphylococcus phage Machias | *Staphylococcus aureus* | Myovirus | Lytic | MW349128.1 | 274478 bp | 263 | 2 |
| Staphylococcus phage vB\_StaM\_PB50 | *Staphylococcus aureus* | Myovirus  | Lytic | OR770614.1 | 273701 bp | 290 | 2(\*) |

**(\*) Predicted using tRNAScan-SE (**[**https://lowelab.ucsc.edu/tRNAscan-SE/**](https://lowelab.ucsc.edu/tRNAscan-SE/)**)**

**Table 1B.** Characteristics of the phages described in the proposal (*Lentusvirus*)

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Staphylococcus phage vB\_StaM\_SA1 | *Staphylococcus lentus* | Myovirus  | Lytic | MW218148.1 | 260727 bp | 258 | 1 |

**(\*) Predicted using tRNAScan-SE (**[**https://lowelab.ucsc.edu/tRNAscan-SE/**](https://lowelab.ucsc.edu/tRNAscan-SE/)**)**

**Table 1C.** Characteristics of the phages described in the proposal (“*Madawaskavirus”*)

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| --- | --- | --- | --- | --- | --- | --- | --- |
| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Staphylococcus phage LY01 | *Staphylococcus aureus* YZ4 | Myovirus | Lytic | OR836606.1 | 258897 bp | 251 | 0 |
| Staphylococcus phage PALS2 | *Staphylococcus aureus* | Myovirus | Lytic | MN091626.1 | 268748 bp | 279 | 1 |
| Staphylococcus phage vB\_SauM-UFV\_DC4 | *Staphylococcus aureus* UFV2030RH1 | Myovirus | Lytic | MZ779063.1 | 263185 bp | 261 | 1 |
| Staphylococcus phage MarsHill | *Staphylococcus aureus* | Myovirus | Lytic | MW248466.1 | 266637 bp | 262 | 0 |
| Staphylococcus phage Madawaska | *Staphylococcus aureus* | Myovirus | Lytic | MW349129.1 | 265446 bp | 264 | 1 |

**Specific References:**

Lee Y, Son B, Cha Y, Ryu S. Characterization and Genomic Analysis of PALS2, a Novel *Staphylococcus* Jumbo Bacteriophage. Front Microbiol. 2021 Mar 8;12:622755. doi: 10.3389/fmicb.2021.622755. PMID: 33763042; PMCID: PMC7982418 [PALS2]

da Silva Duarte V, Treu L, Sartori C, Dias RS, da Silva Paes I, Vieira MS, Santana GR, Marcondes MI, Giacomini A, Corich V, Campanaro S, da Silva CC, de Paula SO. Milk microbial composition of Brazilian dairy cows entering the dry period and genomic comparison between *Staphylococcus aureus* strains susceptible to the bacteriophage vB\_SauM-UFV\_DC4. Sci Rep. 2020 Mar 26;10(1):5520. doi: 10.1038/s41598-020-62499-6. PMID: 32218514; PMCID: PMC7099093. [DC4]

Uchiyama J, Takemura-Uchiyama I, Sakaguchi Y, Gamoh K, Kato S, Daibata M, Ujihara T, Misawa N, Matsuzaki S. Intragenus generalized transduction in *Staphylococcus* spp. by a novel giant phage. ISME J. 2014 Sep;8(9):1949-52. doi: 10.1038/ismej.2014.29. Epub 2014 Mar 6. PMID: 24599069; PMCID: PMC4139722. [S6]

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**Figure 1.** VIRIDIC heat map (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) heatmap for this group of phages. It computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: Stap = *Staphylococcus*; phg = phage.

**Figure 2:** ViPTree analysis (https://www.genome.jp/viptree/; [4]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [5]. The phages of interest are indicated with **red arrowhead**. Abbreviations: Stap = *Staphylococcus*; phg = phage.

**CoreGenes 5 Analysis** [7]: revealed that the phages listed in Table 1 share 163 protein homologs, including DNA-directed RNA polymerase beta subunit, DNA-directed RNA polymerase beta' subunit, DNA-polymerase catalytic subunit, ATP-binding protein, baseplate wedge, RecD-like helicase, tape measure protein, ribonucleoside-diphosphate reductase 1 subunit, ribonucleotide reductase flavodoxin, terminase large subunit, precursor to major capsid protein, prohead core scaffold and protease, Holliday junction resolvase, NAD-dependent DNA-ligase, TelA-like protein, UvsX-like recombinase, DNA gyrase subunits A & B, DNA helicase, guanylate kinase, molecular chaperone GroEL, ribonuclease H, dCMP deaminase, endolysin and portal vertex protein. This indicates that approximately 60.8% of the phage-encoded proteins are conserved.