

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create four new species and abolish one current species in family *Baculoviridae* |
| **Code assigned:**  | 2025.001D.v2.Baculoviridae\_4nsp\_1absp |

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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 | **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** |
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| **Submission date:** |  26/05/2025 |

**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| W - Withdrawn |  |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:**  |
| The minor text edit suggestions have been accepted |

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| **Revision date:** | 26-5-2025 |

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

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon | **X** | 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** |
| *Alphabaculovirus calabietis* | Epithet derived from the host moth species ***Cal****liteara* ***abietis*** |
| *Alphabaculovirus mysequacis* | Epithet derived from the host moth species ***My****thimna* ***sequa****x* |
| *Alphabaculovirus plidaeusalis* | Epithet derived from the host moth species ***Pl****atynota* ***idaeusalis*** |
| *Betabaculovirus plidaeusalis* | Epithet derived from the host moth species ***Pl****atynota* ***idaeusalis*** |

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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*: There are currently 68 species in the genus *Alphabaculovirus* and 29 species in the genus *Betabaculovirus* of the family *Baculoviridae* *Proposed* *taxonomic change(s):* We propose to create three new species in the genus *Alphabaculovirus*, create one new species in the genus *Betabaculovirus*, and abolish one species in the genus *Betabaculovirus**Justification*: Analysis of recently sequenced baculovirus genomes have identified four viruses that each represent a previously undescribed baculovirus species, in accordance with the species demarcation criteria defined for the family *Baculoviridae*. Nucleotide sequences derived from isolates of *Betabaculovirus trini* and *Betabaculovirus myunipunctae* are almost completely identical, indicating that one of these species should be abolished. We have chosen to abolish *Betabaculovirus trini* due to the significant place thatthe exemplar isolate of *Betabaculovirus myunipunctae* occupies in the history of baculovirus research. |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Species*Description of current taxonomy*: The family *Baculoviridae* currently contains 101 species in 4 genera [1]. Most of the species are classified into genera *Alphabaculovirus* and *Betabaculovirus*, which contain 68 and 29 species, respectively. Baculoviruses are classified into one of these two genera if they conform to the following criteria:* Host species of the insect order Lepidoptera
* Circular double-stranded DNA genome ranging in size from 80 to 180 kbp with a gene content characteristic of other alphabaculoviruses or betabaculoviruses;
* Relationships to other alpha- or betabaculoviruses as inferred by molecular phylogeny;
* Occlusion bodies formed within the nucleus (*Alphabaculovirus*) or the nucleocytoplasmic milieu formed after degradation of the nuclear envelope (*Betabaculovirus*), with a shape and size characteristic for the genus;
* Rod-shaped virions consisting of enveloped nucleocapsids, with single (*Betabaculovirus*) or multiple (*Alphabaculovirus*) virions contained in each occlusion body.

Baculovirus isolate names usually include the genus and species of the host of origin. For example, Autographa californica multiple nucleopolyhedrovirus was originally isolated from larvae of *Autographa californica*, a moth known as the alfalfa looper. Specific epithets for member species of *Baculoviridae* are Latinized words formed by merging the first two to four letters of the host genus name with the genitive form of the host specific epithet [2]. For example, the species for alphabaculovirus Autographa californica multiple nucleopolyhedrovirus is *Alphabaculovirus aucalifornicae*. *Proposed* *taxonomic change(s)*: We propose to create the following species for classification in *Alphabaculovirus* or *Betabaculovirus* genera:1) ***Alphabaculovirus calabietis*** **Exemplar isolate:** Calliteara abietis nucleopolyhedrovirus, isolate IOZ-23MG (CaabNPV-IOZ-23MG) [3]**Etymology:** The host epithet “abietis” is already the genitive of “abies”, meaning “fir”, although in this case it refers to the Norway spruce (*Picea abies*), one of the primary plant hosts of *Calliteara abietis* larvae (https://lepidoptera.eu/species/781; last accessed 28 April 2025). 2) ***Alphabaculovirus mysequacis*** **Exemplar isolate:** Mythimna sequax nucleopolyhedrovirus, isolate CNPSo-98 (MysqNPV-CNPSo-98) [4]**Etymology:** “*Sequax*” is the Latin word for "following", which refers to the behavior of the *Mythimna sequax* host larvae (https://bugguide.net/node/view/379966; last accessed 28 April 2025). The genitive form is *sequacis*, thus we’ve adapted *mysequacis* as the epithet for this species.3) ***Alphabaculovirus plidaeusalis*****Exemplar isolate:** Platynota idaeusalis nucleopolyhedrovirus, isolate 2680 (PlidNPV-2680) [5]**Etymology:** “*Idaeusalis*” possibly refers to the red raspberry, *Rubus idaeus*, which is one of host plants of *Platynota idaeusalis* (https://bugguide.net/node/view/25808; last accessed 28 April 2025). The genitive of the suffix *-alis* is *-alis*, so we have adapted *plidaeusalis* as the epithet for this baculovirus species.4) ***Betabaculovirus plidaeusalis*****Exemplar isolate:** Platynota idaeusalis granulovirus, isolate 2683 (PlidGV-2683) [5]**Etymology:** As described above for *Alphabaculovirus plidaeusalis*, with a betabaculovirus from the same host.We also propose to **abolish** species ***Betabaculovirus trini***. *Demarcation criteria:*Species demarcation criteria for baculoviruses are based on pairwise nucleotide distances estimated from alignments of parts of three conserved genes [6] or all 38 core genes of family *Baculoviridae* [7]. With the three-gene alignment, a cut-off value of >0.050 substitutions/site indicates that the viruses being compared belonged to different species, while distances <0.015 indicated that they belonged to the same species. For K2P distances between these two cut-off points, additional evidence is required to support the classification of the isolates being compared into different species. Cut-off points for distances based on a concatenated 38-core gene alignment are <0.021 (same species) and >0.072 (different species) substitutions/site.*Justification*: Phylogenetic inference based on core gene amino acid alignments placed exemplar isolates of the proposed new species in clades with other alphabaculoviruses (Figure 1) or betabaculoviruses (Figure 2). Analysis of their nucleotide sequences yielded K2P distances above the cut-off point for new species in pairwise three-gene alignments, with distances of >0.289 (CaabNPV-IOZ-23MG), >0.072 (MysqNPV-CNPSo-98), >0.33 (PlidNPV-2680), and >0.38 (PlidGV-2683) [3-5]. These values confirm that these viruses represent previously undescribed species in their respective genera.  All the nucleotide sequences for viruses of *Betabaculovirus trini* and *Betabaculovirus myunipunctae* are identical or almost identical [8,9], indicating that these two species are redundant and one of them should be abolished. Although the addition of *Betabaculovirus trini* to the ICTV catalog precedes that of *Betabaculovirus myunipunctae,* the genome sequence for the *Betabaculovirus myunipunctae* exemplar isolate, Pseudaletia unipuncta granulovirus-Hawaiian (PsunGV-H), was released first on GenBank. PsunGV-H was featured in a lot of pioneering work on baculovirus enhancins [10], and we feel that the species for it deserves to be retained in the ICTV catalog. |

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| **References:**  |
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.001D.Nv1.Baculovirdae\_4nsp\_1absp.xlsx | Accompanying Excel sheet |
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| **Tables, Figures:**  |

See next pages **Figure 1.** Phylogeny showing the relationships of baculoviruses belonging to group II of the genus *Alphabaculovirus* (*Lefavirales*: *Baculoviridae*). Shown is a maximum likelihood tree inferred from the concatenated alignments of 38 baculovirus core gene amino acid sequences with RAxML [11] using the Le and Gascuel (LG) substitution model [12]. GenBank accession numbers for genome sequences precede each virus name. Reliability of the tree was assessed with 100 rapid bootstrap replicates, with bootstrap support shown for each node. Clade IIa and clade IIb of the group II alphabaculoviruses are indicated with brackets [13]. Exemplar viruses of currently existing alphabaculovirus species are denoted by blue circles. Currently unclassified viruses are indicated by open circles. Exemplar viruses of proposed alphabaculovirus species are indicated with red bold type.

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**Figure 2.** Phylogeny showing the relationships of baculoviruses belonging to genus *Betabaculovirus* (*Lefavirales*: *Baculoviridae*). Shown is a maximum likelihood tree inferred as described for Figure 1, with bootstrap support shown for each node and genome sequence GenBank accession numbers preceding each virus name. The two basal clades in which betabaculoviruses occur, clade a and clade b [14] are indicated with brackets. Exemplar viruses of currently existing betabaculovirus species are denoted by red circles. Currently unclassified viruses are indicated by open circles. The exemplar virus of the proposed betabaculovirus species are indicated with red bold font. The exemplar virus of the species proposed to be abolished is also indicated by a strikethrough red line.