

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

<https://ictv.global/taxonomy/templates>**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new genus (*Motookavirus*) with two species in the Class *Caudoviricetes* |
| **Code assigned:** | 2025.046B.Motookavirus\_1ng\_2ns | |

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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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| Jakub | Barylski | Institute of Experimental Biology, Adam Mickiewicz University, Poznań, Poland | jakub.barylski@amu.edu.pl |  |
| Hany | Anany | Guelph Research and Development Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada | hany.anany@agr.gc.ca | 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 |  |
| 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| W - Withdrawn |  |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 2:** **GENERAL PROPOSAL**

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

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

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

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**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** |
| **Motookavirus** | **Named after the municipality in Itoshima district, Fukuoka prefecture, Japan where at Katsumi Doi Kyushu University the first virus of its type was isolated** |

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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*: Genus and species  *Description of current taxonomy*: None for these phages  *Proposed* *taxonomic change(s):* To create a new genus (*Motookavirus*) with two species  *Justification*: In accord with our definition of what constitutes a new genus and species [3] these two *Bacillus cereus* phages are classified into a new genus (Motookavirus) of jumbo phages |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: Genus and species  *Description of current taxonomy*: None for these phages  *Proposed* *taxonomic change(s)*: To create a new genus (*Motookavirus*) with two species  *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] – usually calculated using intergenomic distance calculator VIRIDIC [2].  *Justification*: In accord with our definition of what constitutes a new genus and species [3] these two Bacillus cereus phages are classified into a new genus (Motookavirus) of jumbo phages |

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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. 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: 12142423  6. 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** |
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| **Tables, Figures:** |

**Table 1.** Characteristics of the phages described in the proposal

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| Bacillus phage Edson | *Bacillus cereus* | Myovirus | Lytic | PV796108 | 233813 bp | 308 | 0 |
| Bacillus phage vB\_BceM\_WH1 | *Bacillus cereus* | Myovirus | Lytic | LC597490.1 | 229829 bp | 300 | 0 |

A close-up of a document

AI-generated content may be incorrect.A close up of a text

AI-generated content may be incorrect.**Figure 1:** 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 arrowhead**.

A black line with a white background

AI-generated content may be incorrect.

**Figure 2.** The phylogenetic tree was constructed using the major capsid proteins from these and related phages with NGPhylogeny.fr in “one click” mode [6]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. The alignment was exported to iTOL v7 [7]. The red arrowhead indicates the two phages of interest.