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:	***2015.009aS***	(to be completed by ICTV officers)

Short title: 1 new species (*Antheraea pernyi iflavirus*) in the family *Iflaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒ **6** ☐	**2** ☒ **7** ☐	**3** ☐ **8** ☐	**4** ☐ **9** ☐	**5** ☐ **10** ☒

Author(s):

Peng Geng, Wenli Li, Lan Lin, Joachim R. de Miranda, Scott Emrich, Lijia An, Olle Terenius

Corresponding author with e-mail address:

Olle Terenius, olle.terenius@slu.se

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)	*Dicistroviridae* & *Iflaviridae* Study Group

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:	25/06/2015
Date of this revision (if different to above):	29/10/2015

ICTV-EC comments and response of the proposer:

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	***2015.009aS***

(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Iflavirus***
Subfamily:	-
Family:	***Iflaviridae***
Order:	***Picornavirales***

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Antheraea pernyi iflavirus	LnApIV-02	KF751885

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - 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

Species demarcation criteria for the members of the genus *Iflavirus*:

- Natural host range: species can be differentiated on the basis of their natural host range
- Sequence identity between the CPs of isolates and strains of a species is above 90%.

The genome organization, amino acid sequence and phylogenetic analyses suggest that the virus is a novel species (Appendix Figures 1 & 2; Appendix Table 1).

Antheraea pernyi iflavirus (ApIV) is most closely related to the DWV/VDV-1 species complex, but distinct enough to be considered a new species within the *Iflaviridae*.

The virus is monocistronic, with a single-stranded RNA genome of at least 10,163 nucleotides excluding the poly(A) tail and contains a single, large open reading frame encoding a 3,036 amino acid polyprotein containing domains for both structural and non-structural replication proteins.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Geng P, Li W, Lin L, de Miranda JR, Emrich S, Lijia A, Terenius O (2014) Genetic Characterization of a Novel Iflavirus Associated with Vomiting Disease in the Chinese Oak Silkmoth Antheraea pernyi. PLoS ONE 9(3): e92107. doi:10.1371/journal.pone.0092107

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.

Table 1. Percentage amino acid differences between accepted and proposed iflavirus species. Values below 10% are highlighted.

		DWV	EoV	IFV	LlV-1	NlHV-1	PnV	SBV	SBPV	VDV	ApIV	DCPV	LdIV-1	SeIV-1	SeIV-2
Deformed wing virus AJ489744	DWV	0.0	81.1	84.3	83.8	71.5	80.4	80.6	70.9	2.9	66.1	80.2	64.9	85.9	79.8
Ectropis obliqua virus AY365064	EoV	81.1	0.0	84.0	84.9	85.5	9.9	84.4	84.6	80.7	82.7	84.4	83.0	84.4	49.9
Infectious flacherie virus AB000906	IFV	84.3	84.0	0.0	86.8	84.2	84.1	85.3	84.7	83.9	83.6	88.0	84.0	61.9	83.4
Lygus lineolaris virus 1 JF720348	LlV-1	83.8	84.9	86.8	0.0	85.7	85.4	55.8	85.6	83.7	84.6	86.8	84.2	85.0	85.3
Nilaparvata lugens honeydew virus 1 AB766259	NlHV-1	71.5	85.5	84.2	85.7	0.0	85.3	83.9	74.8	72.1	73.7	80.6	74.8	87.1	85.4
Perina nuda virus AF323747	PnV	80.4	9.9	84.1	85.4	85.3	0.0	85.2	83.8	80.2	83.0	84.9	83.1	84.3	51.8
Sacbrood virus AF092924	SBV	80.6	84.4	85.3	55.8	83.9	85.2	0.0	83.8	80.8	82.2	86.3	81.7	85.0	85.7
Slow bee paralysis virus EU035616	SBPV	70.9	84.6	84.7	85.6	74.8	83.8	83.8	0.0	71.0	70.8	80.6	71.4	87.8	83.4
Varroa destructor virus-1 AY251269	VDV	2.9	80.7	83.9	83.7	72.1	80.2	80.8	71.0	0.0	66.2	80.6	64.8	86.1	80.0
Antheraea pernyi iflavirus KF751885	ApIV	66.1	82.7	83.6	84.6	73.7	83.0	82.2	70.8	66.2	0.0	80.5	21.1	83.9	83.2
Dinocampus coccinellae paralysis virus KF843822	DCPV	80.2	84.4	88.0	86.8	80.6	84.9	86.3	80.6	80.6	80.5	0.0	80.6	85.9	86.2
Lymantria dispar iflavirus 1 KJ629170	LdIV-1	64.9	83.0	84.0	84.2	74.8	83.1	81.7	71.4	64.8	21.1	80.6	0.0	84.4	82.3
Spodoptera exigua iflavirus 1 JN091707	SeIV-1	85.9	84.4	61.9	85.0	87.1	84.3	85.0	87.8	86.1	83.9	85.9	84.4	0.0	85.4
Spodoptera exigua iflavirus 2 KJ186788	SeIV-2	79.8	49.9	83.4	85.3	85.4	51.8	85.7	83.4	80.0	83.2	86.2	82.3	85.4	0.0

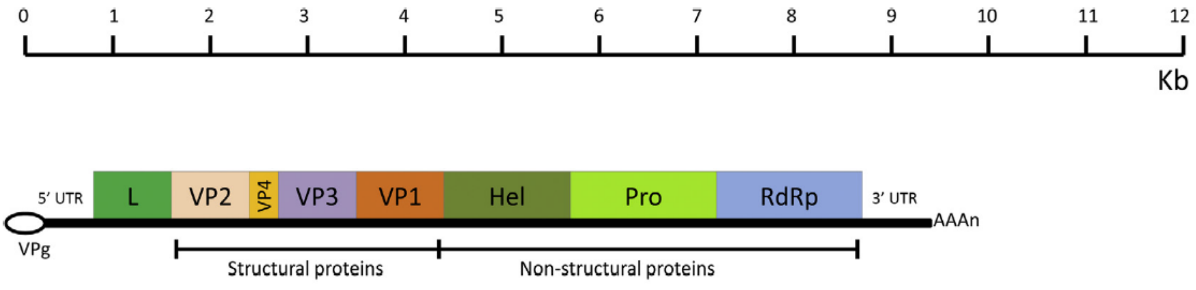

Fig. 1. Iflavirus genome organization.

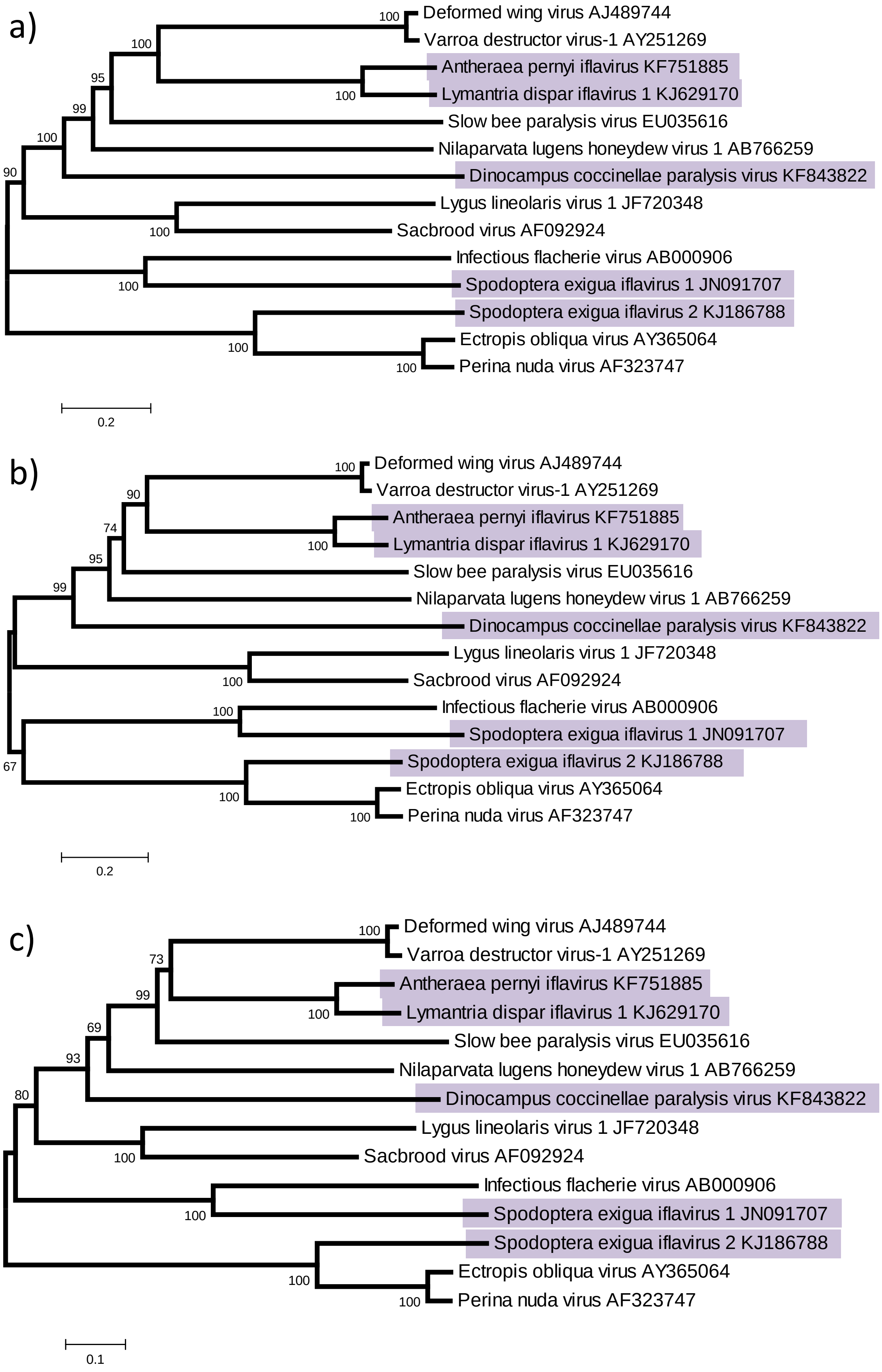

Fig. 2. Neighbor-joining trees showing the relationships between the nine iflavirus species and five proposed species (highlighted). a) complete polyprotein (3783 sites); b) capsid (1172 sites) and c) partial protease/polymerase (522 sites).