

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

|  |  |
| --- | --- |
| **Title:** | To create eleven new species in the Class *Caudoviricetes* |
| **Code assigned:** | 2025.008B.Caudoviricetes\_11ns | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Andrew D. | Millard | Department of Genetics, Genomics, and Cancer Science, University of Leicester, Leicester, UK | adm39@leicester.ac.uk | x |
| Andrew M. | Kropinski | Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com | x |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |
|  |  |  |  |  |

**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:** |
| Caudoviricetes 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:** | 06/05/2025 |

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| W - Withdrawn |  |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

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

|  |
| --- |
| **Response of proposer:** |
|  |

|  |  |
| --- | --- |
| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

|  |
| --- |
| **Abstract for General Proposal:** |
| *Brief description of current situation:*  *Proposed changes:*  *Justification:* |

|  |
| --- |
| **Text of General Proposal:** |
| *Background:*  *Proposed* *changes:*  *Justification:* |

|  |
| --- |
| **References:** |
|  |

|  |  |
| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| **Eleven\_new\_species** | **Specifics on each new species** |
|  |  |

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

<Start here>

**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** |
|  | **Each new species is named after its genus and the name of the phage** |
|  |  |
|  |  |
|  |  |

|  |  |  |
| --- | --- | --- |
| **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*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  The bacterial viruses detailed in this proposal are currently unclassified.  *Proposed* *taxonomic change(s):*   1. Add one new species to the genus *Maaswegvirus* 2. Add one new species to the genus *Efquatrovirus* 3. Add one new species to the genus *Kuravirus* 4. Add one new species to the genus *Gilesvirus* 5. Add one new species to the genus *Karamvirus* 6. Add one new species to the genus Nanditavirus 7. Add one new species to the genus Corndogvirus 8. Add one new species to the genus Birdsnestvirus 9. Add one new species to the genus Przondovirus 10. Add one new species to the genus Rosenblumvirus 11. Add one new species to the genus Tequatrovirus   *Justification*:  These new taxa were identified using taxMyPhage [1] which shows 96.7% accuracy at the genus level and 97.9% accuracy at the species level. The system also detects inconsistencies in current ICTV classifications, identifying cases where genera did not adhere to ICTV’s 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species. Each of the bacteriophages detailed in this proposal fall within the demarcation criteria for inclusion as new species in existing genera within the class *Caudoviricetes*. |

|  |
| --- |
| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  The bacterial viruses detailed in this proposal are currently unclassified.  *Proposed* *taxonomic change(s)*:   1. Add one new species to the genus *Maaswegvirus* 2. Add one new species to the genus *Efquatrovirus* 3. Add one new species to the genus *Kuravirus* 4. Add one new species to the genus *Gilesvirus* 5. Add one new species to the genus *Karamvirus* 6. Add one new species to the genus Nanditavirus 7. Add one new species to the genus Corndogvirus 8. Add one new species to the genus Birdsnestvirus 9. Add one new species to the genus Przondovirus 10. Add one new species to the genus Rosenblumvirus 11. Add one new species to the genus Tequatrovirus   *Demarcation criteria:*  The Bacterial and Archaeal Virus Subcommittee established 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species.  *Justification*:  These new taxa were identified using taxMyPhage [1] which shows 96.7% accuracy at the genus level and 97.9% accuracy at the species level. The system also detects inconsistencies in current ICTV classifications, identifying cases where genera did not adhere to ICTV’s 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species. Each of the bacteriophages detailed in this proposal fall within the demarcation criteria for inclusion as new species in existing genera within the class *Caudoviricetes* (Supplementary Data). |

|  |
| --- |
| **References:** |
| 1. Millard A, Denise R, Lestido M, Thomas MT, Webster D, Turner D, Sicheritz-Pontén T. taxMyPhage: Automated Taxonomy of dsDNA Phage Genomes at the Genus and Species Level. PHAGE 6 (1) https://www.liebertpub.com/doi/10.1089/phage.2024.0050 |

|  |  |
| --- | --- |
| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| Caudoviricetes\_11ns\_supplementary\_figures.zip | Intergenomic similarity data generated by taxMyPhage |
|  |  |

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

<Start here>