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:	***2011.005aI***	(to be completed by ICTV officers)

Short title: create species *Slow bee paralysis virus* in the genus *Iflavirus*, family *Iflaviridae*, order *Picornavirales*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

Dicistroviridae Study Group:
Yanping (Judy) Chen (judy.chen@ars.usda.gov); Nobuhiko Nakashima (nakaji@affrc.go.jp); Peter Christian (tyttenhangerpete@hotmail.co.uk); Tamas Bakonyi (Bakonyi.Tamas@aotk.szie.hu); Bryony C. Bonning (BBonning@iastate.edu); Steven M. Valles (steven.valles@ars.usda.gov); Donald Lightner (dvl@u.arizona.edu)

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* Study Group**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV: Yes
Date of this revision (if different to above):

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	***2011.005aI***	(assigned by ICTV officers)

To create a 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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Slow bee paralysis virus	EU035616

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

The species demarcation criteria in the genus *Iflavirus* are:

- Natural host range: species can be differentiated on the basis of their natural host range.
- Sequence identity at the amino acid level between the capsid proteins (CPs) of isolates and strains of a species is above 90%.

The complete genome sequences of two distinct strains of slow bee paralysis virus (SBPV) of honeybees *Apis mellifera,* have been recently determined and described (de Miranda et al., 2010). The two SBPV strains derived from an English SBPV isolate ((Bailey & Woods, 1974) are labeled as “Rothamsted”and “Harpenden” and registered with GenBank accession # EU035616 and GU938761, respectively. Both stains show the following biological and genomic features that fulfills the *Iflavirus* genus inclusion criteria:

Virus particles: Round, isometric with a diameter of 30 nm.

Genome: Positive-sense, single stranded RNA genome which is approximately 9500 nt long and contains a single open reading frame (ORF). The ORF encodes a polyprotein of 2964 amino acid residues flanked by approximately 300 nt of 5′-UTR and approximately 270 nt of 3′-UTR which terminates in a poly(A) tail. The C-terminal portion of the polyprotein possesses consensus sequences in the order of helicase, protease and RNA-dependent RNA polymerase, similar to those of iflaviruses and other picorna-like viruses. The N-terminal portion of the polyprotein shows homology with the structural CPs of other iflaviruses.

Phylogeny: Phylogenetic tree constructed with the amino acid sequences of viral non-structure proteins at the C-terminal part of the polyprotein displays that SBPVs group together with the members of *Iflaviridae* (Fig. 1). Comparison of the structural CPs (1680 amino acids of the N-terminal region of the polyprotein showed that strains of SBPV are most similar to Deformed wing virus (DWV) and Varroa destructor virus -1 (VDV-1) among existing members of Genus *Iflavirus* (Fig. 2). The sequence identity of the capsid proteins between Rothamsted and DWV or VDV-1 is 26.6% and 26.4%, respectively. The sequence identity of the capsid proteins between Harpenden and DWV or VDV-1 is 26.2% and 26.1%, respectively. However, the amino acids of CPs between Rothamsted and Harpenden are 95.7 % identical.

Natural host range: Both strains of SBPV infect *A. mellifera*. No other hosts or cell lines known to support replication.

The above data suggest that SBPV is an iflavirus and is distinct from any other reported iflaviruses, justifying classification as a novel species in the genus *Iflavirus,* family *Iflaviridae.*

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bailey, L. and Woods, R. D. (1974). Three previously undescribed viruses from the honey bee. J Gen Virol 25, 175–186.

de Miranda, J. R., Dainat, B., Locke, B., Cordoni, G., Berthoud, H., Gauthier, L., Neumann, P., Budge, G.E., Ball, B.V. and Stoltz, D.B. (2010) Genetic characterization of slow bee paralysis virus of the honeybee (*Apis mellifera* L.). J. Gen. Virol. 91(Pt 10):2524-2530.

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.

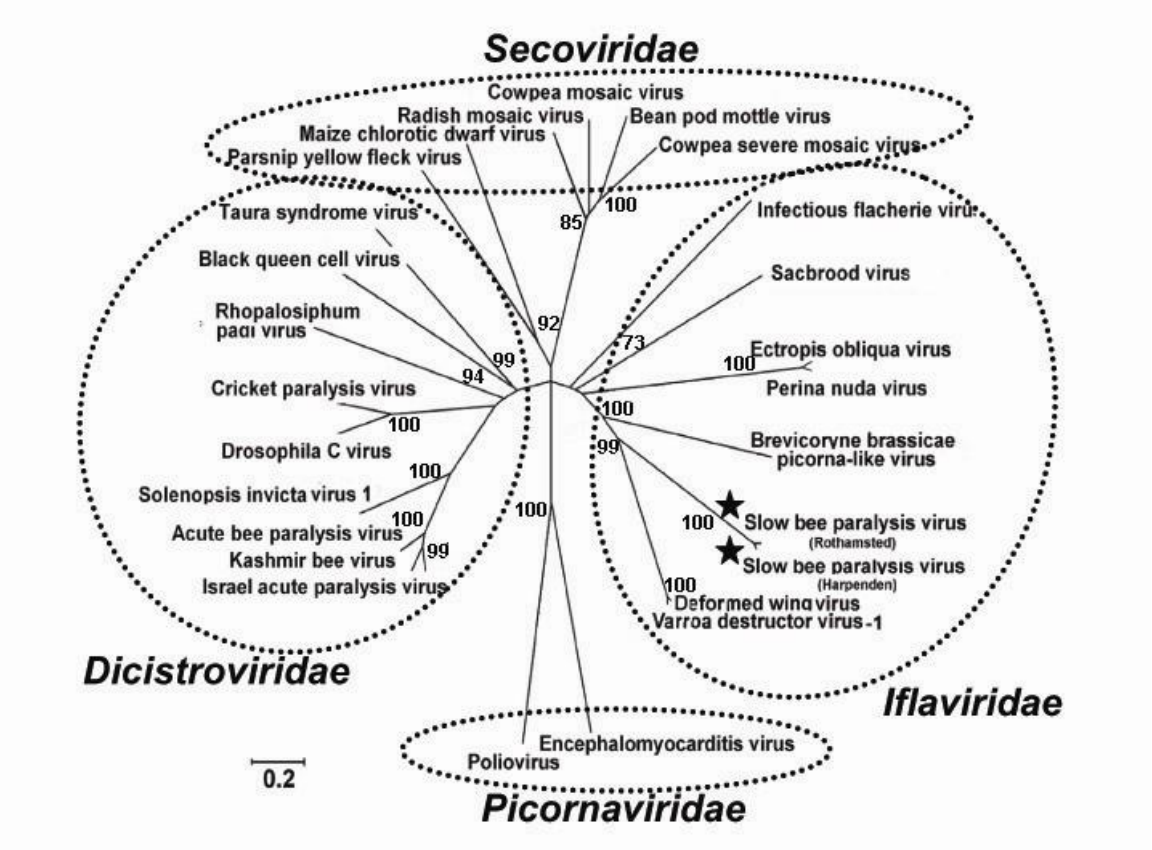

Fig 1. Unrooted phenogram showing the relationship of SBPVs and other viruses in the families *Iflaviridae, Dicistroviridae, Secoviridae* and *Picornaviridae*. The phylogenetic analysis was conducted in MEGA4 (Tamura et al., 2007) based on amino acid sequences of the putative non-structural polyprotein using the Neighbor-Joining method. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The scale bar shows the number of substitutions per base. The neighbour-jointing phenogram was

boostraped 500 times with values greater than 50% given at nodes. Taxa used (with virus name and accession number) were: ***Iflaviridae* -** Deformed wing virus (AY292384), Ectropis obliqua virus (AY365064), Infectious flacherie virus (AB000906), Perina nuda virus (AF323747), Sacbrood virus (AF092924), Varroa destructor virus 1 (AY251269), Brevicoryne brassicae picorna-like virus (EF517277), Slow bee paralysis virus (Rothamsted) (EU035616), and Slow bee paralysis virus (Harpenden) (GU938761); ***Dicistroviridae*** -Acute bee paralysis virus (AF150629), Black queen cell virus (AF183905), Cricket paralysis virus (AF218039), Drosophila C virus (AF014388), Kashmir bee virus (AY27571O), Rhopalosiphum padi virus (AF022937), Solenopsis invicta virus-l (AY6343 14), Taura syndrome virus (AF277675), and Israeli acute paralysis virus (EF219380); ***Secoviridae* -** Parsnip yellow fleck virus (D14066), Cowpea severe mosaic virus (M83830), Maize chlorotic dwarf virus (NP619716), Bean pod mottle virus (NP612349, Radish mosaic virus (YP001911126), and Cowpea mosaic virus (NP613283);***Picornaviridae* -** Poliovirus (VOl149), and Encephalomyocarditis virus (M81861).

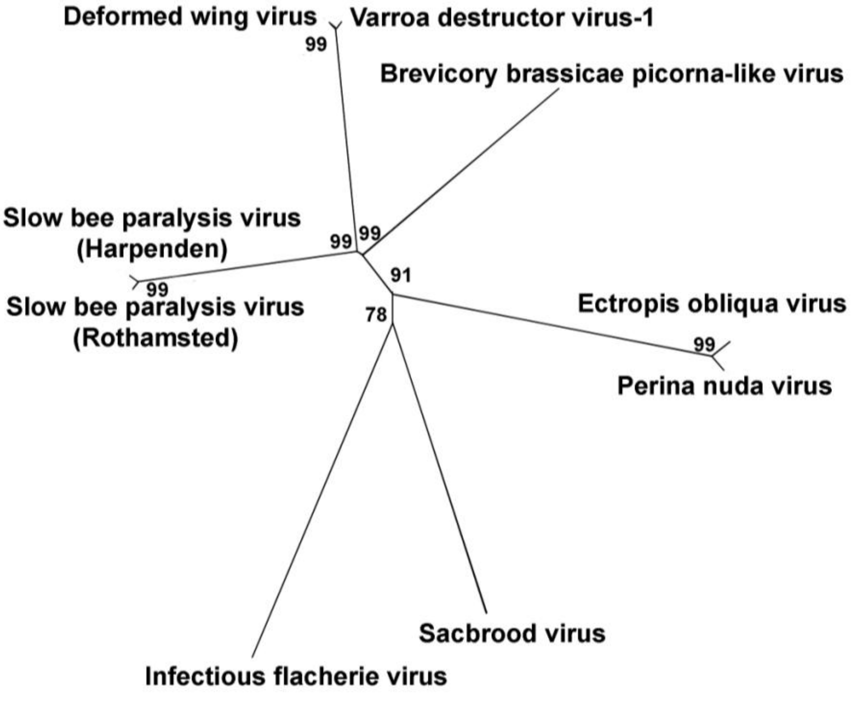

Fig 2. Neighbour-jointing tree showing the relationship between SBPVs and other members of the genus Iflavirus. The phylogenetic analysis was conducted in MEGA4 (Tamura et al., 2007) based on amino acid sequences of the structural capsid proteins. The neighbour-jointing phenogram was bootstraped 500 times with values greater than 50% given at nodes. The names and accession numbers of iflavirus taxa are the same as above Fig. 1.