

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create the new species *Alphabaculovirus alterhycuneae* in the genus *Alphabaculovirus* (*Lefavirales*: *Baculoviridae*) | |
| **Code assigned:** | 2024.001D.N.v1.Alphabaculovirus-1nsp |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Peng X-W | Wuhan Institute of Virology, Chinese Academy of Sciences | [ppxxww@163.com](mailto:ppxxww@163.com) |  |
| Lei C-F | Wuhan Institute of Virology, Chinese Academy of Sciences | [cflei@wh.iov.cn](mailto:cflei@wh.iov.cn) |  |
| Hu J | Wuhan Institute of Virology, Chinese Academy of Sciences | [hujia@wh.iov.cn](mailto:hujia@wh.iov.cn) |  |
| Sun X-L | Wuhan Institute of Virology, Chinese Academy of Sciences | [sunxl@wh.iov.cn](mailto:sunxl@wh.iov.cn) | X |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses | X | Bacterial viruses |  |
| 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:** |
| *Baculoviridae* and *Nudiviridae* 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** |
| *Baculoviridae* and *Nudiviridae* Study Group | 6 | 0 | 2 |
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| **Submission date:** | 05/04/2023 |

**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:** | DD/MM/YYYY |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:** |
| 2024.001D.N.v1.Alphabaculovirus-1nsp.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:** | | **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  In the genus *Alphabaculovirus* (family *Baculoviridae*) there are 65 species*.*  *Proposed* *taxonomic change(s):*  New species  *Justification*:  The genome of the virus (Hypantria cuneae nulceopolyhedrovirus B, (HycuNPV-B)), was fully sequenced using a high-throughput method. The divergence of the phylogenetic tree and the K2P distances based on the 38 core-gene concatenated alignment revealed that the HycuNPV-B isolate belongs to a novel species of *Alphabaculovirus*. For this new species we suggest the species name “Alphabaculovirus alterhycuneae”, following the binomial naming proposal as submitted in 2022 and ratified by the ICTV in April 2023. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Species  *Description of current taxonomy*:  In the genus *Alphabaculovirus* (family *Baculoviridae*) there are 65 species*.*  *Proposed* *taxonomic change(s)*:  New species  *Demarcation criteria:*  The K2P distances proposed by Jehle et al. (2006) based on the *polh/gran*, *lef-8* and *lef-9* are a widely applied method for species demarcation for lepidopteran-specific baculoviruses (Jehle et al., 2006). Wennmann et al. (2018) has adjusted baculovirus species demarcation criteria based on the 38 core-gene data, and the standard thresholds of 0.015 and 0.050 were adjusted to 0.021 and 0.072, respectively, with the K2P demarcation thresholds of below 0.021 for the same species and above 0.072 for distinct species.  *Justification*:  The isolate of the new species proposed for the genus *Alphabaculovirus* (**Table 1**, isolate of proposed species highlighted in yellow) can be classified as belonging to this genus in the family *Baculoviridae* on the basis of the following criteria (Harrison et al., 2019):   * The family *Baculoviridae* comprises large viruses with circular dsDNA genomes ranging from 80 to 180 kbp; * The virions consist of enveloped, rod-shaped nucleocapsids and are embedded in distinctive occlusion bodies measuring 0.15-5 μm; * The occlusion bodies consist of a matrix composed of a single viral protein expressed at high levels during infection; * Members of this family exclusively infect larvae of insect orders Lepidoptera, Hymenoptera and Diptera.   Image of scanning electron microscopy (SEM) and transmission electron microscopy (TEM) observation results for the occlusion bodies of the newly proposed species showed  typical morphological characteristics as observed in other alphabaculoviruses **(Figure 1)**.    **Figure 2** shows the relationship of the representative isolate of the proposed new alphabaculovirus species to representative isolates of recognized species in the family *Baculoviridae*. The phylogenetic analysis was inferred based on the concatenated sequences of 38 baculovirus core genes (Guindon et al., 2010; Katoh et al., 2002).  The K2P distances proposed by Jehle et al. (2006) based on the *polh/gran*, *lef-8* and *lef-9* are a widely applied method for species demarcation for lepidopteran-specific baculoviruses (Jehle et al., 2006). Wennmann et al. (2018) has adjusted baculovirus species demarcation criteria based on the 38 core-gene data, and the standard thresholds of 0.015 and 0.050 were adjusted to 0.021 and 0.072, respectively, with the K2P demarcation thresholds of below 0.021 for the same species and above 0.072 for distinct species. For K2P parameters in-between, more biological information is required to come to a conclusion (Wennmann et al., 2018).  The K2P distances based on the 38 core-gene concatenated alignment among the proposed species’ representative isolates and the representative isolate of the proposed new species of in the genus *Alphabaculovirus* are shown in **Table 2**. The distances measure >0.072 substitutions/site for each locus, indicating that the isolate under consideration is a representative of a new, previously unrecognized species of *Alphabaculovirus* and not a variant of currently existing species. |

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| **References:** |
| Harrison RL, Herniou EA, Jehle JA, Theilmann DA, Burand JP, Becnel JJ, Krell PJ, van Oers MM, Mowery JD, Bauchan GR, and ICTV Report Consortium (2019) ICTV Virus Taxonomy Profile: *Baculoviridae.* J Gen Virol 99:1185-1186. https://doi.org/10.1099/jgv.0.001107  Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: Assessing the performance of PhyML 3.0. Syst Biol 59: 307-321. https://doi.org/10.1093/sysbio/syq010  Jehle JA, Lange M, Wang H, Hu Z, Wang Y, Hauschild R ( 2006) Molecular identification and phylogenetic analysis of baculoviruses from Lepidoptera. Virology 346:180-193. https://doi.org/10.1016/j.virol.2005.10.032  Katoh K, Misawa K, Kuma KI, Miyata T (2002) MAFFT: A novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res 30:3059-3066. https://doi.org/10.1093/nar/gkf436  Wennmann JT, Keilwagen J, Jehle JA (2018) Baculovirus Kimura two-parameter species demarcation criterion is confirmed by the distances of 38 core gene nucleotide sequences. J Gen Virol 99:1307-1320. https://doi.org/10.1099/jgv.0.001100.    Peng XW, Zhang WY, Lei CF, Min SF, Hu J, Wang QH, Sun XL (2022). Genomic analysis of two Chinese isolates of Hyphantria cunea nucleopolyhedrovirus reveals a novel species of alphabaculovirus that infects *Hyphantria cunea drury* (Lepidoptera: Arctiidae). BMC Genomics 23:367. https://doi.org/10.1186/s12864-022-08604-7. |

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| **Tables, Figures:** |

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**Table 1.** Alphabaculovirus genomes used in core gene phylogeny and pairwise distance estimation. Isolate for newly proposed species is highlighted in yellow.

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| **Species** | **Isolate** | **Abbreviation** | **Accession** |
| *Alphabaculovirus aucalifornicae* | Autographa californica multiple nucleopolyhedrovirus C6 | AcMNPV | NC\_001623.1 |
| *Alphabaculovirus angemmatalis* | Anticarsia gemmatalis multiple nucleopolyhedrovirus 37 | AgMNPV | NC\_031761.1 |
| *Alphabaculovirus anpernyi* | Antheraea pernyi nucleopolyhedrovirus Liaoning | AnpeNPV | NC\_008035.3 |
| *Alphabaculovirus bomori* | Bombyx mori nucleopolyhedrovirus T3 | BmNPV | NC\_001962.1 |
| Not assigned | Bombyx mandarina nucleopolyhedrovirus S1 | BomaNPV | FJ882854.1 |
| *Alphabaculovirus capomonae* | Catopsilia pomona nucleopolyhedrovirus 416 | CapoNPV | KU565883.1 |
| *Alphabaculovirus alterchofumiferanae* | Choristoneura fumiferana DEF multiple nucleopolyhedrovirus | CfDEFMNPV | NC\_005137.2 |
| *Alphabaculovirus chofumiferanae* | Choristoneura fumiferana multiple nucleopolyhedrovirus Ireland | CfMNPV | NC\_004778.3 |
| *Alphabaculovirus chomurinanae* | Choristoneura murinana nucleopolyhedrovirus Darmstadt | ChmuNPV | NC\_023177.1 |
| Not assigned | Choristoneura occidentalis nucleopolyhedrovirus BC\_1 | ChocNPV | KC961303.1 |
| *Alphabaculovirus chorosaceanae* | Choristoneura rosaceana nucleopolyhedrovirus NB\_1 | ChroNPV | NC\_021924.1 |
| *Alphabaculovirus covestigialis* | Condylorrhiza vestigialis multiple nucleopolyhedrovirus PR.2002 | CoveMNPV | NC\_026430.1 |
| *Deltabaculovirus cunigripalpi* | Culex nigripalpus nucleopolyhedrovirus Florida1997 | CuniNPV | NC\_003084.1 |
| Not assigned | Dasychira pudibunda nucleopolyhedrovirus ML1 | DapuNPV | KP747440.1 |
| Not assigned | Dendrolimus kikuchii nucleopolyhedrovirus YN | DekiNPV | JX193905.1 |
| *Alphabaculovirus eppostvittanae* | Epiphyas postvittana polyhedrovirus | EppoNPV | NC\_003083.1 |
| *Alphabaculovirus helarmigerae* | Helicoverpa armigera nucleopolyhedrovirus G4 | HearNPV | NC\_002654.2 |
| *Alphabaculovirus lonobliquae* | Lonomia obliqua nucleopolyhedrovirus SP/2000 | LoobNPV | NC\_043520.1 |
| *Alphabaculovirus lydisparis* | Lymantria dispar multiple nucleopolyhedrovirus | LdMNPV | NC\_001973.1 |
| *Alphabaculovirus maconfiguratae* | Mamestra configurata nucleopolyhedrovirus 90/2 | MacoNPV-A | NC\_003529.1 |
| *Alphabaculovirus altermaconfiguratae* | Mamestra configurata nucleopolyhedrovirus 96B | MacoNPV-B | NC\_004117.1 |
| *Alphabaculovirus mavitratae* | Maruca vitrata multiple nucleopolyhedrovirus MV-8 | MaviMNPV | NC\_008725.1 |
| *Alphabaculovirus mabrassicae* | Mamestra brassicae multiple nucleopolyhedrovirus CHb1 | MbMNPV | JX138237.2 |
| *Alphabaculovirus orpseudotsugatae* | Orgyia pseudotsugata multiple nucleopolyhedrovirus | OpMNPV | NC\_001875.2 |
| Not assigned | Philosamia cynthia ricini nucleopolyhedrovirus GX-1 | PhcyNPV | JX404026.1 |
| Not assigned | Plutella xylostella nucleopolyhedrovirus CL3 | PlxyMNPV | DQ457003.1 |
| Belongs to *Alphabaculovirus aucalifornicae* | Rachiplusia ou multiple nucleopolyhedrovirus R1 | RoMNPV | AY145471.1 |
| *Alphabaculovirus spexiguae* | Spodoptera exigua multiple nucleopolyhedrovirus US1 | SeMNPV | NC\_002169.1 |
| *Alphabaculovirus spofrugiperdae* | Spodoptera frugiperda multiple nucleopolyhedrovirus 3AP2 | SfMNPV | NC\_009011.2 |
| Not assigned | Spilosoma obliqua nucleopolyhedrovirus IIPR | SpobNPV | KY550224.1 |
| *Alphabaculovirus thorichlaceae* | Thysanoplusia orichalcea nucleopolyhedrovirus p2 | ThorNPV | NC\_019945.1 |
| *Alphabaculovirus hycuneae* | Hyphantria cunea nucleopolyhedrovirus N9 | HycuNPV | NC\_007767.1 |
| *Alphabaculovirus alterhycuneae* | Hypantria cunea nucleopolyhedrovirus, isolate HB | HycuNPV-B | OL686893.1 |

图片包含 照片, 海胆, 食物, 盘子

描述已自动生成

**Figure 1.** Image of scanning electron microscopy (SEM) and transmission electron microscopy (TEM) observations for the occlusion bodies of the newly proposed species. (A) SEM (× 25,000) showing occlusion body shapes, the rod-shaped indentations on the surfaces of some OBs reveal an immature OB. (B) TEM (× 14,500) showing a cross section of occlusion bodies. ODV: occlusion-derived virus, NC: nucleocapsids, PE: polyhedral envelop, PM: polyhedral matrix (Peng et al., 2022).

A diagram of a number of viruses

Description automatically generated**Figure 2**. Relationships of alphabaculovirus isolates inferred from the predicted amino acid sequences of the 38 baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 38 baculovirus core gene amino acid sequences by maximum likelihood using PhyML 3.1 and the L+G substitution matrix. The representative isolate of the new proposed species is highlighted in red lettering, the deltabaculovirus CuniNPV is used as an outgroup. Bootstrap values are indicated for each interior branch.

**Table 2.** Kimura 2-parameter distances based on concatenated nucleotide sequences of the 38 core genes. The K-2-P values among the representative isolates of currently recognized species are shaded in gray (lower triangle). The other values are the corresponding standard errors (upper triangle). The representative isolate of the newly proposed species was highlighted in red. Distances were estimated with MEGA7 using the Kimura-2-parameter model.

