

Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Genus in an existing Family

Code [†]	2006.0351.04	To create a new genus in the family*	<i>Baculoviridae</i>
Code [†]	2006.0361.04	To name the new genus*	<i>Alphabaculovirus</i>
Code [†]	2006.0371.04	To designate the species	<i>Autographa californica multiple nucleopolyhedrovirus</i>

As the type species of the new genus*

Code [†]	206.0381.04	To designate the following as species of the new genus*:	<i>Adoxophyes honmai</i> NPV, <i>Agrotis ipsilon</i> NPV, <i>Anticarsia gemmatalis</i> MNPV <i>Autographa californica</i> MNPV <i>Bombyx mori</i> NPV, <i>Buzura suppressaria</i> NPV, <i>Choristoneura fumiferana</i> DEF MNPV, <i>Choristoneura fumiferana</i> MNPV, <i>Choristoneura rosaceana</i> NPV, <i>Ectropis obliqua</i> NPV, <i>Epiphyas postvittana</i> NPV, <i>Helicoverpa armigera</i> NPV, <i>Helicoverpa zea</i> NPV, <i>Lymantria dispar</i> MNPV, <i>Mamestra brassicae</i> MNPV, <i>Mamestra configurata</i> NPV-A, <i>Mamestra configurata</i> NPV-B, <i>Orgyia pseudotsugata</i> MNPV, <i>Spodoptera exigua</i> MNPV, <i>Spodoptera frugiperda</i> MNPV, <i>Spodoptera litura</i> NPV, <i>Thysanoplusia orichalcea</i> NPV, <i>Trichoplusia ni</i> SNPV, <i>Wiseana signata</i> NPV
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[†] Assigned by ICTV officers

* repeat these lines and the corresponding arguments for each genus created in the family

Author(s) with email address(es) of the Taxonomic Proposal

J.A. Jehle, G. W. Blissard, B. C. Bonning, J. Cory, E. A. Herniou , G. F. Rohrmann , D. A. Theilmann , S. M. Thiem , and J. M. Vlak

Baculovirus Study Group
Chair: johannes.jehle@dlr.rlp.de

Old Taxonomic Order

Order

Family

Genus

Type Species

Species in the Genus

Baculoviridae

Nucleopolyhedrovirus

Autographa californica multiple nucleopolyhedrovirus

Adoxophyes honmai NPV

Agrotis ipsilon NPV

Anticarsia gemmatalis MNPV

Autographa californica MNPV

Bombyx mori NPV

Buzura suppressaria NPV

Choristoneura fumiferana DEF MNPV

Choristoneura fumiferana MNPV

Choristoneura rosaceana NPV

Culex nigripalpus NPV

Ectropis obliqua NPV

Epiphyas postvittana NPV

Helicoverpa armigera NPV

Helicoverpa zea NPV

Lymantria dispar MNPV

Mamestra brassicae MNPV

Mamestra configurata NPV-A

Mamestra configurata NPV-B

Neodiprion lecontei NPV

Neodiprion sertifer NPV

Orgyia pseudotsugata MNPV

Spodoptera exigua MNPV

Spodoptera frugiperda MNPV

Spodoptera litura NPV

Thysanoplusia orichalcea NPV

Trichoplusia ni SNPV

Wiseana signata NPV

Unassigned Species in the Genus

None

New Taxonomic Order

Order

Family

Genus

Type Species

Species in the Genus

Baculoviridae

Alphabaculovirus

Autographa californica multiple nucleopolyhedrovirus

Adoxophyes honmai NPV

Agrotis ipsilon NPV

Anticarsia gemmatalis MNPV

Autographa californica MNPV

Bombyx mori NPV

Buzura suppressaria NPV

Choristoneura fumiferana DEF MNPV

Choristoneura fumiferana MNPV

Choristoneura rosaceana NPV

Ectropis obliqua NPV

Epiphyas postvittana NPV

Helicoverpa armigera NPV

Helicoverpa zea NPV

Lymantria dispar MNPV

Mamestra brassicae MNPV

Mamestra configurata NPV-A

Mamestra configurata NPV-B

Orgyia pseudotsugata MNPV

Spodoptera exigua MNPV

Spodoptera frugiperda MNPV
Spodoptera litura NPV
Thysanoplusia orichalcea NPV
Trichoplusia ni SNPV
Wiseana signata NPV

Unassigned Species in the family

Culex nigripalpus NPV
Neodiprion lecontei NPV
Neodiprion sertifer NPV

Comment [JJ1]: Is it necessary to indicate them as unassigned species if we create new genera for these species?

Argumentation to choose the type species in the genus

AcMNPV is the best characterized virus of this genus and serves as a model for studying other baculoviruses. Its genome was first sequenced in 1994. AcMNPV is already type species of the existing genus *Nucleopolyhedrovirus*, and so it is proposed as type species for the new genus, *Alphabaculovirus*, which is a revised version of the former genus.

Species demarcation criteria in the genus

Species demarcation criteria within the family *Baculoviridae* have not been well defined. However, the species reported here differ in host range and specificity, DNA restriction profiles, genome sequence, gene content and gene order. As soon as species demarcation criteria based on genetic distance have been developed the list of species will be revised.

List of Species in the created genus

Autographa californica multiple nucleopolyhedrovirus
Adoxophyes honmai NPV
Agrotis ipsilon NPV
Anticarsia gemmatalis MNPV
Autographa californica MNPV
Bombyx mori NPV
Buzura suppressaria NPV
Choristoneura fumiferana DEF MNPV
Choristoneura fumiferana MNPV
Choristoneura rosaceana NPV
Ectropis obliqua NPV
Epiphyas postvittana NPV
Helicoverpa armigera NPV
Helicoverpa za NPV
Lymantria dispar MNPV
Mamestra brassicae MNPV
Mamestra configurata NPV-A
Mamestra configurata NPV-B
Orgyia pseudotsugata MNPV
Spodoptera esigua MNPV
Spodoptera frugiperda MNPV
Spodoptera litura NPV
Thysanoplusia orichalcea NPV
Trichoplusia ni SNPV
Wiseana signata NPV

Argumentation to create a new genus:

The existing genus *Nucleopolyhedrovirus* comprises baculoviruses with polyhedral to globular occlusion bodies (OBs) embedding several to many singly enveloped or multiply enveloped nucleocapsids. Their occlusion body morphology differs from those of the existing genus *Granulovirus*, which have ovicylindrical occlusion bodies, which typically embed a single virion containing only one and in rare cases two nucleocapsids. Viruses in the present genus *Nucleopolyhedrovirus* infect insect hosts in three orders of insects (Lepidoptera, Diptera and Hymenoptera) and one order of the Crustacea.

After more than 25 complete genomes of different baculoviruses have been sequenced, a more comprehensive picture on genome organization, gene content and phylogeny of these viruses became available. Gene content (Table 1) as well as phylogenetic analysis of the 29 core genes that are common in all baculoviruses sequenced so far (Figure 1) clearly indicate that the hymenopteran-specific species *Neodiprion lecontei* NPV and *Neodiprion sertifer* NPV and the dipteran-specific *Culex nigripalpus* nucleopolyhedrovirus (CulexNPV) do not cluster with the lepidopteran-specific NPVs, but form distinct clades. Thus, with respect to the genus *Granulovirus* the present genus *Nucleopolyhedrovirus* are a paraphyletic group of viruses. This is not appropriate for classification.

For that reason we propose to split the existing genus *Nucleopolyhedrovirus* into three genera, which will contain the different NPV species in monophyletic genera. It is proposed to name these genera *Alphabaculovirus*, *Gammabaculovirus* and *Deltabaculovirus* (see propositions for establishing the genera *Gammabaculovirus* and *Deltabaculovirus*).

The genus *Alphabaculovirus* will be defined as follows:

Morphology: Two virion phenotypes, budded viruses (BV) and occlusion derived viruses (ODV) maybe characteristic of a virus species. Virions of the ODV phenotype are embedded within an occlusion body of a crystalline matrix of a single viral protein (polyhedrin) of about 25-33 kDa. Each occlusion body measures about (0.1-) 0.4-3 (-15) μm , matures within the nucleus of infected cells and characteristically contains many enveloped virions. The occluded virions are packaged with either single (S) or multiple (M) nucleocapsids within a single envelope. Nucleocapsids are rod-shaped (30-60 nm x 250-300 nm).

Genome: The genome consists of a single molecule of circular supercoiled dsDNA of 100-180 kbp in size.

Pathology: Viral infections are initiated in the midgut and spread to other organs and tissues. The BV are involved in transmission of infection from cell to cell. OB production only rarely occurs within midgut tissues and the primary locations of OB production are fat body, tracheal cells, muscle, epithelial cells, and other tissues of the hemocoel. Some Alphabaculoviruses, such as AcMNPV and close relatives, utilize GP64 homologues, whereas other NPV use the so-called F proteins.

Host range: Viruses of the proposed genus infect species from the insect Order Lepidoptera.

Origin of the proposed genus name

Alpha: Greek letter α , a

Baculo: from '*baculum*', meaning *stick*, which refers to the morphology of the nucleocapsid

References

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- Theilmann DA, Blissard GW, Bonning B, Jehle JA, O'Reilly DR, Rohrmann GF, Thiem S, Vlak, JM. (2005) Baculoviridae. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger, U, Ball LA (eds.) *Virus Taxonomy - Eighth Report of the International Committee on Taxonomy of Viruses*. Elsevier, Amsterdam, pp. 1129-185.
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Annexes:

Table 1. Common genes identified in 29 baculovirus genomes.

Function	AcMNPV ORF	Name	CuniNPV	Hymenoptera-spec. NPV	Lepidoptera-spec. NPV und GV
Transcription	28	<i>lef-6</i>	-	-	+
	36	<i>pp31/39K</i>	-	-	+
	37	<i>lef-11</i>	-	+	+
	40	<i>P47</i>	+	+	+
	50	<i>lef-8</i>	+	+	+
	62	<i>lef-9</i>	+	+	+
	77	<i>vlf-1</i>	+	+	+
	90	<i>lef-4</i>	+	+	+
	99	<i>lef-5</i>	+	+	+
	Replication	6	<i>lef-2</i>	+	+
14		<i>lef-1</i>	+	+	+
65		<i>dnapol</i>	+	+	+
67		<i>lef-3</i>	-	-	+
95		<i>helicase</i>	+	+	+
139		<i>me53</i>	-	-	+
147		<i>ie-1</i>	-	-	+
25		<i>dbp1</i>	-	+	+
8		<i>polh</i>	(+)*	+	+
10		<i>pk1</i>	-	-	+
Structural proteins	22	<i>pif-2</i>	+	+	+
	23	<i>efp/ld130</i>	+	-	+
	46	<i>odv-e66</i>	-	-	+
	54	<i>vp1054</i>	+	+	+
	61	<i>fp25K</i>	-	-	+
	80	<i>gp41</i>	+	+	+
	83	<i>vp91/p95</i>	+	+	+
	89	<i>vp39</i>	+	+	+
	94	<i>odv-e25</i>	-	-	+
	100	<i>p6.9</i>	+	+	+
	115	<i>pif-3</i>	+	+	+
	119	<i>pif-1</i>	+	+	+
	138	<i>p74 odv-ep</i>	+	+	+
	143	<i>odv-e18</i>	-	+	+

Function	AcMNPV ORF	Name	CuniNPV	Hymenoptera-spec. NPV	Lepidoptera-spec. NPV und GV
	144	<i>odv-e27</i>	+	+	+
	148	<i>odv-e56</i>	+	+	+
Aux. ¹	32	<i>fgf</i>	-	-	+
	35	<i>ubiquitin</i>	-	-	+
	133	<i>alk-exo</i>	+	+	+
Unknown	38		-	-	+
	13	<i>38.7K</i>	-	-	+
	29		-	-	+
	53		-	+	+
	66	<i>desmop</i>	-	-	+
	68		+	+	+
	75		-	+	+
	76		-	+	+
	78		-	+	+
	81		+	+	+
	82	<i>tlp20</i>	-	-	+
	92	<i>p33</i>	+	+	+
	93		-	+	+
	96	<i>19kda</i>	+	+	+
	98	<i>38K</i>	+	+	+
	101	<i>p40</i>	-	+	+
	102	<i>p12</i>	-	-	+
	103	<i>p45</i>	-	+	+
	106		-	+	+
	109		+	+	+
110		-	-	+	
142	<i>p49</i>	+	+	+	
145		-	+	+	
146		-	-	+	

¹ Auxiliary proteins

* non-homologous to polh of other baculoviruses

Figure 1: Neighbour-Joining tree of the amino acid alignment of 29 baculovirus core genes (genes that are present in all sequenced baculovirus genomes) (Table 1) of 29 sequenced baculovirus genomes. The alignment comprised 16349 positions. All branches have bootstrap values exceeding 50%. Bootstrap values >95% are given along the branches.

