

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.004D** |  |
| **Short title:** Create four new species in the genus *Alphabaculovirus* and two new species in the genus *Betabaculovirus* (*Lefavirales*: *Baculoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| *Baculoviridae* and *Nudiviridae* Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** |  |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | 05/28/2021 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2021.004D.R.Baculoviridae\_6nsp.xlsx |

**Abstract**

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| We propose the creation of four new species, *Alphabaculovirus ardigramma, Alphabaculovirus dijuno, Alphabaculovirus ranu* and *Alphabaculovirus speridania-b*  in the genus *Alphabaculovirus*, and two new species, *Betabaculovirus hycunea* and *Betabaculovirus maphaseoli* in the genus *Betabaculovirus*, all in the family *Baculoviridae* (*Naldaviricetes***:** *Lefavirales*). |

**Text of proposal**

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| |  | | --- | | Recently published analyses of baculovirus genome sequences [2, 5-9] support the creation of six new species in family *Baculoviridae*, including four new species in the genus *Alphabaculovirus* (Table 1) and two new species in the genus *Betabaculovirus* (Table 2) (new species highlighted in yellow). Isolates of the proposed species can be classified as belonging to these two genera on the basis of three or more of the following criteria:  • host species of the insect order Lepidoptera;  • circular double-stranded DNA genome ranging in size from 110 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 nucleo-cytoplasmic milieu (*Betabaculovirus*), with a characteristic shape and size (polyhedral, approximately 0.15 to 5 μm in size for alphabaculoviruses; or ovocylindrical, approximately 0.13 x 0.50 μm for betabaculoviruses);  • rod-shaped virions consisting of enveloped nucleocapsids, with multiple virions (*Alphabaculovirus*) or a single virion (*Betabaculovirus*) contained in each occlusion body.  Figures 1 and 2 show the relationships of exemplar isolates of the proposed *Alphabaculovirus* and *Betabaculovirus* species to exemplar isolates of other recognized species in the family *Baculoviridae*. Phylogenies were inferred from the concatenated alignment of the predicted amino acid sequences of 38 baculovirus core genes [1, 3].  Distinctions among species of the *Baculoviridae* have been based on host range, DNA restriction endonuclease fragment patterns, and comparisons of nucleotide and predicted amino acid sequences from various genes. In addition, a species demarcation criterion for baculoviruses have been developed based on pairwise nucleotide distances estimated with the Kimura-2-parameter (K2P) substitution model from partial sequences of three conserved baculovirus genes: *lef-8* and *lef-9* (encoding viral RNA polymerase subunits), and *polyhedrin/granulin* (encoding the viral occlusion body matrix protein) [4]. If nucleotide distances between two viruses are greater than 0.050 substitutions/site at these loci, the viruses are considered to belong to different species. Classification of baculoviruses by this approach has been validated by a broader analysis of K2P distances with all the baculovirus core genes [10].  The range of K2P pairwise nucleotide distances for partial *lef-8*, *lef-9*, and *polyhedrin/granulin* between the proposed species’ exemplar isolates and the representative isolates of the other proposed species and of currently recognized species of genus *Alphabaculovirus* or *Betabaculovirus* are shown in Table 3. The distances measure >0.05 substitutions/site for each locus of each of the exemplar isolates, indicating that the isolates under consideration are representatives of new, previously unrecognized species of *Alphabaculovirus* and *Betabaculovirus* and not variants of currently existing species.  Rationale for the species names in this proposal  The specific epithets used for the species names in this proposal consist of the first two letters of the genus of the host of origin followed by the specific epithet of the host of origin. For example, for the alphabaculovirus species originating from host *Artaxa digramma*, the specific epithet is *ardigramma*. A dash with a letter (e.g. -b) is appended in cases where isolates of more than one species have been identified in the same host.  While the *Baculoviridae* and *Nudiviridae* Study Group has yet to make a final decision on the form of specific epithets for baculovirus and nudivirus species names, the form described above is one option that was discussed by the prior incarnation of the Study Group and is being used on a provisional basis for the purposes of this proposal. A proposal to change all baculovirus and nudivirus species to a binomial format will be developed and submitted at some point before the 2022 EC meeting. | |

**Supporting evidence**

**Table 1.** Exemplar isolates and species of genus *Alphabaculovirus* with complete genome sequences. Proposed new species are highlighted in yellow.

| **Isolate** | **Species** | **Accession no.** | **Abbreviation** |
| --- | --- | --- | --- |
| Adoxophyes honmai nucleopolyhedrovirus ADN001 | *Adoxophyes honmai nucleopolyhedrovirus* | AP006270 | AdhoNPV-ADN001 |
| Agrotis ipsilon multiple nucleopolyhedrovirus Illinois | *Agrotis ipsilon multiple nucleopolyhedrovirus* | EU839994 | AgipMNPV-Illinois |
| Agrotis segetum nucleopolyhedrovirus A | *Agrotis segetum nucleopolyhedrovirus A* | DQ123841 | AgseNPV-A |
| Agrotis segetum nucleopolyhedrovirus B | *Agrotis segetum nucleopolyhedrovirus B* | KM102981 | AgseNPV-B |
| Antheraea pernyi nucleopolyhedrovirus Liaoning | *Antheraea pernyi nucleopolyhedrovirus* | DQ486030 | AnpeNPV-Liaoning |
| Anticarsia gemmatalis multiple nucleopolyhedrovirus 2D | *Anticarsia gemmatalis multiple nucleopolyhedrovirus* | DQ813662 | AgMNPV-2D |
| **Artaxa digramma nucleopolyhedrovirus 424** | ***Alphabaculovirus ardigramma*** | **MN233792** | **ArdiNPV-424** |
| Autographa californica multiple nucleopolyhedrovirus C6 | *Autographa californica multiple nucleopolyhedrovirus* | L22858 | AcMNPV-C6 |
| Bombyx mori nucleopolyhedrovirus T3 | *Bombyx mori nucleopolyhedrovirus* | L33180 | BmNPV-T3 |
| Buzura suppressaria nucleopolyhedrovirus Hubei | *Buzura suppressaria nucleopolyhedrovirus* | KF611977 | BusuNPV-Hubei |
| Choristoneura fumiferana DEF multiple nucleopolyhedrovirus | *Choristoneura fumiferana DEF multiple nucleopolyhedrovirus* | AY327402 | CfDEFNPV |
| Choristoneura fumiferana multiple nucleopolyhedrovirus Ireland | *Choristoneura fumiferana multiple nucleopolyhedrovirus* | AF512031 | CfMNPV-Ireland |
| Choristoneura rosaceana nucleopolyhedrovirus NB1 | *Choristoneura rosaceana nucleopolyhedrovirus* | KC961304 | ChroNPV-NB1 |
| Chrysodeixis chalcites nucleopolyhedrovirus | *Chrysodeixis chalcites nucleopolyhedrovirus* | AY864330 | ChchNPV |
| Choristoneura murinana alphabaculovirus Darmstadt | *Choristoneura murinana nucleopolyhedrovirus* | KF894742 | ChmuNPV-Darmstadt |
| Clanis bilineata nucleopolyhedrovirus DZ1 | *Clanis bilineata nucleopolyhedrovirus* | DQ504428 | ClbiNPV-DZ1 |
| Dasychira pudibunda nucleopolyhedrovirus ML1 | *Orgyia pseudotsugata multiple nucleopolyhedrovirus* | KP747440 | DapuNPV-ML1 |
| **Dione juno nucleopolyhedrovirus Araguari-MG** | ***Alphabaculovirus dijuno*** | **MK558262** | **DijuNPV-Araguari-MG** |
| Ectropis obliqua nucleopolyhedrovirus A1 | *Ectropis obliqua nucleopolyhedrovirus* | DQ837165 | EcobNPV-A1 |
| Epiphyas postvittana nucleopolyhedrovirus | *Epiphyas postvittana nucleopolyhedrovirus* | AY043265 | EppoNPV |
| Euproctis pseudoconspersa nucleopolyhedrovirus Hangzhou | *Euproctis pseudoconspersa nucleopolyhedrovirus* | FJ227128 | EupsNPV-Hangzhou |
| Helicoverpa armigera nucleopolyhedrovirus C1 | *Helicoverpa armigera nucleopolyhedrovirus* | AF271059 | HearNPV-C1 |
| Hyphantria cunea nucleopolyhedrovirus N9 | *Hyphantria cunea nucleopolyhedrovirus* | AP009046 | HycuNPV-N9 |
| Lambdina fiscellaria nucleopolyhedrovirus GR15 | *Lambdina fiscellaria nucleopolyhedrovirus* | KP752043 | LafiNPV-GR15 |
| Leucania separata nucleopolyhedrovirus AH1 | *Leucania separata nucleopolyhedrovirus* | AY394490 | LeseNPV-AH1 |
| Lymantria dispar multiple nucleopolyhedrovirus 5-6 | *Lymantria dispar multiple nucleopolyhedrovirus* | AF081810 | LdMNPV 5-6 |
| Lymantria xylina multiple nucleopolyhedrovirus-5 | *Lymantria xylina nucleopolyhedrovirus* | GQ202541 | LyxyMNPV-5 |
| Mamestra brassicae multiple nucleopolyhedrovirus K1 | *Mamestra brassicae multiple nucleopolyhedrovirus* | JQ798165 | MabrNPV-K1 |
| Mamestra configurata nucleopolyhedrovirus A 90/2 | *Mamestra configurata nucleopolyhedrovirus A* | U59461 | MacoNPV-A 90/2 |
| Mamestra configurata nucleopolyhedrovirus B 96B | *Mamestra configurata nucleopolyhedrovirus B* | AY126275 | MacoNPV-B 96B |
| Maruca vitrata nucleopolyhedrovirus Taiwan | *Maruca vitrata nucleopolyhedrovirus* | EF125867 | MaviNPV-Taiwan |
| Orgyia leucostigma nucleopolyhedrovirus CFS-77 | *Orgyia leucostigma nucleopolyhedrovirus* | EU309041 | OrleNPV-CFS77 |
| Orgyia pseudotsugata multiple nucleopolyhedrovirus | *Orgyia pseudotsugata multiple nucleopolyhedrovirus* | U75930 | OpMNPV |
| Pseudoplusia includens single nucleopolyhedrovirus-IE | *Chrysodeixis includes nucleopolyhedrovirus* | KJ631622 | PsinNPV-IE |
| **Rachiplusia nu nucleopolyhedrovirus VPN54** | ***Alphabaculovirus ranu*** | **MK419956** | **RanuNPV-VPN54** |
| Spodoptera eridania nucleopolyhedrovirus 251 | *Spodoptera eridania nucleopolyhedrovirus* | MH320559 | SperNPV-251 |
| **Spodoptera eridania nucleopolyhedrovirus CNPSo-165** | ***Alphabaculovirus speridania-b*** | **MT040195** | **SperNPV- CNPSo-165** |
| Spodoptera exempta nucleopolyhedrovirus 244.1 | *Spodoptera exempta nucleopolyhedrovirus* | MH717816 | SpexNPV-244.1 |
| Spodoptera exigua multiple nucleopolyhedrovirus Qingdao | *Spodoptera exigua multiple nucleopolyhedrovirus B* | MH370144 | SeMNPV-QD |
| Spodoptera exigua multiple nucleopolyhedrovirus US1 | *Spodoptera exigua multiple nucleopolyhedrovirus A* | AF169823 | SeMNPV-US1 |
| Spodoptera frugiperda multiple nucleopolyhedrovirus 3AP2 | *Spodoptera frugiperda multiple nucleopolyhedrovirus* | EF035042 | SfMNPV-3AP2 |
| Spodoptera litura nucleopolyhedrovirus G2 | *Spodoptera litura nucleopolyhedrovirus* | AF325155 | SpltNPV-G2 |
| Sucra jujuba nucleopolyhedrovirus 473 | *Sucra jujuba nucleopolyhedrovirus* | KJ676450 | SujuNPV-473 |
| Thysanoplusia orichalcea nucleopolyhedrovirus P2 | *Thysanoplusia orichalcea nucleopolyhedrovirus* | JX467702 | ThorNPV-P2 |
| Trichoplusia ni single nucleopolyhedrovirus | *Trichoplusia ni single nucleopolyhedrovirus* | DQ017380 | TnSNPV |

**Table 2.** Exemplar isolates and species of genus *Betabaculovirus* with complete genome sequences. Proposed new species are highlighted in yellow.

|  |  |  |  |
| --- | --- | --- | --- |
| **Isolate** | **Species** | **Accession no.** | **Abbreviation** |
| Adoxophyes orana granulovirus-English | *Adoxophyes orana granulovirus* | AF547984 | AdorGV-English |
| Agrotis segetum granulovirus-DA | *Agrotis segetum granulovirus* | KR584663 | AgseGV-DA |
| Pieris rapae granulovirus-Wuhan | *Artogeia rapae granulovirus* | GQ884143 | PiraGV-Wuhan |
| Choristoneura occidentalis granulovirus | *Choristoneura fumiferana granulovirus* | DQ333351 | ChocGV |
| Clostera anachoreta granulovirus HBHN | *Clostera anachoreta granulovirus* | HQ116624 | ClanGV-HBHN |
| Clostera anastomosis granulovirus Henan | *Clostera anastomosis granulovirus A* | KC179784 | ClasGV-A (CalGV-Henan) |
| Clostera anastomosis granulovirus B | *Clostera anastomosis granulovirus B* | KR091910 | ClasGV-B |
| Cnaphalocrocis medinalis granulovirus-Enping | *Cnaphalocrocis medinalis granulovirus* | KU593505 | CnmeGV-Enping |
| Cryptophlebia leucotreta granulovirus CV3 | *Cryptophlebia leucotreta granulovirus* | AY229987 | CrleGV-CV3 |
| Cydia pomonella granulovirus M1 | *Cydia pomonella granulovirus* | U53466 | CpGV-M1 |
| Diatraea saccharalis granulovirus Parana-2009 | *Diatraea saccharalis granulovirus* | KP296186 | DisaGV-Parana-2009 |
| Epinotia aporema granulovirus Oliveros.Santa Fe | *Epinotia aporema granulovirus* | JN408834 | EpapGV-Oliveros.Santa Fe |
| Erinnyis ello granulovirus S68 | *Erinnyis ello granulovirus* | KJ406702 | ErelGV-S68 |
| Helicoverpa armigera granulovirus | *Helicoverpa armigera granulovirus* | EU255577 | HearGV |
| **Hyphantria cunea granulovirus Hc1** | ***Betabaculovirus hycunea*** | **MH923363** | **HycuGV-Hc1** |
| **Matsumuraeses phaseoli granulovirus IOZ01** | ***Betabaculovirus maphaseoli*** | **MT844067** | **MaphGV-IOZ01** |
| Mocis latipes granulovirus-SouthernBrazil | *Mocis latipes granulovirus* | KR011718 | MolaGV-SouthernBrazil |
| Pseudalatia unipuncta granulovirus Hawaiian | *Mythimna unipuncta granulovirus A* | EU678671 | PsunGV-H |
| Mythimna unipuncta granulovirus #8 | *Mythimna unipuncta granulovirus B* | KX855660 | MyunGV#8 |
| Phthorimaea operculella granulovirus-T | *Phthorimaea operculella granulovirus* | AF499596 | PhopGV-T |
| Plodia interpunctella-Cambridge | *Plodia interpunctella granulovirus* | KX151395 | PiGV-Cambridge |
| Plutella xylostella granulovirus K1 | *Plutella xylostella granulovirus* | AF270937 | PlxyGV-K1 |
| Spodoptera frugiperda granulovirus VG008 | *Spodoptera frugiperda granulovirus* | KM371112 | SpfrGV-VG008 |
| Spodoptera litura granulovirus K1 | *Spodoptera litura granulovirus* | DQ288858 | SpltGV-K1 |
| Trichoplusia ni granulovirus-LBIV-12 | *Trichoplusia ni granulovirus* | KU752557 | TnGV-LBIV-12 |
| Xestia c-nigrum granulovirus 4 | *Xestia c-nigrum granulovirus* | AF162221 | XecnGV-4 |

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**Figure 1.** Relationships of alphabaculovirus isolates (Table 1) inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated MUSCLE alignments of 38 baculovirus core gene amino acid sequences by maximum evolution using the Le and Gascuel (LG) substitution matrix as implemented in MEGA X, with a gamma shape parameter of 0.85. Bootstrap values are shown for each node. Exemplar isolates of the new proposed species are listed in red font.

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**Figure 2.** Relationships of betabaculovirus isolates (Table 2) inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated MUSCLE alignments of 38 baculovirus core gene amino acid sequences by maximum evolution using the Le and Gascuel (LG) substitution matrix as implemented in MEGA X, with a gamma shape parameter of 0.85. Bootstrap values are shown for each node. Exemplar isolates of the new proposed species are listed in red font.

**Table 3.** Ranges of pairwise Kimura-2-parameter nucleotide distances (substitutes/site) between representative isolates of proposed species and established species of *Alphabaculovirus* and *Betabaculovirus*. Distances >0.05 indicate that the viruses being compared belong to different species.

|  |  |  |  |
| --- | --- | --- | --- |
| **Exemplar isolate (genus)** | **Loci** | | |
| ***lef-8*** | ***lef-9*** | ***polh*/*gran*** |
| ArdiNPV-424 (*Alphabaculovirus*) | 0.38 – 1.38 | 0.20 – 0.92 | 0.25 – 0.45 |
| DijuNPV\_Araguari-MG (*Alphabaculovirus*) | 0.21 – 1.71 | 0.12 – 1.23 | 0.15 – 0.50 |
| RanuNPV-VPN54 (*Alphabaculovirus*) | 0.80 – 1.75 | 0.35 – 0.97 | 0.18 – 0.42 |
| SperNPV-CNPSo-165 (*Alphabaculovirus*) | 0.36 – 1.47 | 0.17 – 0.89 | 0.12 – 0.51 |
| HycuGV-Hc1 (*Betabaculovirus*) | 0.76 – 1.61 | 0.55 – 0.77 | 0.46 – 0.65 |
| MaphGV-IOZ01 (*Betabaculovirus*) | 0.64 – 1.20 | 0.37 – 0.77 | 0.21 – 0.44 |

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