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:	***2015.013aS***	(to be completed by ICTV officers)

Short title: 1 new species (*Spodoptera exigua iflavirus 2*) in the family *Iflaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s):

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Corresponding author with e-mail address:

Salva Herrero (sherrero@uv.es)

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):	26/10/2015

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	***2015.013aS***	(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)**
Spodoptera exigua iflavirus 2	SeIV-2 Spanish isolate	KJ186788

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 novel *S. exigua iflavirus* 2 (SeIV-2) has a genome of 9,5 kb and codes for a single polyprotein of 3011 aa. Genome organization of SeIV-2 is very similar to other members of the family Iflaviridae (Appendix Figure 1). Structural proteins are localized at the N-terminal part of the polyprotein and include the L and VP1–VP4 polypeptides. The non-structural proteins, helicase (Hel), protease (Pro) and RNA-dependent RNA polymerase (RdRp) are localized at the C-terminal part of the polyprotein. Hypothetical binding of the small viral protein VPg and sites involved in the separation of the different functional domains in the polyprotein were predicted by comparison with other iflaviruses.

Phylogenetic analysis using the complete polyprotein, capsid and protease/RdRp sequences confirmed that SeIV2 is a new iflavirus independent from a previous iflavirus isolated in the same host (SeIV1) (Appendix Figure 2). It is distinct from other accepted and proposed iflavirus species (Appendix Table 1).

SeIV2 has been detected in field insects as well as in laboratory colonies (Jakubowska et al., 2014; Virto et al., 2014).

SeIV2 has been independely reported by two laboratories (Jakubowska et al., 2014 and Choi et al., 2012)

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Jakubowska AK, D'Angiolo M, González-Martínez RM, Millán-Leiva A, Carballo A,Murillo R, Caballero P, Herrero S. Simultaneous occurrence of covert infections with small RNA viruses in the lepidopteran *Spodoptera exigua*. J Invertebr Pathol. 2014 Sep;121:56-63.
- Virto C, Navarro D, Tellez MM, Herrero S, Williams T, Murillo R, Caballero P. Natural populations of *Spodoptera exigua* are infected by multiple viruses that are transmitted to their offspring. J Invertebr Pathol. 2014 Oct;122:22-7
- Choi, J. Y., Kim, Y. S., Wang, Y., Shin, S. W., Kim, I., Tao, X. Y.,& Je, Y. H. (2012). Complete genome sequence of a novel picorna-like virus isolated from *Spodoptera exigua*. Journal of Asia-Pacific Entomology, 15(2), 259-263.

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	LIV-1	NIHV-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	LIV-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	NIHV-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

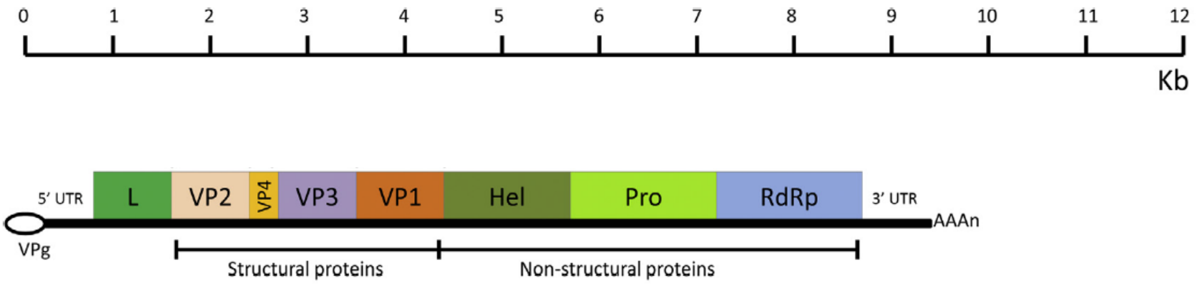

Fig. 1. Iflavirus genome organization.

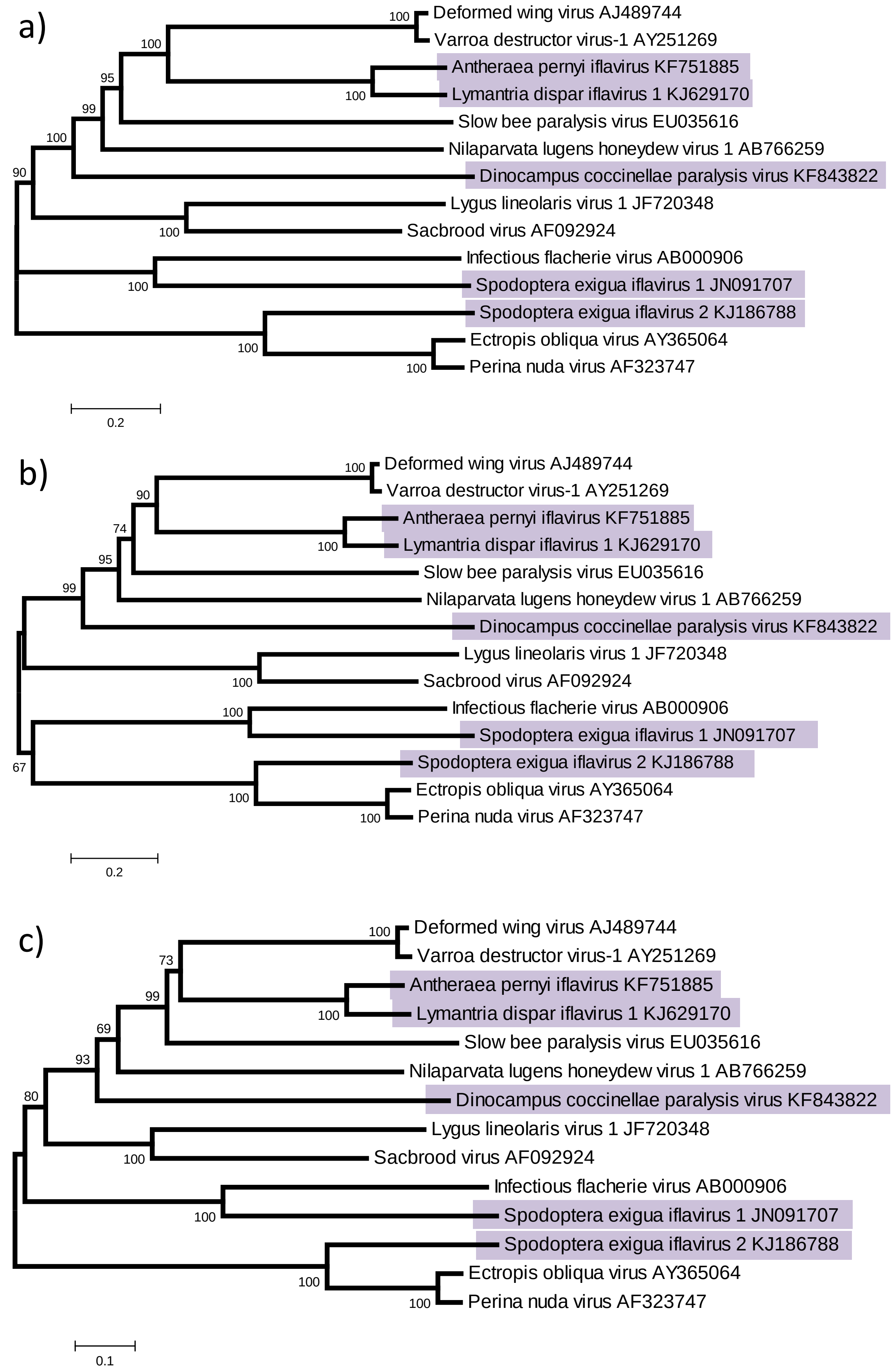

Fig. 2. Neighbor-joining trees showing the relationships between the nine iflavirus species and five proposed species (highlighted). a) complete polyprotein (3783 sites); b) capsid (1172 sites) and c) partial protease/polymerase (522 sites).