

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 species in the genus *Tequintavirus* |
| **Code assigned:** | 2025.076B.A.v2.Tequintavirus\_1ns | |

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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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**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:** <https://ictv.global/sc> |
|  |
| **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:** | 29/08/2024 |

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| W - Withdrawn |  |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

**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** |
| *Tequintavirus vipecosubii* | The proposed binomial name of the new species is derived from the site of isolation in the Philippines: *Tequintavirus vipecosubii* isolated from a sewage facility in Subic. |
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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*:  Species  *Description of current taxonomy*:  The genus *Tequintavirus* is classified within the subfamily *Markadamsvirinae*, family *Demerecviridae*. The genus is currently comprised of 70 species.  *Proposed* *taxonomic change(s):*  Create one new species *Tequintavirus vipecosubii* in the genus *Tequintavirus*.  *Justification*:  A new species, represented by Escherichia phage vB\_EcoS\_I14, is proposed based on a 95% intergenomic similarity threshold. This newly identified species is most closely related to *Tequintavirus S131* (GenBank MH370378.1), sharing 80.1% similarity. This taxonomic proposal is grounded in the principles of phylogenetic analysis and genomic comparison, providing a robust classification for this newly isolated bacteriophage. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  The genus *Tequintavirus* is classified within the subfamily *Markadamsvirinae*, family *Demerecviridae*. The genus is currently comprised of 70 species.  *Proposed* *taxonomic change(s):*  Create one new species *Tequintavirus vipecosubii* in the genus *Tequintavirus*.  *Demarcation criteria:*  Species demarcation: Two phages are classified as the same species if their genomes share more than 95% identity across their entire length, as determined by VIRIDIC. [1, 2].  *Justification*:  A new species, represented Escherichia phage vB\_EcoS\_I14, is proposed based on a 95% intergenomic similarity threshold. This newly identified species is most closely related to *Tequintavirus S131* (GenBank MH370378.1), sharing 80.1% similarity (Figure 1, Figure 2). This taxonomic proposal is grounded in the principles of phylogenetic analysis and genomic comparison, providing a robust classification for this newly discovered bacteriophage. All annotated sequences and raw reads were compiled and deposited into GenBank with accession numbers as listed in Table 1. |
| **References:** |
| 1. Turner D., Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy Viruses, 13(3), 506. https://doi.org/10.3390/v13030506  2. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC — A Novel Tool to Calculate the Intergenomic Similarities of prokaryote-infecting viruses. Viruses 12(11):1268. https://doi.org/10.3390/v12111268 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
|  |  |
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| **Tables, Figures:** |

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**Figure 1. Intergenomic similarity scores (VIRIDIC) of phages classified within the genus *Tequintavirus*.**

A screenshot of a computer

AI-generated content may be incorrect.

**Figure 2. Closeup image from Figure 1 of closely related species of Escherichia phage vB\_EcoS\_I14**

**Table 1. Summary of molecular features of Escherichia phage vB\_EcoS\_I14.**

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|  | **Escherichia phage vB\_EcoS\_I14** |
| Genome size (bp)  GC content (%)  Coverage  No. of CDS  No. of genes with predicted function  No. of tRNAs  Lifestyle prediction  Taxonomic identity  Temperate marker genes  Presence of antibiotic resistance genes  Presence of virulence genes  BioProject accession no.  SRA accession no.  GenBank accession no. | 97,251  38.88%  68.328727x  169  69  25  lytic  *Tequintavirus sp.*  *-*  *-*  *-*  [PRJNA1123417](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1123417)  [SRR30124319](https://trace.ncbi.nlm.nih.gov/Traces/?view=run_browser&acc=SRR30124319&display=metadata)  [PP892525](https://www.ncbi.nlm.nih.gov/nuccore/PP892525) |