



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:	2014.002aI	(to be completed by ICTV officers)			
Short title: Removal of species <i>Helicoverpa zea single nucleopolyhedrovirus</i> from the genus <i>Alphabaculovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input type="checkbox"/> 7 <input checked="" type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input 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 (the members of which are also authors of this proposal)

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:

7/1/13

Date of this revision (if different to above):

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2014.002aI	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Helicoverpa zea single nucleopolyhedrovirus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Alphabaculovirus</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Baculoviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		YES

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

The current species list for genus *Alphabaculovirus* in family *Baculoviridae* contains two species, *Helicoverpa armigera nucleopolyhedrovirus* and *Helicoverpa zea single nucleopolyhedrovirus*, that should be considered the same species for the following reasons:

- 1) Isolates of these two virus species display little difference in biological activity, and are able to cross-infect and kill host larvae of both *H. zea* and *H. armigera* with similar levels of pathogenicity (LD₅₀/LC₅₀) and virulence (survival time/LT₅₀) (Hughes et al., 1983; Ignoffo et al., 1983; Rowley et al., 2011; Williams and Payne, 1984).
- 2) Isolates of the two species exhibit nearly identical restriction endonuclease fragment patterns (Gettig and McCarthy, 1982). Also, the complete genome sequences of isolates from both virus species exhibit high levels of nucleotide and predicted amino acid sequence similarities and extensive co-linearity of ORF distribution (Chen et al., 2001; Chen et al., 2002; Ogembo et al., 2009; Zhang et al., 2005).
- 3) When evaluated by a proposed criterion for baculovirus species demarcation (Jehle et al., 2006), isolates of the two species appear to be variants of one species, rather than representatives of two separate species.

The species demarcation criterion was originally developed from comparisons of sequences from 117 separate baculovirus isolates and has been used by other researchers to make decisions about the taxonomic status of baculoviruses. It is based on pairwise comparison of nucleotide distances estimated from alignments of partial *lef-8*, *lef-9*, and *polh* genes using the Kimura 2-parameter model of nucleotide substitution. According to this criterion, if nucleotide distances between two

baculoviruses at these loci are less than 0.015 substitutions/site, the two baculoviruses being compared 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, such as host range, are considered when making a decision about their taxonomic status.

Phylogenetic inference of relationships among baculovirus isolates from *H. zea* and *H. armigera* places these isolates into separate groups (Figure 1). However, pairwise Kimura-2-parameter distances calculated for these isolates range from 0.00 – 0.016 substitutions/site, indicating that these isolates are variants of the same species (Rowley et al., 2011). Table 1 shows pairwise Kimura-2-parameter distances for a selection of the isolates portrayed in Figure 1.

Of the two heliothine alphabaculovirus species currently listed, we recommend that *Helicoverpa zea single nucleopolyhedrovirus* be removed from the *Alphabaculovirus* species list. We recommend that *Helicoverpa armigera nucleopolyhedrovirus* should be retained as a species because (a) a paper on the reference sequence for *Helicoverpa armigera nucleopolyhedrovirus* (Chen et al., 2001) was published prior to that for *Helicoverpa zea single nucleopolyhedrovirus* (Chen et al., 2002), and (b) isolates of *Helicoverpa armigera nucleopolyhedrovirus* have played a more prominent role in basic research on baculoviruses and are more frequently used as tools for insect pest management than those of *Helicoverpa zea single nucleopolyhedrovirus*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Biological activities of *H. zea* and *H. armigera* alphabaculovirus isolates

Hughes, P.R., Gettig, R.R., McCarthy, W.J., 1983. Comparison of the time-mortality response of *Heliothis zea* to 14 isolates of *Heliothis* nuclear polyhedrosis virus. J. Invert. Path. 41, 256-261.

Ignoffo, C.M., McIntosh, A.H., Garcia, C., 1983. Susceptibility of larvae of *Heliothis zea*, *H. virescens*, and *H. armigera* [Lep.: Noctuidae] to 3 baculoviruses. Entomophaga 28, 1-8.

Rowley, D.L., Popham, H.J., Harrison, R.L., 2011. Genetic variation and virulence of nucleopolyhedroviruses isolated worldwide from the heliothine pests *Helicoverpa armigera*, *Helicoverpa zea*, and *Heliothis virescens*. J Invertebr Pathol 107, 112-126.

Williams, C.F., Payne, C.C., 1984. The susceptibility of *Heliothis armigera* larvae to three nuclear polyhedrosis viruses. Annals of Applied Biology 104, 405-412.

Analyses of *H. zea* and *H. armigera* alphabaculovirus genomes

Chen, X., WF, I.J., Tarchini, R., Sun, X., Sandbrink, H., Wang, H., Peters, S., Zuidema, D., Lankhorst, R.K., Vlak, J.M., Hu, Z., 2001. The sequence of the *Helicoverpa armigera* single nucleocapsid nucleopolyhedrovirus genome. J. Gen. Virol. 82, 241-257.

Chen, X., Zhang, W.J., Wong, J., Chun, G., Lu, A., McCutchen, B.F., Presnail, J.K., Herrmann, R., Dolan, M., Tingey, S., Hu, Z.H., Vlak, J.M., 2002. Comparative analysis of the complete genome sequences of *Helicoverpa zea* and *Helicoverpa armigera* single-nucleocapsid nucleopolyhedroviruses. J. Gen. Virol. 83, 673-684.

Gettig, R.R., McCarthy, W.J., 1982. Genotypic variation among wild isolates of *Heliothis* spp nuclear polyhedrosis viruses from different geographical regions. Virology 117, 245-252.

Ogembo, J.G., Caoili, B.L., Shikata, M., Chaeychomsri, S., Kobayashi, M., Ikeda, M., 2009. Comparative genomic sequence analysis of novel *Helicoverpa armigera* nucleopolyhedrovirus (NPV) isolated from Kenya and three other previously sequenced *Helicoverpa* spp. NPVs. Virus Genes.

Zhang, C.X., Ma, X.C., Guo, Z.J., 2005. Comparison of the complete genome sequence between C1 and G4 isolates of the *Helicoverpa armigera* single nucleocapsid nucleopolyhedrovirus. Virology 333, 190-199.

Proposed baculovirus 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.

Annex:

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.

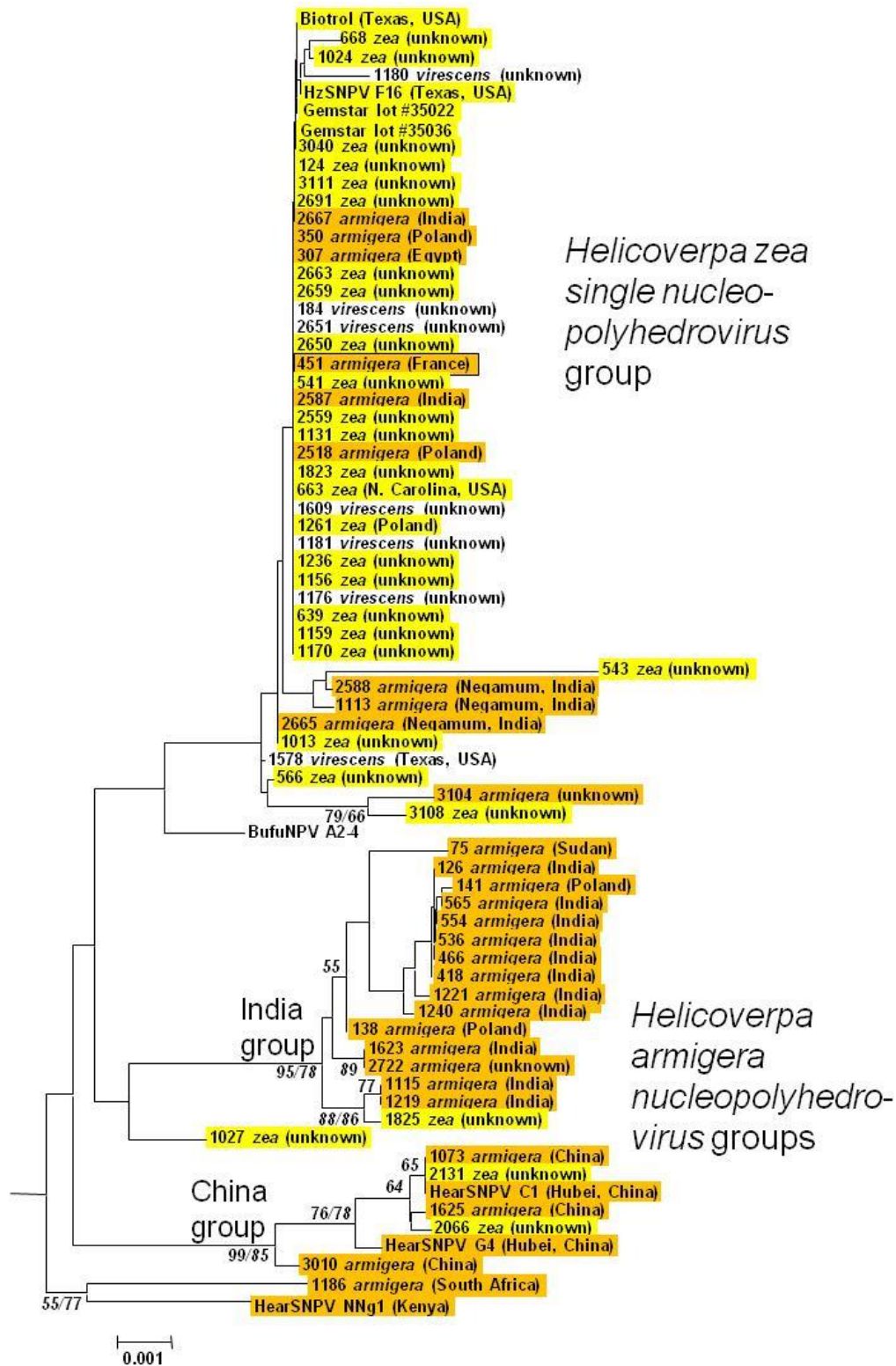


Figure 1. Phylogenetic tree of NPV isolates from *Helicoverpa zea* (yellow background) and *Helicoverpa armigera* (orange background) based on concatenated alignments of partial nucleotide sequences of the genes *lef-8*, *lef-9*, and *polh*. Also included are NPVs from *Heliothis virescens* (clear background) and *Busseola fusca* (BufuNPV A2-4; Jehle et al., 2006), as well as sequences from the genomes of *Helicoverpa zea* single nucleopolyhedrovirus strain HzSNPV F16 (Chen et al., 2002) and *Helicoverpa armigera* nucleopolyhedrovirus strains HearSNPV-C1 (Zhang et al., 2005), HearSNPV-G4 (Chen et al., 2001), and HearNPV-NNg1 (Ogembo et al.,

2009). Bootstrap values $\geq 50\%$ for minimum evolution (ME) and maximum parsimony (MP) trees are shown at each node where available (either ME/MP, or just ME). Adapted from Rowley et al., 2011.

Table 1. Pairwise nucleotide distances of selected *H. armigera* and *H. zea* alphabaculoviruses from Figure 1, calculated from concatenated partial *lef-8*, *lef-9*, and *polh* sequence alignments.

<i>lef8-lef9-polh</i>	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. zea (Biotrol)																
2. 75 armigera (Sudan)	0.011															
3. 126 armigera (India)	0.011	0.003														
4. 543 zea (unknown)	0.005	0.016	0.015													
5. 663 zea (N. Carolina)	0.000	0.011	0.011	0.005												
6. 668 zea (unknown)	0.001	0.011	0.011	0.006	0.001											
7. 1027 zea (unknown)	0.003	0.007	0.007	0.009	0.003	0.004										
8. 1113 armigera (India)	0.002	0.010	0.009	0.006	0.002	0.003	0.004									
9. 1186 armigera (S. Africa)	0.009	0.014	0.014	0.014	0.009	0.009	0.011	0.009								
10. 1623 armigera (India)	0.009	0.005	0.002	0.013	0.009	0.009	0.005	0.007	0.012							
11. 3010 armigera (China)	0.008	0.012	0.012	0.013	0.008	0.009	0.007	0.009	0.011	0.010						
12. 3108 zea (unknown)	0.003	0.012	0.012	0.008	0.003	0.003	0.006	0.003	0.010	0.010	0.009					
13. zea (GemStar)	0.000	0.011	0.011	0.005	0.000	0.001	0.003	0.002	0.009	0.009	0.008	0.003				
14. HaNPV-C1 (China)	0.011	0.015	0.015	0.016	0.011	0.011	0.010	0.011	0.014	0.013	0.003	0.012	0.011			
15. HaNPV-G4 (China)	0.009	0.014	0.014	0.014	0.009	0.009	0.009	0.009	0.013	0.012	0.005	0.010	0.009	0.002		
16. HaNPV-NNg1 (Kenya)	0.008	0.012	0.012	0.013	0.008	0.009	0.009	0.009	0.007	0.011	0.011	0.009	0.008	0.013	0.014	
17. HzSNPV F16 (Texas)	0.000	0.011	0.011	0.005	0.000	0.001	0.003	0.002	0.009	0.009	0.008	0.003	0.000	0.011	0.009	0.008