This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.



For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.008D*** | | | | (to be completed by ICTV officers) |
| **Short title:** Two new species in genus *Betabaculovirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Robert L. Harrison  Elisabeth A. Herniou  Peter J. Krell  David A. Theilmann  James J. Becnel  Johannes A. Jehle  John 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 Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 5/27/2017 | |
| Date of this revision (if different to above): | | | | 14/06/2017 | |

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

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.008D.N.v1.Betabaculovirus\_2sp1ren |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| ***Baculoviridae* core genes, *Betabaculovirus* characteristics, and proposed species demarcation criterion**  Jehle, J.A., Lange, M., Wang, H., Hu, Z., Wang, Y., Hauschild, R., 2006. Molecular  identification and phylogenetic analysis of baculoviruses from Lepidoptera. Virology 346, 180-193.  Garavaglia, M.J., Miele, S.A., Iserte, J.A., Belaich, M.N., Ghiringhelli, P.D., 2012. The ac53, ac78, ac101, and ac103 genes are newly discovered core genes in the family *Baculoviridae*. J Virol 86, 12069-12079.  Javed, M.A., Biswas, S. Willis, L.G., Harris, S., Pritchard, C., van Oers, M.M., Donly, C., Erlandson, M.A., Hegedus, D.D., Theilmann, D.A., 2017. Autographa californica multiple nucleopolyhedrovirus AC83 is a *per os* infectivity factor (PIF) protein required for occlusion-derived virus (ODV) and budded virus nucleocapsid assembly as well as assembly of the PIF complex in ODV envelopes. J Virol 91, e02115-16.  Herniou, E.A., Arif, B.M., Becnel, J.J., Blissard, G.W., Bonning, B., Harrison, R.L., Jehle, J.A., Theilmann, D.A., Vlak, J.M., 2011. Baculoviridae, in: King, A.M.Q., Adams, M.J., Carstens, E.B., Lefkowitz, E.J. (Eds.), Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier, Oxford, pp. 163-174.  ***Cnaphalocrocis medinalis granulovirus***  Pang, Y., Lai, Y., Liu, J., Ye, Y., 1981. A new granulovirus from naturally infected Asiatic rice leafroller, *Cnaphalocrocis medinalis* (Guenee). Microbiology China 2, 103-104.  Zhang, X., Zhu, Z., Sun, S., Chen, Q., Deng, F., Yang, K., 2015. Genome sequencing and analysis of a granulovirus isolated from the Asiatic rice leafroller, *Cnaphalocrocis medinalis.* Virol Sin 30, 417-424.  ***Mythimna unipuncta granulovirus B***  Harrison, R.L., Rowley, D.L., Mowery, J., Bauchan, G.R., Theilmann, D.A., Rohrmann, G.F., Erlandson, M.A., 2017. The complete genome sequence of a second distinct betabaculovirus from the true armyworm, *Mythimna unipuncta*. PLoS ONE 12, e0170510. |

|  |
| --- |
| **Annex:**  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 proposed species *Cnaphalocrocis medinalis* *granulovirus* and *Mythimna unipuncta* *granulovirus B* can be identified as belonging to the genus *Betabaculovirus* of 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 100 to 180 kbp with a

gene content characteristic of other betabaculoviruses;

* relationships to other baculoviruses as inferred by molecular phylogeny;
* occlusion bodies formed within the nucleus with a characteristic shape and size (ovocylindrical, approximately 0.13 x 0.50 μm);
* rod-shaped virions consisting of a single enveloped nucleocapsid, with a single virion contained in each occlusion body.

Figure 1 shows the relationships of representative isolates of the proposed species to representative isolates of other recognized species in the genus *Betabaculovirus* (Table 1), as well as a selection of representative isolates for the other three genera of *Baculoviridae* (*Alphabaculovirus*, *Gammabaculovirus*, and *Deltabaculovirus*), determined from the concatenated alignment of the predicted amino acid sequences of 38 baculovirus core genes (Garavaglia et al., 2012; Javed et al., 2017). The tree shows that the representatives of the two proposed *Betabaculovirus* species group with other betabaculoviruses.

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 *granulin* (*polh*)(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 *granulin* (*polh*) between the proposed species’ representative isolates and other representative isolates of genus *Betabaculovirus* are shown in Table 2. The distances measure >0.05 substitutions/site for each locus, indicating that the isolates under consideration are representatives of new, previously unrecognized species of *Betabaculovirus* and not variants of currently existing species.

We also propose to rename *Pseudalatia unipuncta granulovirus* as *Mythimna unipuncta granulovirus A*, to reflect the fact that the new species *Mythimna unipuncta granulovirus B* is the second distinct betabaculovirus to be isolated from the host *Mythimna (Pseudoletia) unipuncta*.

**Table 1.** Betabaculovirus isolates used in core gene phylogeny and pairwise distance estimation. Isolates for newly proposed species are indicated in bold type with a yellow background.

|  |  |  |  |
| --- | --- | --- | --- |
| **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 |
| 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 |
| Mocis sp. granulovirus | - | KR011718 | MospGV |
| **Mythimna unipuncta granulovirus #8** | ***Mythimna unipuncta granulovirus B*** | **KX855660** | **MyunGV#8** |
| Phthorimaea operculella granulovirus-T | *Phthorimaea operculella granulovirus* | AF499596 | PhopGV-T |
| Pieris rapae granulovirus-Wuhan | *Artogeia rapae granulovirus* | GQ884143 | PiraGV-Wuhan |
| Plodia interpunctella-Cambridge | *Plodia interpunctella granulovirus* | KX151395 | PiGV-Cambridge |
| Plutella xylostella granulovirus K1 | *Plutella xylostella granulovirus* | AF270937 | PlxyGV-K1 |
| Pseudalatia unipuncta granulovirus Hawaiian | *Mythimna unipuncta granulovirus A* | EU678671 | PsunGV-H |
| Spodoptera frugiperda granulovirus VG008 | *Spodoptera frugiperda granulovirus* | KM371112 | SpfrGV-VG008 |
| Spodoptera litura granulovirus K1 | *Spodoptera litura granulovirus* | DQ288858 | SpltGV-K1 |
| Trichoplusia ni granulovirus M10-5 | *Trichoplusia ni granulovirus* | AY519201-AY519203 | TnGV M10-5 |
| Xestia c-nigrum granulovirus 4 | *Xestia c-nigrum granulovirus* | AF162221 | XecnGV-4 |

*Clostera anastomosis granulovirus B*

,

*Erinnyis ello granulovirus*

*Choristoneura fumiferana granulovirus*

*Artogeia rapae granulovirus*

*Clostera anastomosis granulovirus A*

*Clostera anachoreta granulovirus*

*Cydia pomella granulovirus*

*Cryptophlebia leucotreta granulovirus*

*Diatraea saccharalis granulovirus*

*Plodia interpuctella granulovirus*

*Adoxophyes orana granulovirus*

***Cnaphalocrocis medinalis granulovirus***

*Phthorimaea operculella granulovirus*

*Epinotia aporema granulovirus*

*Agrotis segetum granulovirus*

*Plutella xylostella granulovirus*

*Spodoptera litura granulovirus*

***Mythimna unipuncta granulovirus B***

*Spodoptera frugiperda granulovirus*

Mocis sp. granulovirus

*Mythimna unipuncta granulovirus A*

*Helicoverpa armigera granulovirus*

*Xestia c-nigrum granulovirus*

*Alphabaculovirus*

*Gammabaculovirus*

*Deltabaculovirus*

**100**

**100**

**96**

**100**

**88**

**100**

**96**

**100**

**64**

**66**

**89**

**100**

**100**

**55**

**79**

**100**

**100**

**100**

**100**

**100**

**92**

**100**

**100**

**100**

**100**

0.5

*Betabaculovirus*

**Figure 1.** Relationships among betabaculovirus species and betabaculovirus isolate Mocis sp. granulovirus, inferred from representative isolate core gene amino acid sequence alignments (see Table 1 for species and isolate names). The proposed species are listed in bold font and highlighted in yellow. The phylogenetic tree was constructed from the concatenated alignments of 38 baculovirus core gene amino acid sequences with the minimum-evolution method using the James-Taylor-Thornton substitution model in MEGA7. Bootstrap values are shown for each node. In addition to genus *Betabaculovirus*, clades formed by isolates from the other three genera of *Baculoviridae* are indicated.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Virus isolates** | **Loci** | | |
| ***lef-8*** | ***lef-9*** | ***granulin*** |
| CnmeGV-Enping | 0.817 – 2.148 | 0.572 – 1.912 | 0.565 – 1.261 |
| MyunGV#8 | 0.632 – 4.191 | 0.675 – 2.264 | 0.200 – 1.004 |

\* Distances were estimated with MEGA6 using the Kimura 2-parameter model.