



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:	2012.001aI	(to be completed by ICTV officers)			
Short title: Eight new species in 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"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <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 (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: May, 2012
Date of this revision (if different to above): 25 July 2012

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	2012.001aI	(assigned by ICTV officers)
To create 8 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:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Agrotis segetum nucleopolyhedrovirus</i>		DQ123841
<i>Antheraea pernyi nucleopolyhedrovirus</i>		DQ486030
<i>Chrysodeixis chalcites nucleopolyhedrovirus</i>		AY864330
<i>Clanis bilineata nucleopolyhedrovirus</i>		DQ504428
<i>Euproctis pseudoconspersa nucleopolyhedrovirus</i>		FJ227128
<i>Hyphantria cunea nucleopolyhedrovirus</i>		AP009046
<i>Leucania separata nucleopolyhedrovirus</i>		AY394490
<i>Maruca vitrata nucleopolyhedrovirus</i>		EF125867

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria. ○ If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria. • Further material in support of this proposal may be presented in the Appendix, Module 9
<p>Isolates of the proposed species can be identified as belonging to the genus <i>Alphabaculovirus</i> 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 proposed species to other recognized species in the <i>Baculoviridae</i>, as determined from the concatenated alignment of the predicted amino acid sequences of 28 baculovirus core genes (van Oers and Vlcek 2007). Reference isolates for all eight of the proposed species occur in the <i>Alphabaculovirus</i> clade in the Figure 1 phylogram.</p> <p>Distinctions among species of the <i>Baculoviridae</i> have been based on host range, DNA</p>

restriction endonuclease fragment patterns, and comparisons of nucleotide and predicted amino acid sequences from various genes. A proposed species demarcation criterion was published in 2006 that is based on pairwise nucleotide distances estimated using the Kimura 2-parameter model of nucleotide substitution (Jehle et al 2006). According to this criterion, if nucleotide distances between two baculoviruses, estimated from alignments of partial *lef-8*, *lef-9*, and *polh* genes, are less than 0.015 substitutions/site, the two baculoviruses are considered to be the same species. If pairwise nucleotide distances between two viruses at these loci 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 are considered. The proposed criterion was originally based on comparisons of sequences from 117 separate baculovirus isolates, and researchers have applied this criterion to other isolates to identify potential new baculovirus species and variants of currently recognized species.

Isolates of all of the proposed species have been identified from different lepidopteran host species. Pairwise Kimura 2-parameter distances for reference isolates of the eight proposed species are listed in Tables 1 and 2. Distances calculated from alignments of the individual *lef-8*, *lef-9*, and *polh* sequences are reported along with distances calculated from alignments that have been concatenated together, as genetic distances for the three loci can vary considerably due to different rates of evolution as well as homologous recombination with other baculoviruses. All of the pairwise distances of the eight proposed species for both the single-locus and the concatenated alignments are well in excess of 0.05 substitutions/site (Tables 1 and 2, red type). Branch lengths in the Figure 1 phylogram separating these eight viruses from their closest relatives are in a range that is comparable to the branch lengths separating other recognized alphabaculovirus species. Distinctive genome features and gene compositions for these viruses are detailed in the publications describing the genomes of these viruses.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Baculoviridae core genes and proposed species demarcation criterion

Jehle, J. A., Lange, M., Wang, H., Hu, Z., Wang, Y., and Hauschild, R. (2006). Molecular identification and phylogenetic analysis of baculoviruses from Lepidoptera. *Virology* 346, 180-93.

van Oers, M., and Vlak, J. M. (2007). Baculovirus genomics. *Current Drug Targets* 8, 1051-1068.

Agrotis segetum nucleopolyhedrovirus A

Jakubowska, A., van Oers, M. M., Ziemnicka, J., Lipa, J. J., and Vlak, J. M. (2005). Molecular characterization of *Agrotis segetum* nucleopolyhedrovirus from Poland. *Journal of Invertebrate Pathology* 90, 64-68.

Jakubowska, A. K., Peters, S. A., Ziemnicka, J., Vlak, J. M., and van Oers, M. M. (2006). Genome sequence of an enhancin gene-rich nucleopolyhedrovirus (NPV) from *Agrotis segetum*: collinearity with *Spodoptera exigua* multiple NPV. *Journal of General Virology* 87, 537-551.

Antheraea pernyi nucleopolyhedrovirus

Fan, Q., Li, S., Wang, L., Zhang, B., Ye, B., Zhao, Z., and Cui, L. (2007). The genome sequence of the multinucleocapsid nucleopolyhedrovirus of the Chinese oak silkworm *Antheraea pernyi*. *Virology* 366, 304-315.

Nie, Z. M., Zhang, Z. F., Wang, D., He, P. A., Jiang, C. Y., Song, L., Chen, F., Xu, J., Yang, L., Yu, L. L., Chen, J., Lv, Z. B., Lu, J. J., Wu, X. F., and Zhang, Y. Z. (2007). Complete sequence and organization of *Antheraea pernyi* nucleopolyhedrovirus, a dr-rich baculovirus. *BMC Genomics* 8, 248.

Chrysodeixis chalcites nucleopolyhedrovirus

van Oers, M. M., Herniou, E. A., Usmany, M., Messelink, G. J., and Vlak, J. M. (2004). Identification and characterization of a DNA photolyase-containing baculovirus from *Chrysodeixis chalcites*. *Virology* 330, 460-470.

van Oers, M. M., Abma-Henkens, M. H., Herniou, E. A., de Groot, J. C., Peters, S., and Vlak, J. M. (2005). Genome sequence of *Chrysodeixis chalcites* nucleopolyhedrovirus, a baculovirus with two DNA photolyase genes. *Journal of General Virology* 86, 2069-2080.

Clanis bilineata nucleopolyhedrovirus

Wang, L., Yi, J., Zhu, S., Li, B., Chen, Y., Shen, W., and Wang, W. (2008). Identification of a single-nucleocapsid baculovirus isolated from *Clanis bilineata tsingtauica* (Lepidoptera: Sphingidae). *Archives of Virology* 153, 1557-1561.

Zhu, S. Y., Yi, J. P., Shen, W. D., Wang, L. Q., He, H. G., Wang, Y., Li, B., and Wang, W. B. (2009). Genomic sequence, organization and characteristics of a new nucleopolyhedrovirus isolated from *Clanis bilineata* larva. *BMC Genomics* 10, 91.

Euproctis pseudoconspersa nucleopolyhedrovirus

additional material in support of this proposal

References:

Tang, X. D., Xiao, Q., Ma, X. C., Zhu, Z. R., and Zhang, C. X. (2009). Morphology and genome of *Euproctis pseudoconspersa* nucleopolyhedrovirus. *Virus Genes* 38, 495-506.

Hyphantria cunea nucleopolyhedrovirus

Kamiya, K., Okimoto, N., Ikeda, M., Kunimi, Y., Kobayashi, M., and Kawamura, S. (2003). Genotypic variation of a wild isolate of *Hyphantria cunea* nucleopolyhedrovirus. *Journal of Insect Biotechnology and Sericology* 72, 57-64.

Ikeda, M., Shikata, M., Shirata, N., Chaeychomsri, S., and Kobayashi, M. (2006). Gene organization and complete sequence of the *Hyphantria cunea* nucleopolyhedrovirus genome. *Journal of General Virology* 87, 2549-2562.

Leucania separata nucleopolyhedrovirus

Wang, J. W., Qi, Y. P., Huang, Y. X., and Li, S. D. (1995). Nucleotide sequence of a 1446 base pair Sall fragment and structure of a novel early gene of *Leucania separata* nuclear polyhedrosis virus. *Archives of Virology* 140, 2283-2291.

Xiao, H., and Qi, Y. (2007). Genome sequence of *Leucania seperata* nucleopolyhedrovirus. *Virus Genes* 35, 845-856.

Maruca vitrata nucleopolyhedrovirus

Lee, S. T., Srinivasan, R., Wu, W. J., and Talekar, N. S. (2007). Occurrence and characterization of a nucleopolyhedrovirus from *Maruca vitrata* (Lepidoptera, Pyralidae) isolated in Taiwan. *BioControl* 52, 801-809.

Chen, Y. R., Wu, C. Y., Lee, S. T., Wu, Y. J., Lo, C. F., Tsai, M. F., and Wang, C. H. (2008). Genomic and host range studies of *Maruca vitrata* nucleopolyhedrovirus. *Journal of General Virology* 89, 2315-2330.

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.

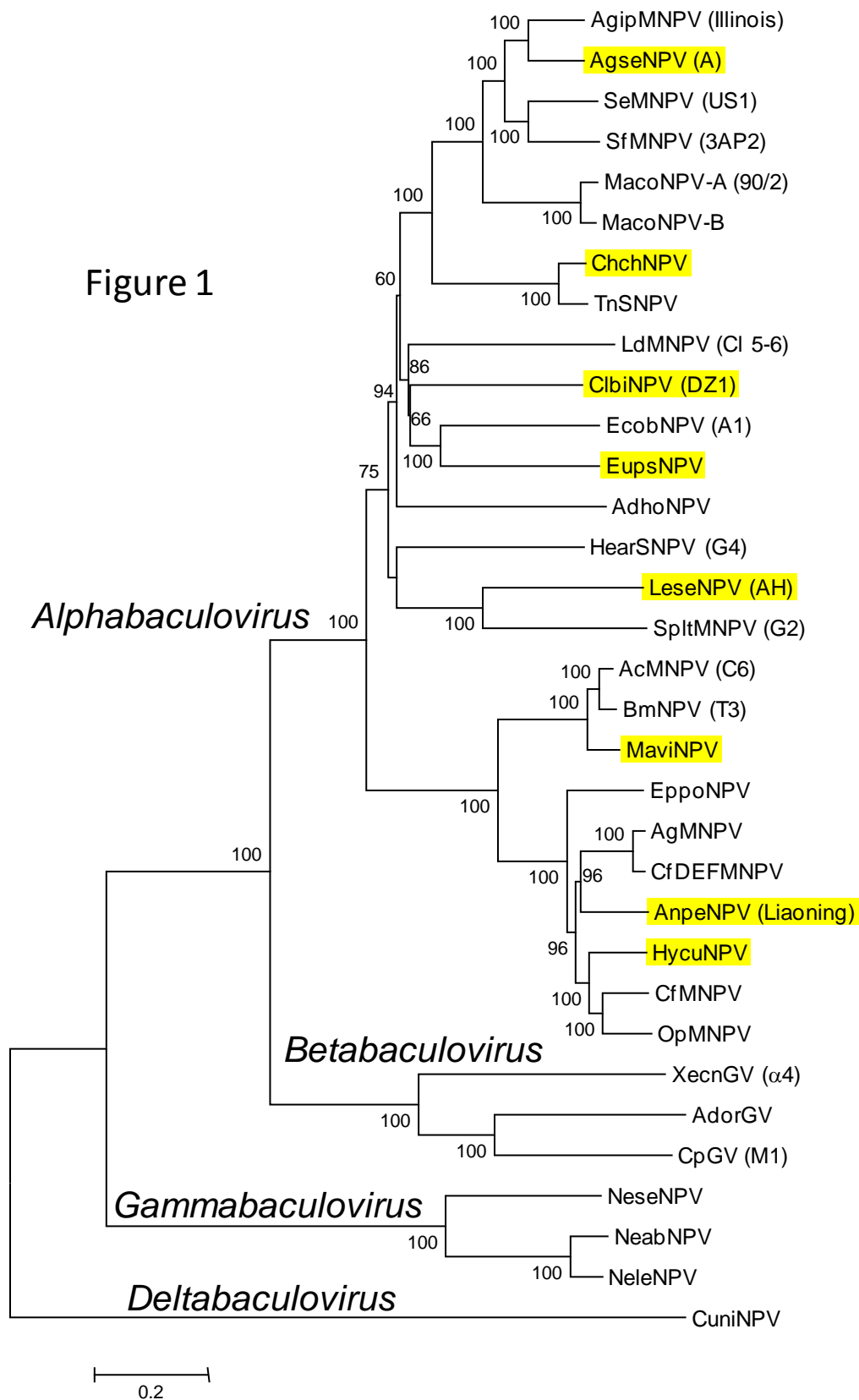


Figure 1. Relationships of recognized and proposed baculovirus species, inferred from the predicted amino acid sequences of baculovirus core genes. Phylogenetic tree was constructed from the concatenated alignments of 28 baculovirus core gene amino acid sequences using the minimum-evolution method. Proposed species are highlighted in yellow, and clades corresponding to the four genera of *Baculoviridae*

are indicated. Virus taxa include *Adoxophyes orana granulovirus* (AdorGV), *Adoxophyes honmai nucleopolyhedrovirus* (AdhoNPV), *Agrotis ipsilon multiple nucleopolyhedrovirus* (AgipMNPV), *Agrotis segetum nucleopolyhedrovirus* (AgseNPV), *Antheraea pernyi nucleopolyhedrovirus* (AnpeNPV), *Anticarsia gemmatalis multiple nucleopolyhedrovirus* (AgMNPV), *Autographa californica multiple nucleopolyhedrovirus* (AcMNPV), *Bombyx mori nucleopolyhedrovirus* (BmNPV), *Choristoneura fumiferana multiple nucleopolyhedrovirus* (CfMNPV), *Choristoneura fumiferana DEF multiple nucleopolyhedrovirus* (CfDEFNPV), *Chrysodeixis chalcites nucleopolyhedrovirus* (ChchNPV), *Clanis bilineata nucleopolyhedrovirus* (CibiNPV), *Culex nigripalpus nucleopolyhedrovirus* (CuniNPV), *Cydia pomonella granulovirus* (CpGV), *Ecotropis obliqua nucleopolyhedrovirus* (EcobNPV), *Epiphyas postvittana nucleopolyhedrovirus* (EppoNPV), *Euproctis pseudoconspersa nucleopolyhedrovirus* (EupsNPV), *Helicoverpa armigera nucleopolyhedrovirus* (HearSNPV), *Hyphantria cunea nucleopolyhedrovirus* (HycuNPV), *Leucania separata nucleopolyhedrovirus* (LeseNPV), *Lymantria dispar multiple nucleopolyhedrovirus* (LdMNPV), *Mamestra configurata nucleopolyhedroviruses -A and -B* (MacoNPV-A and -B), *Maruca vitrata nucleopolyhedrovirus* (MaviNPV), *Neodiprion abietis nucleopolyhedrovirus* (NeabNPV), *Neodiprion lecontei nucleopolyhedrovirus* (NeleNPV), *Neodiprion sertifer nucleopolyhedrovirus* (NeseNPV), *Spodoptera exigua multiple nucleopolyhedrovirus* (SeMNPV), *Spodoptera frugiperda multiple nucleopolyhedrovirus* (SfMNPV), *Spodoptera litura multiple nucleopolyhedrovirus* (SpltMNPV), *Trichoplusia ni single nucleopolyhedrovirus* (TnSNPV), and *Xestia c-nigrum granulovirus* (XecnGV).

Table 1. Pairwise nucleotide distances calculated from partial *lef-8* and *lef-9* sequence alignments*

<i>lef8</i>	<i>lef9</i>	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
1 AcMNPV		0.457	0.435	0.412	0.316	0.230	0.031	0.230	0.291	0.387	0.734	0.409	0.253	0.475	0.492	0.323	0.395	0.469	0.434	0.393	0.122	0.282	0.403	0.423	0.545	0.379	
2 AdhoNPV		0.705		0.378	0.328	0.493	0.513	0.414	0.492	0.523	0.315	0.534	0.378	0.471	0.360	0.376	0.514	0.447	0.388	0.312	0.292	0.439	0.500	0.337	0.362	0.487	0.370
3 AgipMNPV		0.716	0.839		0.175	0.310	0.385	0.394	0.401	0.359	0.335	0.566	0.331	0.438	0.372	0.438	0.367	0.298	0.298	0.236	0.265	0.405	0.309	0.243	0.228	0.393	0.298
4 AgseNPV		0.727	0.820	0.300		0.359	0.408	0.373	0.416	0.350	0.383	0.500	0.356	0.480	0.373	0.504	0.352	0.273	0.344	0.247	0.249	0.408	0.336	0.229	0.209	0.457	0.382
5 AnpeNPV		0.684	0.790	0.606	0.706		0.188	0.303	0.172	0.132	0.428	0.645	0.412	0.264	0.459	0.487	0.157	0.344	0.397	0.366	0.389	0.319	0.127	0.411	0.367	0.516	0.442
6 AgMNPV		0.609	0.722	0.685	0.747	0.345		0.218	0.023	0.166	0.385	0.750	0.432	0.166	0.451	0.463	0.155	0.407	0.483	0.409	0.409	0.261	0.171	0.424	0.397	0.580	0.431
7 BmNPV		0.038	0.695	0.750	0.747	0.677	0.627		0.219	0.292	0.371	0.686	0.408	0.235	0.446	0.474	0.309	0.393	0.434	0.402	0.371	0.123	0.256	0.386	0.375	0.504	0.371
8 CfDEFMNPV		0.603	0.691	0.698	0.775	0.314	0.040	0.621		0.150	0.416	0.754	0.423	0.160	0.459	0.455	0.155	0.400	0.466	0.401	0.401	0.289	0.155	0.440	0.412	0.590	0.473
9 CfMNPV		0.548	0.705	0.645	0.650	0.330	0.337	0.572	0.319		0.479	0.747	0.434	0.230	0.463	0.516	0.132	0.353	0.436	0.409	0.451	0.344	0.103	0.401	0.391	0.502	0.492
10 ChchNPV		0.743	0.653	0.699	0.689	0.817	0.730	0.737	0.720	0.736		0.529	0.385	0.489	0.341	0.296	0.429	0.426	0.338	0.349	0.316	0.379	0.459	0.291	0.303	0.425	0.088
11 CibiNPV		0.775	0.625	0.764	0.821	0.906	0.720	0.781	0.731	0.761	0.580		0.552	0.761	0.648	0.433	0.651	0.615	0.421	0.552	0.589	0.675	0.692	0.565	0.530	0.469	0.541
12 EcobNPV		0.708	0.613	0.677	0.665	0.753	0.674	0.715	0.665	0.691	0.581	0.504		0.434	0.303	0.411	0.469	0.346	0.357	0.332	0.370	0.470	0.467	0.360	0.324	0.446	0.354
13 EppoNPV		0.558	0.693	0.781	0.842	0.376	0.306	0.579	0.293	0.376	0.764	0.731	0.721		0.499	0.430	0.247	0.467	0.523	0.459	0.410	0.293	0.237	0.523	0.436	0.613	0.476
14 EupsNPV		0.675	0.647	0.643	0.682	0.738	0.643	0.684	0.667	0.643	0.620	0.543	0.501	0.684		0.416	0.445	0.412	0.411	0.373	0.381	0.421	0.461	0.333	0.359	0.453	0.386
15 HearSNPV		0.791	0.702	0.677	0.763	0.763	0.753	0.812	0.775	0.749	0.618	0.628	0.628	0.671	0.492		0.506	0.462	0.378	0.359	0.330	0.447	0.550	0.399	0.405	0.374	0.335
16 HycuNPV		0.586	0.741	0.666	0.731	0.383	0.316	0.610	0.295	0.246	0.704	0.803	0.692	0.353	0.654	0.681		0.351	0.444	0.426	0.435	0.308	0.084	0.404	0.375	0.533	0.460
17 LdMNPV		0.761	0.776	0.539	0.631	0.575	0.681	0.784	0.678	0.607	0.600	0.636	0.677	0.787	0.505	0.572	0.696		0.333	0.326	0.362	0.361	0.325	0.293	0.344	0.387	0.377
18 LeseNPV		0.727	0.846	0.517	0.541	0.663	0.782	0.781	0.768	0.692	0.669	0.821	0.767	0.767	0.703	0.758	0.792	0.579		0.321	0.357	0.496	0.351	0.325	0.362	0.284	0.319
19 MacoNPV-A		0.743	0.783	0.569	0.566	0.815	0.882	0.764	0.887	0.781	0.703	0.721	0.763	0.832	0.742	0.694	0.765	0.675	0.625		0.061	0.394	0.378	0.272	0.232	0.344	0.328
20 MacoNPV-B		0.792	0.797	0.538	0.540	0.831	0.896	0.802	0.880	0.791	0.692	0.717	0.716	0.862	0.734	0.656	0.787	0.688	0.641	0.105		0.386	0.433	0.294	0.232	0.378	0.322
21 MaviNPV		0.101	0.653	0.737	0.736	0.665	0.580	0.122	0.584	0.557	0.704	0.806	0.665	0.535	0.651	0.728	0.569	0.787	0.769	0.728	0.768		0.311	0.442	0.375	0.538	0.393
22 OpMNPV		0.625	0.821	0.590	0.636	0.272	0.331	0.647	0.307	0.196	0.735	0.779	0.743	0.416	0.680	0.744	0.268	0.554	0.652	0.862	0.852	0.631		0.385	0.382	0.484	0.456
23 SeMNPV		0.796	0.836	0.390	0.441	0.709	0.812	0.797	0.784	0.779	0.696	0.793	0.704	0.847	0.700	0.768	0.746	0.651	0.620	0.579	0.577	0.770	0.776		0.204	0.386	0.293
24 SfMNPV		0.733	0.811	0.567	0.534	0.875	0.809	0.751	0.818	0.834	0.704	0.677	0.649	0.817	0.659	0.786	0.841	0.757	0.681	0.569	0.572	0.777	0.908	0.319		0.357	0.311
25 SplitMNPV		0.796	0.840	0.401	0.462	0.743	0.819	0.803	0.802	0.803	0.779	0.770	0.695	0.830	0.720	0.801	0.826	0.681	0.656	0.585	0.587	0.773	0.816	0.163	0.296		0.416
26 TnSNPV		0.757	0.671	0.704	0.714	0.857	0.733	0.744	0.705	0.766	0.160	0.582	0.623	0.743	0.679	0.613	0.733	0.637	0.711	0.694	0.678	0.714	0.770	0.736	0.653	0.739	

*The number of base substitutions per site between pairs of sequences are shown. Abbreviations of the taxa are as listed for Figure 1. Analyses were conducted using the Kimura 2-parameter model in MEGA5. Pairwise distances for *lef-8* (Table 1) and the concatenated *lef-8/lef-9/polh* (Table 2) sequences are listed below the diagonal lines, and *lef-9* (Table 1) and *polh* (Table 2) distances are listed above the diagonal lines. Values for the proposed species are in red bold type.

Table 2. Pairwise nucleotide distances calculated from partial *polh* sequence alignments and partial *lef-8*, *lef-9*, and *polh* sequence alignments that have been concatenated together*

<i>polh</i>	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
<i>lef8-lef9-polh</i>																										
1 AcMNPV		0.297	0.219	0.244	0.297	0.311	0.302	0.304	0.277	0.192	0.341	0.257	0.337	0.382	0.366	0.284	0.315	0.263	0.178	0.193	0.296	0.253	0.269	0.212	0.292	0.177
2 AdhoNPV	0.489		0.275	0.266	0.323	0.319	0.382	0.321	0.295	0.278	0.306	0.270	0.332	0.305	0.310	0.262	0.340	0.317	0.247	0.233	0.364	0.283	0.264	0.273	0.280	0.233
3 AgipMNPV	0.450	0.503		0.144	0.291	0.305	0.287	0.274	0.300	0.235	0.263	0.252	0.321	0.334	0.325	0.312	0.304	0.217	0.181	0.204	0.272	0.270	0.177	0.168	0.279	0.241
4 AgseNPV	0.462	0.482	0.219		0.281	0.306	0.292	0.278	0.298	0.249	0.291	0.257	0.291	0.360	0.317	0.316	0.310	0.225	0.207	0.230	0.295	0.261	0.215	0.193	0.269	0.250
5 AnpeNPV	0.453	0.536	0.423	0.463		0.141	0.201	0.147	0.193	0.312	0.338	0.321	0.157	0.405	0.367	0.208	0.293	0.287	0.268	0.274	0.180	0.174	0.291	0.290	0.340	0.292
6 AgMNPV	0.414	0.516	0.473	0.497	0.237		0.203	0.046	0.201	0.293	0.333	0.300	0.168	0.353	0.335	0.180	0.322	0.273	0.276	0.299	0.175	0.190	0.280	0.309	0.314	0.284
7 BmNPV	0.116	0.515	0.485	0.483	0.402	0.370		0.191	0.228	0.311	0.330	0.307	0.202	0.386	0.386	0.228	0.322	0.290	0.305	0.295	0.105	0.221	0.306	0.302	0.373	0.300
8 CfDEFMNPV	0.409	0.502	0.465	0.494	0.224	0.039	0.362		0.201	0.280	0.345	0.288	0.142	0.362	0.334	0.166	0.294	0.265	0.271	0.272	0.178	0.182	0.275	0.279	0.313	0.276
9 CfMNPV	0.392	0.499	0.451	0.449	0.240	0.254	0.379	0.243		0.319	0.331	0.266	0.195	0.344	0.342	0.204	0.320	0.266	0.252	0.288	0.218	0.155	0.289	0.303	0.290	0.296
10 ChchNPV	0.434	0.434	0.434	0.446	0.527	0.481	0.488	0.478	0.514		0.293	0.271	0.318	0.355	0.298	0.319	0.321	0.305	0.223	0.214	0.295	0.279	0.279	0.208	0.308	0.126
11 CibiNPV	0.581	0.480	0.513	0.533	0.608	0.561	0.570	0.571	0.573	0.456		0.341	0.363	0.281	0.287	0.349	0.400	0.337	0.258	0.249	0.345	0.330	0.292	0.271	0.362	0.290
12 EcobNPV	0.463	0.431	0.437	0.440	0.508	0.477	0.488	0.466	0.466	0.422	0.450		0.273	0.249	0.285	0.265	0.277	0.235	0.210	0.205	0.307	0.268	0.238	0.251	0.215	0.243
13 EppoNPV	0.411	0.503	0.522	0.532	0.270	0.228	0.357	0.211	0.280	0.525	0.580	0.479		0.377	0.349	0.183	0.322	0.299	0.299	0.281	0.165	0.166	0.281	0.312	0.308	0.344
14 EupsNPV	0.520	0.452	0.468	0.493	0.550	0.491	0.520	0.506	0.489	0.460	0.452	0.366	0.526		0.287	0.338	0.420	0.356	0.296	0.276	0.344	0.375	0.303	0.389	0.338	0.344
15 HearSNPV	0.559	0.479	0.491	0.530	0.549	0.526	0.571	0.531	0.537	0.428	0.455	0.453	0.497	0.400		0.340	0.436	0.346	0.310	0.282	0.349	0.337	0.297	0.312	0.325	0.332
16 HycuNPV	0.416	0.493	0.465	0.485	0.272	0.234	0.396	0.221	0.209	0.494	0.583	0.472	0.269	0.487	0.511		0.329	0.299	0.250	0.269	0.210	0.165	0.283	0.278	0.336	0.304
17 LdMNPV	0.502	0.528	0.401	0.430	0.418	0.482	0.512	0.466	0.443	0.456	0.539	0.448	0.528	0.457	0.501	0.476		0.278	0.258	0.310	0.348	0.288	0.331	0.279	0.303	0.299
18 LeseNPV	0.482	0.527	0.358	0.379	0.459	0.508	0.504	0.495	0.466	0.456	0.538	0.461	0.523	0.508	0.518	0.515	0.412		0.219	0.262	0.281	0.264	0.198	0.235	0.169	0.274
19 MacoNPV-A	0.437	0.458	0.347	0.361	0.491	0.524	0.501	0.520	0.482	0.431	0.493	0.442	0.532	0.485	0.474	0.480	0.433	0.401		0.091	0.299	0.245	0.187	0.170	0.273	0.209
20 MacoNPV-B	0.451	0.450	0.354	0.362	0.504	0.539	0.501	0.519	0.512	0.417	0.493	0.434	0.520	0.475	0.442	0.497	0.470	0.434	0.092		0.307	0.267	0.208	0.196	0.277	0.183
21 MaviNPV	0.167	0.497	0.475	0.488	0.392	0.351	0.116	0.359	0.379	0.470	0.584	0.483	0.337	0.484	0.519	0.374	0.517	0.508	0.485	0.499		0.230	0.274	0.310	0.321	0.296
22 OpMNPV	0.406	0.526	0.408	0.425	0.208	0.248	0.393	0.232	0.164	0.490	0.571	0.490	0.284	0.516	0.539	0.193	0.404	0.434	0.495	0.516	0.403		0.246	0.246	0.279	0.281
23 SeMNPV	0.494	0.488	0.282	0.315	0.479	0.509	0.508	0.501	0.497	0.443	0.536	0.445	0.538	0.469	0.508	0.486	0.453	0.394	0.361	0.375	0.495	0.472		0.148	0.209	0.278
24 SfMNPV	0.449	0.490	0.336	0.334	0.518	0.516	0.489	0.506	0.518	0.413	0.480	0.423	0.528	0.493	0.515	0.504	0.471	0.434	0.339	0.353	0.500	0.506	0.232		0.252	0.230
25 SpltMNPV	0.534	0.530	0.355	0.388	0.535	0.561	0.569	0.555	0.527	0.514	0.546	0.449	0.565	0.516	0.524	0.563	0.473	0.382	0.417	0.426	0.539	0.522	0.213	0.290		0.250
26 TnSNPV	0.428	0.430	0.430	0.455	0.530	0.487	0.485	0.482	0.516	0.135	0.458	0.418	0.527	0.487	0.449	0.502	0.450	0.451	0.417	0.398	0.477	0.502	0.456	0.410	0.471	

* See footnote for Table 1.