

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create a new genus, *Cepavirus,* with two species (Caudoviricetes; *Autographiviridae*; *Slopekvirinae*) and a new species in the genera *Suseptimavirus* (*Caudoviricetes; Gordonclarkvirinae*) and *Uetakevirus* (*Caudoviricetes*). | |
| **Code assigned:** | 2024.006B |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Pas C | Ghent University, Department of Biotechnology, Valentin Vaerwyckweg 1, 9000 Gent, Belgium | celia.pas@ugent.be |  |
| Fieseler L | ZHAW School of Life Sciences and Facility Management, Centre for Food Safety and Quality Management, Einsiedlerstrasse 31, 8820 Wädenswil, Switzerland | lars.fieseler@zhaw.ch |  |
| Briers Y | Ghent University, Department of Biotechnology, Valentin Vaerwyckweg 1, 9000 Gent, Belgium | yves.briers@ugent.be | **X** |
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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:** |
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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:** | 27/11/2023 |

**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:** |
| 2024.006B.A.v1.Cepavirus\_Suseptimavirus\_Uetakevirus\_4ns.xlsx |

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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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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus and species.  *Description of current taxonomy*:  The bacterial viruses in this proposal are currently unclassified.  *Proposed* *taxonomic change(s):*  1. Creation of a new genus, *Cepavirus*, within the subfamily *Slopekvirinae*, family *Autographiviridae*.  2. Assign Escherichia phage vB\_EcoP\_PAS7 as a new species in the new genus, *Cepavirus*  3. Assign Escherichia phage vB\_EcoP\_PAS59 as a new species in the genus *Suseptimavirus*, subfamily *Gordonclarkvirinae*.  4. Assign Escherichia phage vB\_EcoP\_PAS6 as a new species within the genus *Uetakevirus*.  *Justification*:  These bacterial viruses fall within current genus and species demarcation criteria for inclusion within existing genera. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus and species.  *Description of current taxonomy*:  The subfamily *Slopekvirinae* in the family *Autographiviridae* was established in 2019, proposal 2019.103B.  The subfamily *Gordonclarkvirinae* was established in 2022, proposal 2022.034B.  The genus *Uetakevirus* was established in 2018, proposal 2018.007B.A.v4, renaming the historical genus Epsilon15virus.  *Proposed* *taxonomic change(s)*:  1. Creation of a new genus, *Cepavirus*, within the subfamily *Slopekvirinae*, family *Autographiviridae*.  2. Assign Escherichia phage vB\_EcoP\_PAS7 as a new species in the new genus, *Cepavirus*  3. Assign Escherichia phage vB\_EcoP\_PAS59 as a new species in the genus *Suseptimavirus*, subfamily *Gordonclarkvirinae*.  4. Assign Escherichia phage vB\_EcoP\_PAS6 as a new species within the genus *Uetakevirus*.  *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.  Genus demarcation criteria: 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.  *Justification*:  Taxonomic relatives of the isolated phages were first identified using BLASTn within the class *Caudoviricetes* (taxid:2731619) (Sayers et al., 2022). VICTOR phylogeny (Meier-Kolthoff & Göker, 2017) was then used to establish a phylogenetic tree of the phages and their phage relatives (Figure 1). Additionally, intergenomic similarity scores were obtained through VIRIDIC alignment (Figure 2) (Moraru et al., 2020).  Escherichia phage vB\_EcoP\_PAS7 (PAS7; OQ921331) is related to phages of different genera within the *Slopekvirinae* phage subfamily, with its closest relatives Enterobacter phages ENC16 (OL355133) and phiKDA1 (NC\_027980.1) of the *Koutsourouvirus* genus, with similarity scores of 36.0 and 35.2 % respectively (Figure 1,2). These scores are lower than 70 %, indicating that this phage isolate belongs to a different genus than its taxonomically related phages. We therefore propose a new viral genus *Cepavirus* within the *Slopekvirinae* subfamily, and a complementing new species *Cepavirus PAS7* within this new genus with phage PAS7 as its exemplar virus. We chose this genus name for its easy pronounceability, named after the Spanish translation of ‘strain’, referring to the strain specific nature of phages, with phage PAS7 as an exemplar phage that infects only specific *E. coli* strains.  The close relatives of Escherichia phage vB\_EcoP\_PAS59 (PAS59; OQ921332) all belong to the lytic phage subfamily *Gordonclarkvirinae*. With an intergenomic similarity score of 86.0 %, Escherichia phage EK010 (LC553734) is its closest relative (Figure 1,2). Phage EK010 is currently classified in the genus *Suseptimavirus* within the subfamily *Gordonclarkvirinae.* As the closest phage relative has less than 95 % similarity with phage PAS59, we propose a new phage species *Suseptimavirus PAS59* within the genus *Suseptimavirus.*  The closely related phages of Escherichia phage vB\_EcoP\_PAS61 (PAS61; OQ921333) all belong to the temperate phage genus *Uetakevirus* (Figure 1,2). With a similarity score of 78.7 % with its closest relative phage phiV10 (NC\_007804.2), we propose a new phage species *Uetakevirus PAS61* within the genus *Uetakevirus* with phage PAS61 as its exemplar virus. |

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| **References:** |
| Meier-Kolthoff, J. P., & Göker, M. (2017). VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics, 33(21), 3396–3404. https://doi.org/10.1093/BIOINFORMATICS/BTX440  Moraru, C., Varsani, A., & Kropinski, A. M. (2020). VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses, 12(11). https://doi.org/10.3390/v12111268  Sayers, E. W., Bolton, E. E., Brister, J. R., Canese, K., Chan, J., Comeau, D. C., Connor, R., Funk, K., Kelly, C., Kim, S., Madej, T., Marchler-Bauer, A., Lanczycki, C., Lathrop, S., Lu, Z., Thibaud-Nissen, F., Murphy, T., Phan, L., Skripchenko, Y., … Sherry, S. T. (2022). Database resources of the national center for biotechnology information. Nucleic Acids Research, 50(D1), D20–D26. <https://doi.org/10.1093/NAR/GKAB1112>  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:** |

A screenshot of a computer

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Figure 1: VICTOR phylogeny of the isolated phage genomes and their respective taxonomic relatives. Phage isolates for taxonomy proposal are outlined. This tool uses the Genome Blast Distance Phylogeny approach to calculate intergenomic distances, including 100 pseudo-bootstrap replicates for calculating branch support (Meier-Kolthoff & Göker, 2017).

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Figure 2: Genomic similarities of the isolated phage genomes to their respective taxonomic relatives through VIRIDIC genome alignment (Moraru et al., 2020). Isolated phages are indicated using orange, purple and green ellipses. Intergenomic similarity scores of 36.0, 78.1 and 86.0 % were identified between the isolated phage genomes and their closest taxonomic relatives (phages ENC16, EK010 and phiV10 respectively).