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:	***2015.010aS***	(to be completed by ICTV officers)

Short title: 1 new species (*Dinocampus coccinellae paralysis virus*) 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** ☒

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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)	*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	***2015.010aS***	(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)**
Dinocampus coccinellae paralysis virus	From Dinocampus coccinellae, Canada	KF843822

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

DcPV is an Iflavirus

The genome of DcPV is composed of 10,168 nt, not including the poly(A) tail. It has a low G + C content (32.9% A, 15.6% C, 19.2% G, and 31.8% U) and contains one large Open Reading Frame (ORF), 820–9840 nt, encoding a predicted polyprotein of 3007 aa. The structural proteins are encoded by the 5' half of the sequence, and the non-structural helicase, protease, and RNA-dependent RNA polymerase (RdRp) are encoded by the 3' half of the sequence. The 5' and the 3' non-translated regions (NTR) have lengths of 819 and 325 nt, respectively (without the poly(A) tail) (Appendix Figure 1)

Based on the predicted polyprotein, the predicted structural and non-structural DcPV proteins contain functional motifs and domains shared by picorna-like viruses and picornaviruses of the order *Picornavirales*.

Alignement of DcPV structural proteins with other picornaviruses confirmed that it conserved all key features (data not shown)

A phylogenetic analysis was performed on the complete polyprotein, capsid and protease/RdRp sequences and confirmed that DcPV is an Iflavirus (Appendix Figure 2).

DcPV is a new species associated to the parasitoid wasp *Dinocampus coccinellae*

List of Species Demarcation Criteria in 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%.

DcPV is highly dissimilar to all other known picornaviruses (less than 90% identity for all

predicted structural) (Appendix Table 1).
DcPV is the first virus found in the parasitoid wasp *Dinocampus coccinellae* and in the ladybeetle *Coleomegilla macualata*. It is more closely related to VcPLV and NvitV-1, which have been found in the ichneumonid *Venturia canescens* and the pteromalid *Nasonia vitripennis*, respectively. Its absence in healthy ladybeetles further suggests that the virus is associated with the parasitoid wasp *Dinocampus coccinellae*.

DcPV name:
DcPV stands for Dinocampus coccinellae paralysis virus. It aims at providing clues on the remarkable role of DcPV in participating in the behavioral manipulation of the parasitic wasp host (see Dheilly et al., 2015).

MODULE 10: **APPENDIX**: supporting material

The Dinocampus coccinellae paralysis virus (*Dc*PV) has recently been found associated with the parasitic wasp *Dinocampus coccinellae*. Evidences suggest that DcPV is transmitted to the host of *Dinocampus coccinellae*, the ladybeetle *Coleomegilla maculata* during the course of parasitosis and replicates in the ladybeetle nervous tissue resulting in the ladybeetle paralysis. The paralyzed ladybeetle is then used as a bodyguard by the pupating wasp. The larva spins a cocoon between the legs of the immobilized ladybeetle and is thus protected from predators. Interestingly, some ladybeetles survive the infection and behavior manipulation; they eliminate the virus and recover a normal behavior. Further researches are necessary to determine the nature of the interaction between the parasitic wasp and the virus (mutualism, commensalism or parasitism) but it appears that the behavior manipulation allowed by the virus replication in the nervous system of the ladybeetle reduces the predation pressure on the wasp progeny.

The genome of DcPV is composed of 10,168 nt, not including the poly(A) tail. It has a low G + C content (32.9% A, 15.6% C, 19.2% G, and 31.8% U) and contains one large Open Reading Frame (ORF), 820–9840 nt, encoding a predicted polyprotein of 3007 aa (Figure 1). The structural proteins are encoded by the 5' half of the sequence, and the non-structural helicase, protease, and RNA-dependent RNA polymerase (RdRp) are encoded by the 3' half of the sequence (Figure 1). The 5' and the 3' non-translated regions (NTR) have lengths of 819 and 325 nt, respectively (without the poly(A) tail) (Figure 1) .

Based on the predicted polyprotein, the predicted structural and non-structural DcPV proteins contain functional motifs and domains shared by picorna-like viruses and picornaviruses of the order Picornavirales (Figure 1). DcPV RdRp (aa 2920-3220) contains the eight domains originally found in all RdRp from these families of viruses. The three domains of Helicase described by (aa 1834-1986) were also detected, but the most interesting feature is the presence of the nucleoside triphosphate binding residue GxxGxGKS of domain A that is highly conserved. In addition, both the cysteine protease motif GxCG and the substrate-binding residues GxHxxG, of the 3C protease are conserved (aa 2555-2730). In addition, VP2, VP3, and VP1 were found in positions 596–778, 872–1076, and 1296–1494 of the polyprotein, respectively, and the key motifs characteristic of picornaviruses were also identified: NxNxFQxG for VP2, $WxGxLx_3FxFx_7Gx_5YxP$ for VP3, and FxRG for VP1.

additional material in support of this proposal

References:

Dheilly NM, Maure F, Ravallec M, Galinier R, Doyon J, Duval D, Leger L, Volkoff A-N, Misse D, Nidelet S, Demolomb V, Brodeur J, Gourbal B, Thomas F, Mitta G. **2015** Who is the puppet master? Replication of a parasitic wasp-associated virus correlates with host behavior manipulation. *Proceedings of the Royal Society B Biological Sciences.* DOI: 10.1098/rspb.2014.2773
http://rspb.royalsocietypublishing.org/content/282/1803/20142773

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	NlHV-1	PnV	SBV	SBPV	VDV	AplV	DCPV	LdlV-1	SelV-1	SelV-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	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	AplV	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	LdlV-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	SelV-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	SelV-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

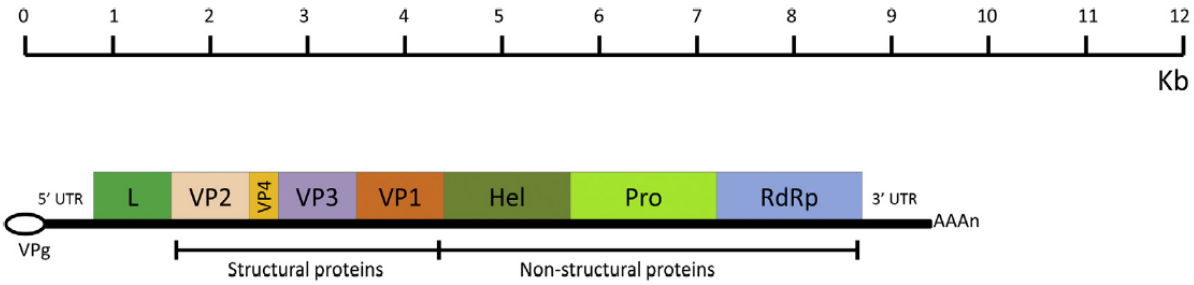

Fig. 1. Iflavirus genome organization.

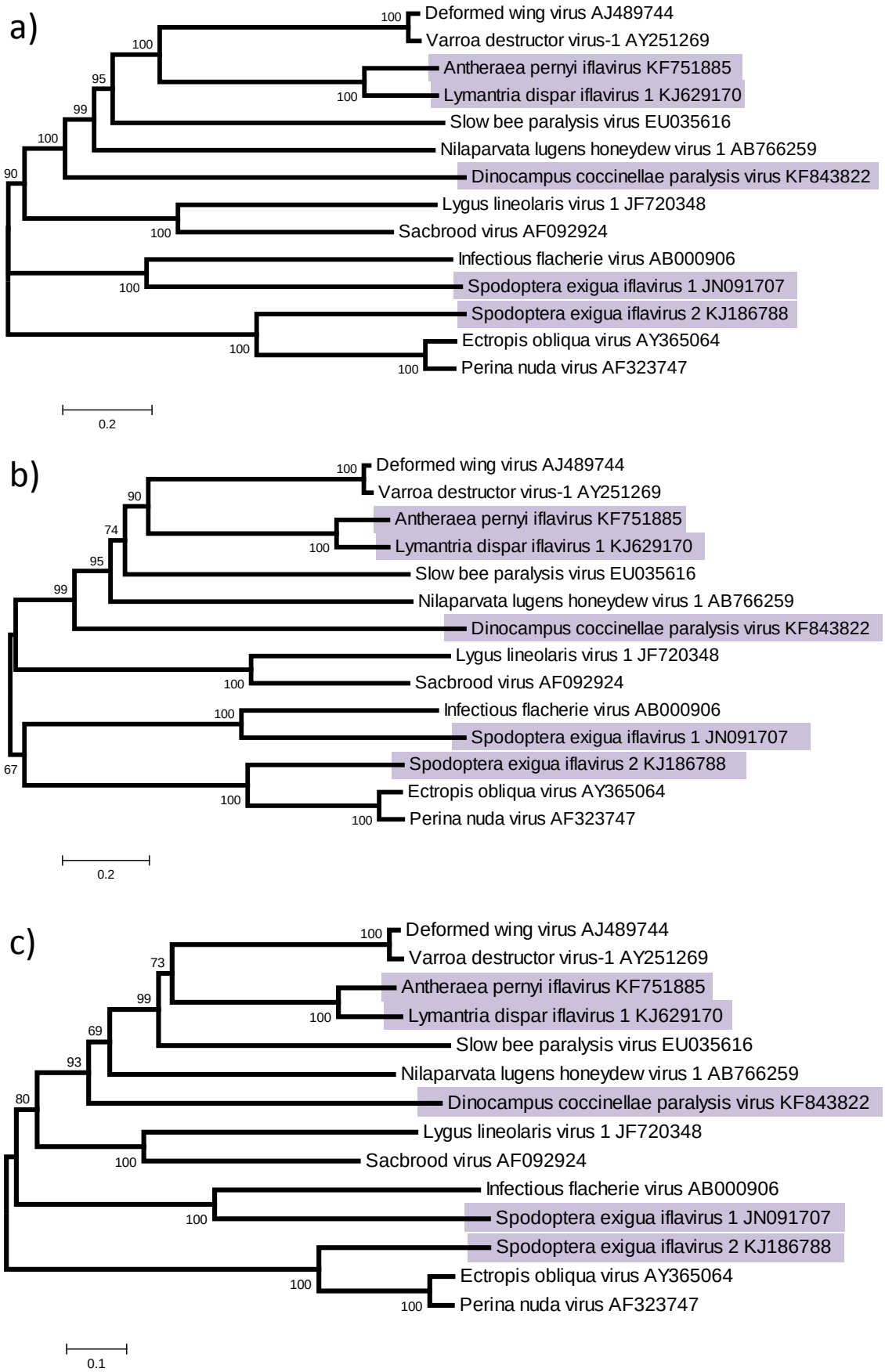

Fig. 2. Neighbor-joining trees showing the relationships between the nine iflavirus species and five proposed species (highlighted). a) complete polyprotein (3783 sites); b) capsid (1172 sites) and c) partial protease/polymerase (522 sites).