



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	2015.002a,bD	(to be completed by ICTV officers)			
Short title: One new species, <i>Agrotis segetum nucleopolyhedrovirus B</i>, in the genus <i>Alphabaculovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input checked="" type="checkbox"/>	4 <input type="checkbox"/> 9 <input type="checkbox"/>	5 <input type="checkbox"/> 10 <input checked="" type="checkbox"/>

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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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Baculoviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: 6/22/15
Date of this revision (if different to above): 9/23/15

ICTV-EC comments and response of the proposer:

7/21/2015: Add scale to Figure 1.
8/7/2015: Figure 1 with scale was supplied by corresponding author Johannes Jehle.
9/22/2015: Figure 1 was replaced with a tree (with scale bar) which indicated that the new species of this proposal is different and distinct from the two other new *Alphabaculovirus* species discussed at EC47, *Chrysodeixis includens nucleopolyhedrovirus* and *Sucra jujuba nucleopolyhedrovirus*.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2015.002aD	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Alphabaculovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ (new) ” after its proposed name. • If no genus is specified, enter “ unassigned ” in the genus box.
Subfamily:		
Family:	<i>Baculoviridae</i>	
Order:		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Agrotis segetum nucleopolyhedrovirus B</i>	Agrotis segetum nucleopolyhedrovirus B (AgseNPV-B)	KM102981

Reasons to justify the creation and assignment of the new species:

- Isolates of the proposed species can be identified as belonging to the genus *Alphabaculovirus* 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 110–170 kbp with a gene content characteristic of other alphabaculoviruses; relationships to other baculoviruses as inferred by molecular phylogeny; occlusion bodies formed within the nucleus with a characteristic size and shape; and rod-shaped virions consisting of nucleocapsids enveloped singly or in bunches. Figure 1 shows the relationships of the isolate of the proposed species to other baculoviruses, as determined from the concatenated alignment of the predicted amino acid sequences of 37 baculovirus core genes of (Wennmann et al., 2015).
- Agrotis segetum nucleopolyhedrovirus was originally isolated from infected *Agrotis segetum* larvae. Two isolates (English or Oxford isolate and French isolate) were described in the literature. Both showed the same endonuclease restriction profiles of their DNA (Allaway and Payne, 1983; Jakubowska et al., 2005, 2006). After an isolate of AgseNPV from Poland (Lipa, 1971, Jakubowska et al., 2005, 2006) showed a distinct restriction profile, the Polish isolate was termed AgseNPV-A and the English isolate was termed AgseNPV-B (Jakubowska et al., 2005, 2006). Eventually, the Polish isolate was accepted as a new *Alphabaculovirus* species, termed *Agrotis segetum nucleopolyhedrovirus*. Another isolate, isolated from *Agrotis ipsilon* and named Agrotis ipsilon nucleopolyhedrovirus (AgipNPV) has an overlapping host range as it also infects larvae of *Agrotis segetum*. AgipNPV significantly differs in restriction profile and genome sequence from AgseNPV-A and AgseNPV-B. The species *Agrotis ipsilon multiple nucleopolyhedrovirus* was established for the isolate AgipNPV.
- Complete genome sequencing of AgipNPV-B (Accession number KM102981) revealed significant differences in nucleotide sequence and open reading frame composition from AgseNPV-A and AgipNPV (Wennmann et al., 2014). For baculoviruses the Kimura-2-parameter (K-2-P) of *polh*, *lef-8*, and *lef-9* was suggested as one species demarcation criterion (Jehle et al., 2006b). If the K-2-P distance is larger than 0.050, two baculoviruses were regarded to belong to distinct species. According to the K-2-P differences, calculated from concatenated alignments of partial *lef-8*, *lef-9*, and *polh* genes, AgseNPV-B is distinct from AgseNPV-A (K-2-P

= 0.214) and from AgipNPV (K-2-P = 0.090).

- This new species is also different and distinct from the two other *Alphabaculovirus* species proposed in 2015, *Chrysodeixis includens nucleopolyhedrovirus* and *Sucra jujuba nucleopolyhedrovirus* (Figure 1).

MODULE 8: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

Renaming one or more taxa

Code	2015.002bD	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current name		Proposed name
<i>Agrotis segetum nucleopolyhedrovirus</i>		<i>Agrotis segetum nucleopolyhedrovirus A</i>

Reasons to justify the renaming:

The species *Agrotis segetum nucleopolyhedrovirus* was previously established for the (Polish) isolate of *Agrotis segetum nucleopolyhedrovirus A* (AgseNPV-A). After finding that *Agrotis segetum nucleopolyhedrovirus B* (AgseNPV-B) should belong to a different species, we propose to rename the species *Agrotis segetum nucleopolyhedrovirus* to *Agrotis segetum nucleopolyhedrovirus A* and to establish a new species, *Agrotis segetum nucleopolyhedrovirus B*, for the one isolate, AgseNPV-B.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Allaway, G.P., Payne, C.C., 1983. A biochemical and biological comparison of three European isolates of NPV virus from *Agrotis segetum*. Arch. Virol. 75, 43–54.
- Garavaglia, M.J., Miele, S.A.B., Iserete, 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.
- Jakubowska, A., van Oers, M. M., Ziemnicka, J., Lipa, J. J., Vlak, J. M., 2005. Molecular characterization of *Agrotis segetum* nucleopolyhedrovirus from Poland. J. Invertebr. Pathol. 90, 64-68.
- Jakubowska, A. K., Peters, S. A., Ziemnicka, J., Vlak, J. M., van Oers, M. M., 2006. Genome sequence of an enhancin gene-rich nucleopolyhedrovirus (NPV) from *Agrotis segetum*: collinearity with *Spodoptera exigua* multiple NPV. J. Gen. Virol. 87, 537–551.
- 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.
- Lipa, J.J., Ziemnicka, J., Gudz-Gorban, A.P., 1971. Electron microscopy of nuclear polyhedrosis virus from *Agrotis segetum* Schiff. and *A. exclamatoris* L. (Lepidoptera, Noctuidae). Acta Microbiol. Pol. Ser. B 3, 55–61.
- Miele, S.A.B., Garavaglia, M.J., Belaich, M.N., Ghiringhelli, P.D., 2011. Baculovirus: Molecular insights on their diversity and conservation. Int. J. Evol. Biol. 2011, 1–15.
- Wennmann, J. T., Gueli Alletti, G. Jehle, J.A. (2015). The genome sequence of *Agrotis segetum* nucleopolyhedrovirus B (AgseNPV-B) reveals a new baculovirus species within the *Agrotis* baculovirus complex. Virus Genes 50, 260–276.

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

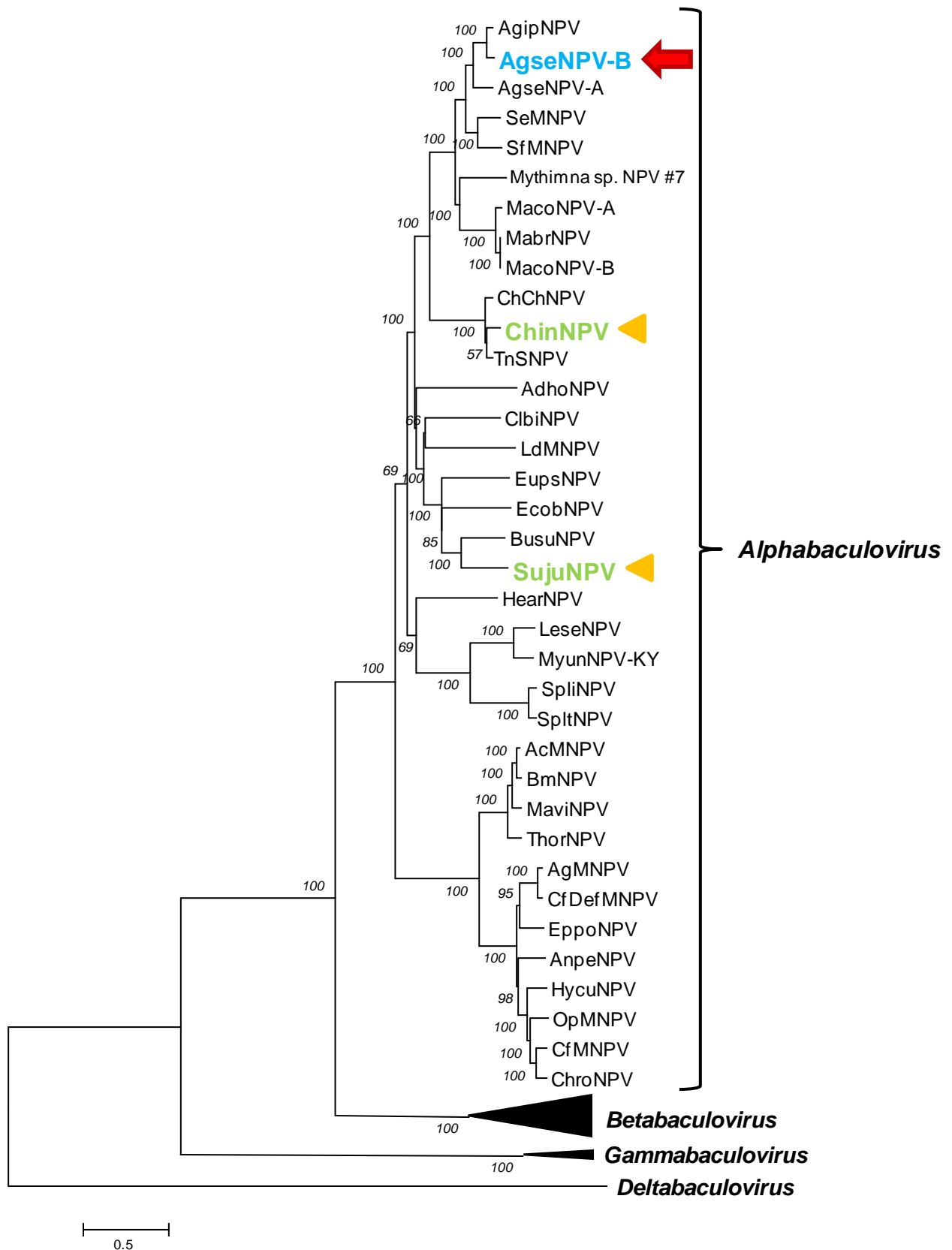


Figure 1. Relationships of baculovirus species and other isolates, inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 34 baculovirus core gene amino acid sequences using the minimum-evolution method using the James-Taylor-Thornton substitution model and a gamma parameter of

0.85 (estimated from the *dnapol* alignment). Bootstrap values are shown for each node. Clades corresponding to the four genera of *Baculoviridae* are indicated. The proposed species is listed in blue font and denoted with a red arrow. Additional new *Alphabaculovirus* species discussed at EC47 are listed in green font and denoted with an orange arrowhead. *Alphabaculovirus* taxa include the reference isolates (abbreviations for the corresponding viruses are in brackets) for species *Adoxophyes honmai nucleopolyhedrovirus* (AdhoNPV), *Agrotis ipsilon multiple nucleopolyhedrovirus* (AgipNPV), *Agrotis segetum nucleopolyhedrovirus A* (AgseNPV-A), *Agrotis segetum nucleopolyhedrovirus B* (AgseNPV-B), *Antheraea pernyi nucleopolyhedrovirus* (AnpeNPV), *Anticarsia gemmatalis multiple nucleopolyhedrovirus* (AgMNPNV), *Autographa californica multiple nucleopolyhedrovirus* (AcMNPNV), *Bombyx mori nucleopolyhedrovirus* (BmNPV), *Buzura suppressaria nucleopolyhedrovirus* (BusuNPV), *Choristoneura fumiferana multiple nucleopolyhedrovirus* (CfMNPNV), *Choristoneura fumiferana DEF multiple nucleopolyhedrovirus* (CfDEFNPV), *Chrysodeixis chalcites nucleopolyhedrovirus* (ChchNPV), *Chrysodeixis includens nucleopolyhedrovirus* (ChinNPV), *Clanis bilineata nucleopolyhedrovirus* (ClbiNPV), *Choristoneura rosaceana nucleopolyhedrovirus* (ChroNPV), *Ecotropis obliqua nucleopolyhedrovirus* (EcobNPV), *Epiphyas postvittana nucleopolyhedrovirus* (EppoNPV), *Euproctis pseudoconspersa nucleopolyhedrovirus* (EupsNPV), *Helicoverpa armigera nucleopolyhedrovirus* (HearNPV), *Hyphantria cunea nucleopolyhedrovirus* (HycuNPV), *Leucania separata nucleopolyhedrovirus* (LeseNPV), *Lymantria dispar multiple nucleopolyhedrovirus* (LdMNPNV), *Mamestra configurata nucleopolyhedroviruses A and B* (MacoNPV-A and -B), *Maruca vitrata nucleopolyhedrovirus* (MaviNPV), *Spodoptera exigua multiple nucleopolyhedrovirus* (SeMNPNV), *Spodoptera frugiperda multiple nucleopolyhedrovirus* (SfMNPNV), *Spodoptera litura nucleopolyhedrovirus* (SpltNPV), and *Sucra jujuba nucleopolyhedrovirus* (SujuNPV), *Thysanoplusia orichalcea nucleopolyhedrovirus* (ThorNPV), and *Trichoplusia ni single nucleopolyhedrovirus* (TnSNPNV), as well as isolates *Mythimna* spp. nucleopolyhedrovirus #7 (*Mythimna* sp. NPV #7), and *Mythimna unipuncta nucleopolyhedrovirus* (MyunNPV-KY).
