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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.001D*** |  |
| **Short title:** Create eight new species and rename one species in the genus *Alphabaculovirus* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Harrison RL, Herniou EA, Jehle JA, Theilmann DA, Burand JP, Krell PJ, van Oers MM | Robert.L.Harrison@ars.usda.gov; elisabeth.herniou@univ-tours.fr; Johannes.Jehle@julius-kuehn.de; David.Theilmann@AGR.GC.CA; jburand@microbio.umass.edu; pkrell@uoguelph.ca; Monique.vanOers@wur.nl  |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| USDA-ARS Beltsville Agricultural Research Center, Beltsville, MD, USA (RLH); Institut de Recherche sur la Biologie de l’Insecte, Tours, France (EAH); Julius Kühn Institute, Darmstadt, Germany (JAJ); AAFC Summerland Research and Development Centre, Summerland, BC, Canada (DAT); University of Massachusetts-Amherst, Amherst, MA, USA (JPB); University of Guelph, Guelph, ON, Canada (PJK); Wageningen University, Wageningen, The Netherlands (MMVO) |

 |
| **Corresponding author** |
| Robert L. Harrison |
| **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 and Nudiviridae SG** |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: | 20 May 2019 |
| Date of this revision (if different to above): |  6 June 2019 |

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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:** 2019.001D.A.v1.8newsp\_Alphabaculovirus.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_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, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

Isolates of the eight new species proposed for genus *Alphabaculovirus* (Table 1, isolates of proposed species highlighted in yellow) can be classified as belonging to this genus in the family *Baculoviridae* on the basis of three or more of the following criteria (Harrison et al., 2018):

* 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;
* relationships to other alphabaculoviruses as inferred by molecular phylogeny;
* occlusion bodies formed within the nucleus with a characteristic shape and size (polyhedral, approximately 0.15 to 3 μm in size);
* rod-shaped, enveloped virions containing one or more nucleocapsids, with multiple virions contained in each occlusion body.

Figure 1 shows the relationships of representative isolates of the proposed *Alphabaculovirus* 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).

According to these criteria, 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. A recent analysis of pairwise nucleotide distances for the full-length sequences of all 38 core genes among 172 fully sequenced baculovirus genomes has largely confirmed the species assignments that have been made using these criteria (Wennmann et al., 2018).

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 2. Except for CoveMNPV-PR.2002, the distances measure >0.05 substitutions/site for each locus, clearly indicate that the isolates under consideration are representatives of new, previously undescribed species of *Alphabaculovirus* and not variants of members of currently existing species.

Although Castro et al. (2017) had assessed pairwise distances between CoveMNPV-PR.2002 and CfDEFMNPV (Choristoneura fumiferana DEF MNPV) at the *lef-9* and *polh* loci to be 0.081 and 0.082 substitutions/site, respectively, our calculations showed these distances to measure 0.033 and 0.047 substitutions/site, while distance at the *lef-8* locus measured 0.138 subtitutions/site. While this analysis indicates that CoveMNPV-PR.2002 and CfDEFMNPV are related, differences in the host of origin and ORF content (Castro et al., 2017) and evidence from core gene phylogenetic inference (Figure 1) and pairwise distances of all 38 core genes (Wennmann et al., 2018) support the conclusion that these two viruses are members of different species.

Finally, because MyunNPV-KY310 represents the second distinct alphabaculovirus species to be isolated from the host *Mythimna unipuncta*, we propose to rename species *Mythimna unipuncta nucleopolyhedrovirus* as *Mythimna unipuncta nucleopolyhedrovirus A* to distinguish it from *Mythimna unipuncta nucleopolyhedrovirus B*.

**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 |
| **Condylorrhiza vestigialis multiple nucleopolyhedrovirus PR.2002** | ***Condylorrhiza vestigialis nucleopolyhedrovirus*** | **CoveMNPV-PR.2002** |
| **Cryptophlebia peltastica nucleopolyhedrovirus SA** | ***Cryptophlebia peltastica nucleopolyhedrovirus*** | **CrpeNPV-SA** |
| **Cyclophragma undans nucleopolyhedrovirus Whiov** | ***Cyclophragma undans nucleopolyhedrovirus***  | **CyunNPV-Whiov** |
| 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 |
| **Hyposidra talaca nucleopolyhedrovirus India001** | ***Hyposidra talaca nucleopolyhedrovirus*** | **HytaNPV-India001** |
| 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 A* | MyunNPV#7 |
| **Mythimna unipuncta nucleopolyhedrovirus KY310** | ***Mythimna unipuncta nucleopolyhedrovirus B*** | **MyunNPV-KY310** |
| 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 eridania nucleopolyhedrovirus 251** | ***Spodoptera eridania nucleopolyhedrovirus*** | **SperNPV-251** |
| **Spodoptera exempta nucleopolyhedrovirus 244.1** | ***Spodoptera exempta nucleopolyhedrovirus***  | **SpexNPV-244.1** |
| 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 |
| Spodoptera litura nucleopolyhedrovirus II | Not assigned | SpltNPV-II |
| Sucra jujuba nucleopolyhedrovirus 473 | *Sucra jujuba nucleopolyhedrovirus* | SujuNPV-473 |
| Thysanoplusia orichalcea nucleopolyhedrovirus P1 | *Thysanoplusia orichalcea nucleopolyhedrovirus* | ThorNPV-P1 |
| Trichoplusia ni single nucleopolyhedrovirus | *Trichoplusia ni single nucleopolyhedrovirus* | TnSNPV |
| **Urbanus proteus nucleopolyhedrovirus-Southern Brazil** | ***Urbanus proteus nucleopolyhedrovirus*** | **UrprNPV-Southern Brazil** |



**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 likelihood using the Le and Gascuel (LG) substitution matrix as implemented in RAxML. Bootstrap values are shown for each node. Representative isolates of the new proposed species are listed in red font. With the exception of Spodoptera litura nucleopolyedrovirus II, the other viruses in the tree are representative isolates of current species.

**Table 2.** The range of Kimura-2-parameter nucleotide distances (in substitutions/site) between the listed isolates of the proposed species and other alphabaculoviruses at three different loci \*

|  |  |
| --- | --- |
| **Virus isolates** | **Loci** |
| *lef-8* | *lef-9* | *polyhedrin/granulin* |
| CoveMNPV-PR.2002 | 0.138 – 1.434 | 0.033 – 1.035 | 0.047 – 0.465 |
| CrpeNPV-SA | 0.770 – 1.435 | 0.313 – 0.731 | 0.226 – 0.437 |
| CyunNPV-Whiov | 0.502 – 1.467 | 0.278 – 0.800 | 0.278 – 0.466 |
| HytaNPV-India001 | 0.295 – 1.216 | 0.153 – 0.807 | 0.193 – 0.463 |
| MyunNPV-KY310 | 0.331 – 1.460 | 0.198 – 0.746 | 0.209 – 0.496 |
| SperNPV-251 | 0.192 – 1.514 | 0.114 – 0.837 | 0.161 – 0.490 |
| SpexNPV-244.1 | 0.558 – 1.388 | 0.199 – 0.935 | 0.184 – 0.421 |
| UrprNPV-Southern Brazil | 0.761 – 1.621 | 0.321 – 0.818 | 0.271 – 0.515 |

\*Distances were estimated with MEGA X using the Kimura-2-parameter model. Distances >0.050 indicate that the isolates being compared belong to different species, while distances <0.015 indicate that they belong to the same species. The distances include estimated distances for all possible pairwise comparisons between isolates of the proposed species.

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| --- |
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