

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

Code <sup>†</sup>	<b>2006.040I.04</b>	To create a new genus in the family*	<i>Baculoviridae</i>
Code <sup>†</sup>	<b>2006.041I.04</b>	To name the new genus*	<i>Gammabaculovirus</i>
Code <sup>†</sup>	<b>2006.042I.04</b>	To designate the species As the type species of the new genus*	<i>Neodiprion lecontei nucleopolyhedrovirus</i>
Code <sup>†</sup>	<b>2006.043I.04</b>	To designate the following as species of the new genus*:	<i>Neodiprion lecontei nucleopolyhedrovirus</i> <i>Neodiprion sertifer nucleopolyhedrovirus</i>

<sup>†</sup> Assigned by ICTV officers

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

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### Old Taxonomic Order

<b>Order</b>	
<b>Family</b>	<i>Baculoviridae</i>
<b>Genus</b>	<i>Nucleopolyhedrovirus</i>
<b>Type Species</b>	<i>Autographa californica multiple nucleopolyhedrovirus</i>
<b>Species in the Genus</b>	<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>Culex nigripalpus</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>Neodiprion lecontei</i> NPV <i>Neodiprion sertifer</i> NPV <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

*Trichoplusia ni* SNPV  
*Wiseana signata* NPV

**Tentative Species in the Genus**

*Aedes sollicitans*  
*Hyphantria cunea* NPV  
*Orgyia pseudotsugata* SNPV  
*Panaeus monodon* NPV  
*Panolis flammea* NPV

**New Taxonomic Order**

**Order**

**Family**

*Baculoviridae*

**Genus**

*Gammabaculovirus*

**Type Species**

*Neodiprion lecontei nucleopolyhedrovirus*

**Species in the Genus**

*Neodiprion sertifer nucleopolyhedrovirus*

**Argumentation to choose the type species in the genus**

We have chosen *Neodiprion lecontei nucleopolyhedrovirus* as the type species since it was the first virus in this proposed genus that was fully sequenced, reported to the scientific community and published in 2004.

**Species demarcation criteria in the genus**

Species demarcation criteria within the family *Baculoviridae* have not been well defined. However, the species reported here differ from all other reported baculoviruses 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**

*Neodiprion lecontei nucleopolyhedrovirus*  
*Neodiprion sertifer nucleopolyhedrovirus*

## Argumentation to create a new genus:

Based on biochemical properties of the occlusion body protein, histopathology as well as genome sequence analyses we propose that these hymenopteran-specific baculoviruses comprise a distinct genus within the *Baculoviridae*.

The proposed genus *Gammabaculovirus* should comprise the hymenopteran-specific baculoviruses, *Neodiprion lecontei nucleopolyhedrovirus* and *Neodiprion sertifer nucleopolyhedrovirus*.

Other Hymenopteran-specific baculoviruses may also belong to this taxa (Herniou et al., 2004). Viruses belonging to this genus have polyhedral OBs of about 0.4-1.1  $\mu\text{m}$  in mean size with single enveloped nucleocapsids (SNPV) in their virions (Ackermann & Smirnov, 1983). The genomes of *Neodiprion lecontei nucleopolyhedrovirus* (NeleNPV) and *Neodiprion sertifer nucleopolyhedrovirus* (NeseNPV) are about 82-86 kbp and appear to be smaller on average than those of lepidopteran-specific NPVs. Neither budded virions nor F or GP64 genes have been identified in current members of this group, suggesting that a BV phenotype may be absent (Lauzon et al., 2004; Garcia-Maruniak et al., 2004). Phylogenetic analyses based on 29 core genes that are conserved in all baculovirus genomes indicate clearly that NeleNPV and NeseNPV form a monophyletic cluster that is distinct from other NPVs (Lauzon et al., 2004; Jehle et al., 2006).

Key descriptors of the proposed genus are:

**Morphology:** 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 0.4 – 1.1  $\mu\text{m}$  in mean size. Occlusion bodies characteristically contain many enveloped virions. The occluded virions contain single (S) nucleocapsids within a single envelope. Existence of budded virions (BV) has not been demonstrated.

**Genome:** The genome consists of a single molecule of circular supercoiled dsDNA. The genomes of NeleNPV and NeseNPV are about 82-86 kbp.

**Pathology:** Viral infection is restricted to epithelial cells in the midgut. No systemic spread of infection to tissues within the hemocoel have been observed. Neither F nor GP64 protein genes are present in the genomes.

**Host range:** Viruses in the proposed genus have been observed infecting insects only in the Order Hymenoptera.

## Origin of the proposed genus name

Gamma: Greek letter  $\alpha$ , a

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

## References

- Ackermann, H-W, Smirnoff, WA (1983) A morphological investigation of 23 baculoviruses. *Journal of invertebrate Pathology* 41: 269-280.
- Garcia-Maruniak A, Maruniak JE, Zannotto PM, Doumbouya AE, Liu JC, Merritt TM, Lanoie JS (2004) Sequence analysis of the genome of the *Neodiprion sertifer* nucleopolyhedrovirus. *Journal of Virology* 78: 7036-51.
- Herniou EA, Olszewski JA, O'Reilly DR, Cory JS (2004) Ancient coevolution of baculoviruses and their insect hosts. *Journal of Virology* 78: 3244-51.
- Jehle JA, Blissard GW, Bonning BC, Cory J, Herniou EA, Rohrmann GF, Theilmann DA, Thiem SM, Vlak JM (2006). On the classification and nomenclature of baculoviruses: A proposal for revision. *Archives of Virology* 151:1 257-66.
- Lauzon HA, Lucarotti CJ, Krell PJ, Feng Q, Retnakaran A, Arif BM (2004) Sequence and organization of the *Neodiprion lecontei* nucleopolyhedrovirus genome. *Journal of Virology* 78: 7023-35.
- Rohrmann GF, Pearson MN, Bailey TJ, Becker RR, Beaudreau GS (1981) N-Terminal polyhedrin sequences and occluded Baculovirus evolution. *Journal of Molecular Evolution* 17, 329-333.

## 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>pp31/39 K</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>	-	+	+
Structural proteins	8	<i>polh</i>	(+)*	+	+
	10	<i>pk1</i>	-	-	+
	22	<i>pif-2</i>	+	+	+
	23	<i>efp/ld13 0</i>	+	-	+
	46	<i>odv-e66</i>	-	-	+
	54	<i>vp1054</i>	+	+	+
	61	<i>fp25K</i>	-	-	+
	80	<i>gp41</i>	+	+	+
	83	<i>vp91/p9 5</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>	-	+	+	
Aux. <sup>1</sup>	144	<i>odv-e27</i>	+	+	+
	148	<i>odv-e56</i>	+	+	+
	32	<i>fgf</i>	-	-	+
	35	<i>ubiquitin</i>	-	-	+
	133	<i>alk-exo</i>	+	+	+
	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		-	+	+
Unkown	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		-	-	+	

<sup>1</sup> Auxiliary proteins

\* non-homologous to *polh* of other baculoviruses

Figure 1: Neighbour Joining tree of the amino acid alignment of 29 baculovirus core genes (Table1) 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.

