This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| --- | --- | --- |
| **Code assigned:** | ***2018.002D*** | (to be completed by ICTV officers) |
| **Short title:** 7 new species in genus *Alphabaculovirus* and 1 new species in genus *Betabaculovirus* of family *Baculoviridae* |
|  |
| **Author(s):** |
| Robert L. Harrison Elisabeth A. Herniou Peter J. KrellDavid A. Theilmann James J. Becnel Johannes A. Jehle Monique M. van OersJohn P. Burand |
| **Corresponding author with e-mail address:** |
| Robert L. Harrison (Robert.L.Harrison@ars.usda.gov) |
| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | ***Baculoviridae/Nudiviridae*** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 6/8/18 |
| Date of this revision (if different to above): |       |

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

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2018.002D.N.v1.Baculoviridae\_8sp |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.
 |

Isolates of the seven new species proposed for genus *Alphabaculovirus* (Table 1, isolates of proposed species highlighted in yellow) and the single new species proposed for the genus *Betabaculovirus* (Table 2) can be classified as belonging to these genera in the family *Baculoviridae* on the basis of three or more of the following criteria (Herniou et al., 2011):

* host species of the insect orderLepidoptera;
* 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 baculoviruses 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 15 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 representative isolates of the proposed Alphabaculovirus and Betabaculovirus species to representative 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 (Garavaglia et al., 2012; Javed et al., 2017).

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, species demarcation criteria for baculoviruses have been proposed that rely upon pairwise nucleotide distances estimated with the Kimura-2-parameter 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) (Jehle et al., 2006). If nucleotide distances between two viruses are less than 0.015 substitutions/site, the two baculoviruses are considered to be the same species. If nucleotide distances between two viruses are greater than 0.05 substitutions/site, the viruses are considered to be different species. If the nucleotide distances lie between 0.015 and 0.050 substitutions/site, additional characteristics of the two viruses (*i.e.* host range) must be considered to make a decision about their taxonomic status. The proposed criterion was originally based on an alignment of sequences from 117 separate baculovirus isolates and the phylogeny inferred from this alignment. Researchers have applied this criterion to other isolates to identify many new baculovirus species and variants of currently recognized species.

The range of Kimura-2-parameter pairwise nucleotide distances for *lef-8*, *lef-9*, and *polyhedrin/granulin* between the proposed species’ representative 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, indicating that the isolates under consideration are representatives of new, previously unrecognized species of *Alphabaculovirus* and *Betabaculovirus* and not variants of currently existing species.

**Table 1.** Alphabaculovirus isolates used in core gene phylogeny and pairwise distance estimation. Isolates for newly proposed species are highlighted in yellow.

|  |  |  |
| --- | --- | --- |
| **Isolate** | **Species** | **Abbreviation** |
| Adoxophyes honmai nucleopolyhedrovirus ADN001 | *Adoxophyes honmai nucleopolyhedrovirus* | AdhoNPV-ADN001 |
| Agrotis ipsilon multiple nucleopolyhedrovirus Illinois | *Agrotis ipsilon multiple nucleopolyhedrovirus* | AgipMNPV-Illinois |
| Agrotis segetum nucleopolyhedrovirus A | *Agrotis segetum nucleopolyhedrovirus A* | AgseNPV-A |
| Agrotis segetum nucleopolyhedrovirus B | *Agrotis segetum nucleopolyhedrovirus B* | AgseNPV-B |
| Antheraea pernyi nucleopolyhedrovirus Liaoning | *Antheraea pernyi nucleopolyhedrovirus* | AnpeNPV-Liaoning |
| Anticarsia gemmatalis multiple nucleopolyhedrovirus 2D | *Anticarsia gemmatalis multiple nucleopolyhedrovirus* | AgMNPV-2D |
| Autographa californica multiple nucleopolyhedrovirus C6 | *Autographa californica multiple nucleopolyhedrovirus* | AcMNPV-C6 |
| Bombyx mori nucleopolyhedrovirus T3 | *Bombyx mori nucleopolyhedrovirus* | BmNPV-T3 |
| Buzura suppressaria nucleopolyhedrovirus Hubei | *Buzura suppressaria nucleopolyhedrovirus* | BusuNPV-Hubei |
| Catopsilia pomona nucleopolyhedrovirus-416 | *Catopsilia pomona nucleopolyhedrovirus* | CapoNPV-416 |
| Choristoneura fumiferana DEF multiple nucleopolyhedrovirus | *Choristoneura fumiferana DEF multiple nucleopolyhedrovirus* | CfDEFNPV |
| Choristoneura fumiferana multiple nucleopolyhedrovirus Ireland | *Choristoneura fumiferana multiple nucleopolyhedrovirus* | CfMNPV-Ireland |
| Choristoneura murinana nucleopolyhedrovirus-Darmstadt | *Choristoneura murinana nucleopolyhedrovirus* | ChmuNPV-Darmstadt |
| Choristoneura rosaceana nucleopolyhedrovirus NB1 | *Choristoneura rosaceana nucleopolyhedrovirus* | ChroNPV-NB1 |
| Chrysodeixis chalcites nucleopolyhedrovirus | *Chrysodeixis chalcites nucleopolyhedrovirus* | ChchNPV |
| Pseudoplusia includens single nucleopolyhedrovirus-IE  | *Chrysodeixis includens nucleopolyhedrovirus* | PsinNPV-IE |
| Clanis bilineata nucleopolyhedrovirus DZ1 | *Clanis bilineata nucleopolyhedrovirus* | ClbiNPV-DZ1 |
| Ectropis obliqua nucleopolyhedrovirus A1 | *Ectropis obliqua nucleopolyhedrovirus* | EcobNPV-A1 |
| Epiphyas postvittana nucleopolyhedrovirus | *Epiphyas postvittana nucleopolyhedrovirus* | EppoNPV |
| Euproctis pseudoconspersa nucleopolyhedrovirus Hangzhou | *Euproctis pseudoconspersa nucleopolyhedrovirus* | EupsNPV-Hangzhou |
| Helicoverpa armigera nucleopolyhedrovirus G4 | *Helicoverpa armigera nucleopolyhedrovirus* | HearNPV-G4 |
| **Hemileuca sp. nucleopolyhedrovirus-MEM** | ***Hemileuca species nucleopolyhedrovirus*** | **HespNPV-MEM** |
| Hyphantria cunea nucleopolyhedrovirus N9 | *Hyphantria cunea nucleopolyhedrovirus* | HycuNPV-N9 |
| Lambdina fiscellaria nucleopolyhedrovirus GR15 | *Lambdina fiscellaria nucleopolyhedrovirus* | LafiNPV-GR15 |
| Leucania separata nucleopolyhedrovirus AH1 | *Leucania separata nucleopolyhedrovirus* | LeseNPV-AH1 |
| **Lonomia obliqua multiple nucleopolyhedrovirus-SP/2000** | ***Lonomia obliqua nucleopolyhedrovirus*** | **LoobNPV-SP/2000** |
| Lymantria dispar multiple nucleopolyhedrovirus 5-6 | *Lymantria dispar multiple nucleopolyhedrovirus* | LdMNPV 5-6 |
| Lymantria xylina multiple nucleopolyhedrovirus-5 | *Lymantria xylina nucleopolyhedrovirus* | LyxyMNPV-5 |
| Mamestra brassicae multiple nucleopolyhedrovirus K1 | *Mamestra brassicae multiple nucleopolyhedrovirus* | MabrNPV-K1 |
| Mamestra configurata nucleopolyhedrovirus A 90/2 | *Mamestra configurata nucleopolyhedrovirus A* | MacoNPV-A 90/2 |
| Mamestra configurata nucleopolyhedrovirus B 96B | *Mamestra configurata nucleopolyhedrovirus B* | MacoNPV-B 96B |
| Maruca vitrata nucleopolyhedrovirus Taiwan | *Maruca vitrata nucleopolyhedrovirus* | MaviNPV-Taiwan |
| **Mythimna unipuncta nucleopolyhedrovirus #7** | ***Mythimna unipuncta nucleopolyhedrovirus*** | **MyunNPV#7** |
| **Operophtera brumata nucleopolyhedrovirus-MA** | ***Operophtera brumata nucleopolyhedrovirus*** | **OpbuNPV-MA** |
| Orgyia leucostigma nucleopolyhedrovirus CFS-77 | *Orgyia leucostigma nucleopolyhedrovirus* | OrleNPV-CFS77 |
| Orgyia pseudotsugata multiple nucleopolyhedrovirus | *Orgyia pseudotsugata multiple nucleopolyhedrovirus* | OpMNPV |
| **Oxyplax ochracea nucleopolyhedrovirus-435** | ***Oxyplax ochracea nucleopolyhedrovirus*** | **OxocNPV-435** |
| **Peridroma species nucleopolyhedrovirus-GR167** | ***Peridroma saucia nucleopolyhedrovirus*** | **PespNPV-GR167** |
| **Perigonia lusca single nucleopolyhedrovirus** | ***Perigonia lusca nucleopolyhedrovirus*** | **PeluSNPV** |
| Spodoptera exigua multiple nucleopolyhedrovirus US1 | *Spodoptera exigua multiple nucleopolyhedrovirus* | SeMNPV-US1 |
| Spodoptera frugiperda multiple nucleopolyhedrovirus 3AP2 | *Spodoptera frugiperda multiple nucleopolyhedrovirus* | SfMNPV-3AP2 |
| Spodoptera littoralis nucleopolyhedrovirus AN1956 | *Spodoptera littoralis nucleopolyhedrovirus* | SpliNPV-AN1956 |
| Spodoptera litura nucleopolyhedrovirus G2 | *Spodoptera litura nucleopolyhedrovirus* | SpltNPV-G2 |
| Sucra jujuba nucleopolyhedrovirus 473 | *Sucra jujuba nucleopolyhedrovirus* | SujuNPV-473 |
| Thysanoplusia orichalcea nucleopolyhedrovirus P1 | *Thysanoplusia orichalcea nucleopolyhedrovirus* | ThorNPV-P1 |
| Trichoplusia ni single nucleopolyhedrovirus Canada | *Trichoplusia ni single nucleopolyhedrovirus* | TnSNPV-Canada |

**Table 2.** Betabaculovirus isolates used in core gene phylogeny and pairwise distance estimation. The isolate for the newly proposed species is indicated in bold type with a yellow background.

|  |  |  |
| --- | --- | --- |
| **Isolate** | **Species** | **Abbreviation** |
| Adoxophyes orana granulovirus-English | *Adoxophyes orana granulovirus* | AdorGV-English |
| Agrotis segetum granulovirus-DA | *Agrotis segetum granulovirus* | AgseGV-DA |
| Pieris rapae granulovirus-Wuhan | *Artogeia rapae granulovirus* | PiraGV-Wuhan |
| Choristoneura occidentalis granulovirus | *Choristoneura fumiferana granulovirus* | ChocGV |
| Clostera anachoreta granulovirus HBHN | *Clostera anachoreta granulovirus* | ClanGV-HBHN |
| Clostera anastomosis granulovirus Henan | *Clostera anastomosis granulovirus A* | ClasGV-A (CalGV-Henan) |
| Clostera anastomosis granulovirus B | *Clostera anastomosis granulovirus B* | ClasGV-B |
| Cnaphalocrocis medinalis granulovirus-Enping | *Cnaphalocrocis medinalis granulovirus* | CnmeGV-Enping |
| Cryptophlebia leucotreta granulovirus CV3 | *Cryptophlebia leucotreta granulovirus* | CrleGV-CV3 |
| Cydia pomonella granulovirus M1 | *Cydia pomonella granulovirus* | CpGV-M1 |
| Diatraea saccharalis granulovirus Parana-2009 | *Diatraea saccharalis granulovirus* | DisaGV-Parana-2009 |
| Epinotia aporema granulovirus Oliveros.Santa Fe | *Epinotia aporema granulovirus* | EpapGV-Oliveros.Santa Fe |
| Erinnyis ello granulovirus S68 | *Erinnyis ello granulovirus* | ErelGV-S68 |
| Helicoverpa armigera granulovirus | *Helicoverpa armigera granulovirus* | HearGV |
| **Mocis latipes granulovirus-SouthernBrazil** | ***Mocis latipes granulovirus*** | **MolaGV-SouthernBrazil** |
| Pseudalatia unipuncta granulovirus Hawaiian | *Mythimna unipuncta granulovirus A* | PsunGV-H |
| Mythimna unipuncta granulovirus #8 | *Mythimna unipuncta granulovirus B* | MyunGV#8 |
| Phthorimaea operculella granulovirus-T | *Phthorimaea operculella granulovirus* | PhopGV-T |
| Plodia interpunctella-Cambridge | *Plodia interpunctella granulovirus* | PiGV-Cambridge |
| Plutella xylostella granulovirus K1 | *Plutella xylostella granulovirus* | PlxyGV-K1 |
|  |  |  |
| Spodoptera frugiperda granulovirus VG008 | *Spodoptera frugiperda granulovirus* | SpfrGV-VG008 |
| Spodoptera litura granulovirus K1 | *Spodoptera litura granulovirus* | SpltGV-K1 |
| Trichoplusia ni granulovirus-LBIV-12 | *Trichoplusia ni granulovirus* | TnGV-LBIV-12 |
| Xestia c-nigrum granulovirus 4 | *Xestia c-nigrum granulovirus* | XecnGV-4 |

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 alignments of 38 baculovirus core gene amino acid sequences by maximum likelihood using RAxML and the Le and Gascuel (LG) substitution matrix. Bootstrap values are shown for each node. Representative isolates of the new proposed species are listed in red font.

Clades corresponding to isolates of the genera *Betabaculovirus* and *Gammabaculovirus* are also shown, as the unclassified baculovirus isolate Mythimna unipuncta nucleopolyhedrovirus-KY310 (MyunNPV-KY310). The tree is rooted against the lone representative isolate of the genus *Deltabaculovirus* (not shown).



| Figure 2. Relationships of betabaculovirus isolates (Table 2) inferred from the predicted amino acid sequences of baculovirus core genes inferred as described in the Figure 1 legend. The representative isolate of the new proposed betabaculovirus species is listed in red font.**Table 3.** The range of Kimura-2-parameter nucleotide distances (in substitution/site) between the listed isolates of the proposed species and other alpha- or betabaculoviruses at three different loci \*

|  |  |
| --- | --- |
| **Virus isolates** | **Loci** |
| *lef-8* | *lef-9* | *polyhedrin/granulin* |
| HespNPV-MEM | 0.767 – 1.800 | 0.367 – 1.341 | 0.331 –0.780 |
| LoobMNPV | 0.595 – 2.228 | 0.408 – 1.697 | 0.378 –1.040 |
| MyunNPV#7 | 0.514 – 2.179 | 0.226 – 1.517 | 0.218 – 0.799 |
| OpbuNPV-MA | 1.069 – 2.109 | 0.557 – 1.589 | 0.442 – 1.139 |
| OxocNPV-435 | 0.748 – 3.010 | 0.520 – 1.932 | 0.403 – 1.364 |
| PeluSNPV | 0.910 – 1.779 | 0.432 – 0.929 | 0.268 – 0.900 |
| PespNPV-GR167 | 0.403 – 1.799 | 0.226 – 1.172 | 0.246 – 1.136 |
| MolaGV-SouthernBrazil | 0.454 – 2.120 | 0.511 – 2.044 | 0.200 –1.001 |

\*Distances were estimated with MEGA7 using the Kimura-2-parameter model. Distances >0.050 indicate that the isolates being compared belong to different species. The distances include estimated distances for all possible pairwise comparisons between isolates of the proposed species. |
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| **References:** |
| --- |

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