

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

- Code<sup>†</sup>  To create a new genus in the family\*
- Code<sup>†</sup>  To name the new genus\*
- Code<sup>†</sup>  To designate   
as the type species of the new genus\*
- Code<sup>†</sup>  To designate the following as species of the new genus\*:

<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

Order	
Family	<i>Baculoviridae</i>
Genus	<i>Nucleopolyhedrovirus</i>
Type Species	<i>Autographa californica multiple nucleopolyhedrovirus</i>
Species in the Genus	<i>Adoxophyes honmai NPV</i> <i>Agrotis ipsilon NPV</i> <i>Anticarsia gemmatalis MNPV</i> <i>Autographa californica MNPV</i> <i>Bombyx mori NPV</i> <i>Buzura suppressaria NPV</i> <i>Choristoneura fumiferana DEF MNPV</i> <i>Choristoneura fumiferana MNPV</i> <i>Choristoneura rosaceana NPV</i> <u><i>Culex nigripalpus NPV</i></u> <i>Ectropis obliqua NPV</i> <i>Epiphyas postvittana NPV</i> <i>Helicoverpa armigera NPV</i> <i>Helicoverpa zea NPV</i> <i>Lymantria dispar MNPV</i> <i>Mamestra brassicae MNPV</i> <i>Mamestra configurata NPV-A</i> <i>Mamestra configurata NPV-B</i> <i>Neodiprion lecontei NPV</i> <i>Neodiprion sertifer NPV</i> <i>Orgyia pseudotsugata MNPV</i>

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

**Tentative Species in the Genus**

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

**New Taxonomic Order**

<b>Order</b>	
<b>Family</b>	<i>Baculoviridae</i>
<b>Genus</b>	<i>Deltabaculovirus</i>
<b>Type Species</b>	<i>Culex nigripalpus nucleopolyhedrovirus</i>
<b>Species in the Genus</b>	<i>Culex nigripalpus nucleopolyhedrovirus</i>

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

We have chosen *Culex nigripalpus nucleopolyhedrovirus* as the type species since it was the first virus in this genus that was fully sequenced and published in 2002.

**Species demarcation criteria in the genus**

Species demarcation criteria within this genus are not yet developed since genus contains only one type species and one tentative species.

**List of Species in the created genus**

*Culex nigripalpus 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 dipteran-specific *Culex nigripalpus nucleopolyhedrovirus* comprises a distinct genus within the *Baculoviridae*.

The proposed genus should only include the species *Culex nigripalpus nucleopolyhedrovirus* at this time. Two virus phenotypes may be characteristic of a virus species: budded virions and occluded virions. *Culex nigripalpus nucleopolyhedrovirus* (CuniNPV) has globular OBs of about 400 nm in diameter. Infection of host mosquito larvae by CuniNPV is restricted to epithelial cells of the larval midgut (Moser et al., 2001). The occlusion body protein of CuniNPV is not homologous to the polyhedrin or granulin genes of the baculoviruses infecting Lepidoptera and Hymenoptera (Perera et al., 2006).

The polyhedral OB protein of CuniNPV is about 90 kDa in size and is non-homologous to the 25-33 kDa OB protein of lepidopteran- and hymenopteran-specific baculoviruses (Perera et al., 2006). The genome of CuniNPV shares only 30 ORFs with other lepidopteran-specific NPVs and GVs. This indicates that the phylogenetic distance between CuniNPV and lepidopteran NPVs is much greater than between lepidopteran NPVs and GVs.

Key descriptors of the proposed genus *Deltabaculovirus* are:

**Morphology:** Eventually two virus phenotypes, budded virions (BV) and occluded virions (ODV) may exist, though evidence for existence of BV is not conclusive. Virions of the ODV phenotype are embedded within a globular occlusion body of a crystalline matrix of a single viral protein (polyhedron). The polyhedrin protein of CuniNPV is not a homologue of Polyhedrins of baculoviruses from lepidopteran, and hymenopteran hosts. The occlusion body measures about 0.4  $\mu\text{m}$  in mean size. Occlusion bodies characteristically contain several enveloped virions. The occluded virions are packaged with single (S) nucleocapsids within a single envelope.

**Genome:** The genome consists of a single molecule of circular supercoiled dsDNA. The genome of CuniNPV is about 80 kbp and is similar in size to genomes of those baculoviruses with smaller genomes.

**Pathology:** Viral infection is restricted to epithelial cells in the midgut. No systemic spread of infection was observed. An F protein gene is present in the genome but budded virions have not yet been isolated and characterized.

**Host range:** Viruses in the proposed genus infect insects in the Order Diptera.

## Origin of the proposed genus name

Delta: Greek letter  $\delta$ , d

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

## References

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- Afonso CL, Tulman ER, Lu Z, Balinsky CA, Moser BA, Becnel JJ, Rock DL, Kutish GF (2001) Genome sequence of a baculovirus pathogenic for *Culex nigripalpus*. *Journal of Virology* 75: 11157-11165.
- Herniou EA, Olszewski JA, O'Reilly DR, Cory JS (2004) Ancient coevolution of baculoviruses and their insect hosts. *Journal of Virology* 78: 3244-51.
- Moser BA, Becnel JJ, White SE, Afonso C, Kutish G, Shanker S, Almira E (2001) Morphological and molecular evidence that *Culex nigripalpus* baculovirus is an unusual member of the family Baculoviridae. *Journal of General Virology* 82: 283-297.
- Perera OP, Valles SM, Green TB, White S, Strong CA, Becnel JJ (2006) Molecular analysis of an occlusion body protein from *Culex nigripalpus* nucleopolyhedrovirus (CuniNPV). *Journal of Invertebrate Pathology* 91: 35-42.
- 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. *Arch Virol.* 151:1 257-66.
- 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>	-	-	+
Structural proteins	25	<i>dbp1</i>	-	+	+
	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>	-	+	+	
Function	AcMNPV ORF	Name	CuniNPV	Hymenoptera-spec. NPV	Lepidoptera-spec. NPV und GV
Aux. <sup>1</sup>	144	<i>odv-e27</i>	+	+	+
	148	<i>odv-e56</i>	+	+	+
	32	<i>fgf</i>	-	-	+
Unkown	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		-	+	+
	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.

