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:	***2016.003aS***	(to be completed by ICTV officers)

Short title: Create species *Brevicoryne brassicae virus* in the genus *Iflavirus*, family *Iflaviridae*, order *Picornavirales*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

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Corresponding author with e-mail address: Eugene Ryabov (eugene.ryabov@gmail.com)

Eugene.ryabov@gmail.com

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** (Animal ssRNA+ Viruses Subcommittee)

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

Date first submitted to ICTV: 15 May 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

Please replace GenBank RefSeq numbers with accession numbers.

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	***2016.003aS***	(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)**
Brevicoryne brassicae virus	Brevicoryne brassicae virus - UK	EF517277

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 11

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 Brevicoryne brassicae virus (BrBV) of the cabbage aphid, *Brevicoryne brassicae* (Linnaeus, 1758) have been determined and described. This include the BrBV strains isolated in the Warwickshire, United Kingdom in 2006, BrBV-UK, GenBank accession number EF517277 (Ryabov, 2007) and a strain identified in various locations throughout Israel in 2009-2012, BrBV-IL, GenBank accession number KP777548 (Luria et al., 2016). Both BrBV stains show the following biological and genomic features fulfilling the genus *Iflavirus* inclusion criteria:

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

Genome: Positive-sense, single-stranded RNA genome with the 3′ terminal poly(A) tail, which is approximately 10,161 nt long (excluding the 3′ poly(A) tail) and contains a single uninterrupted open reading frame (ORF) (Fig. 1). The ORFs of the both strains encode a

polyprotein of approximately 2,983 amino acid residues flanked by approximately 792 nt of 5′-UTR and approximately 417 nt of 3′-UTR preceding the poly(A) tail. The BrBV-UK and BrBV-IL have 95% nt identity, the ORF-encoded polypeptides have 98% aa identity. The C-terminal part of the BrBV polyprotein contains regions of sequence homology to the crucial catalytic amino acids of the RNA helicase, a chymotrypsin-like protease and an RNA-dependent RNA polymerase (RdRp) of iflaviruses and other picorna-like viruses. The N-terminal portion of the polyprotein shows homology with the structural CPs of other iflaviruses (Ryabov, 2007; Luria et al., 2016).

Phylogeny: Phylogenetic tree constructed with the amino acid sequences of the viral polyproteins displays that BrBV showed highest sequence similarity with the members of the genus *Iflavirus* (Fig. 2). Comparison of the structural CPs (1,113 amino acids of the N-terminal region of the polyprotein) showed that BrBV strains showed about 20 to 29 % amino acids identity, indicating that BrBV strains are significantly different from other *Iflavirus* members. For example, BrBV strains showed 27% amino acid identity with the structural gene block of the deformed wing virus-Italy (GenBank accession number AJ489744), the highest amino acid identity was observed with the structural proteins of the unclassified putative *Iflavirus* members Graminella nigrifrons virus 1 isolate Ohio, GenBank accession number KP866792 (29%); Diaphorina citri picorna-like virus isolate BR1, GenBank accession number KT698837 (28%).

Natural host range: Both strains of BrBV infect of the cabbage aphid, *Brevicoryne brassicae* (Linnaeus, 1758). No other hosts or cell lines known to support replication. It was specifically demonstrated that BrBV present at high levels in the individual aphids which were not parasitized by parasitoid wasps *(Hymenoptera: Aphidiinae sp.)* (Ryabov, 2007), also no BrBV was detected in the plant tissues, confirming that BrBV is a virus which infects the cabbage aphid.

The above data suggest that BrBV possess all characteristics of the genus *Iflavirus* and is distinct from any other members of this genus, justifying classification as a novel species in the genus *Iflavirus*, family *Iflaviridae*, order *Picornavirales*

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ryabov, E.V., 2007. A novel virus isolated from the aphid *Brevicoryne* brassicae with similarity to Hymenoptera picorna-like viruses. *J. Gen. Virol.* 88:2590-2595. DOI 10.1099/vir.0.83050-0. PMID: 17698671

Luria, N., Reingold, V., Lachman, O., Sela, N., Dombrovsky, A., 2016. Extended phylogenetic analysis of a new Israeli isolate of Brevicoryne brassicae virus (BrBV-IL) suggests taxonomic revision of the genus Iflavirus. *Virol. J.* 13:50. doi: 10.1186/s12985-016-0500-z . PMID: 27000790

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.

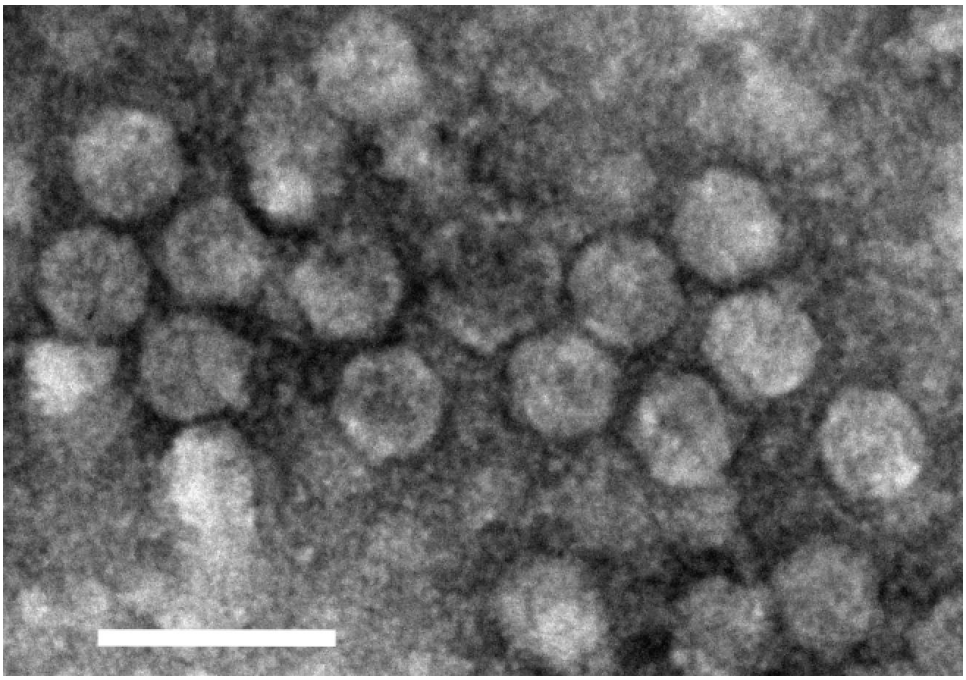

Figure 1. Transmission electron microscopy of purified BrBV particles isolated from *Brevicoryne brassicae* aphids, bar represents 50 nm.

Figure 2

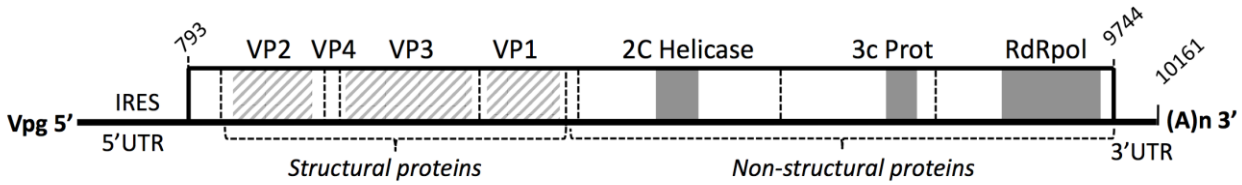

Figure 2. Organization of the BrBV genomic RNA (BrBV-UK GenBank accession numbers EF517277). The long box represents the single open reading frame with the conserved domains indicated, the vertical dotted lines indicate putative proteolytic cleavage sites. The capsid proteins are encoded in the order VP2–VP4–VP3–VP1, the striped boxes indicate three major capsid proteins with the beta-barrel domains. The arrangement of the BrBV capsid proteins in the virion is likely to be similar to that of the cricket paralysis virus capsid proteins with the same names, with the VP1 at the 5-fold axis. The dark boxes in the non-structural part are picorna-like 2C helicase, 3C protease (3c Prot), and RNA-dependent RNA polymerase (RdRpol) domains.

Figure 3

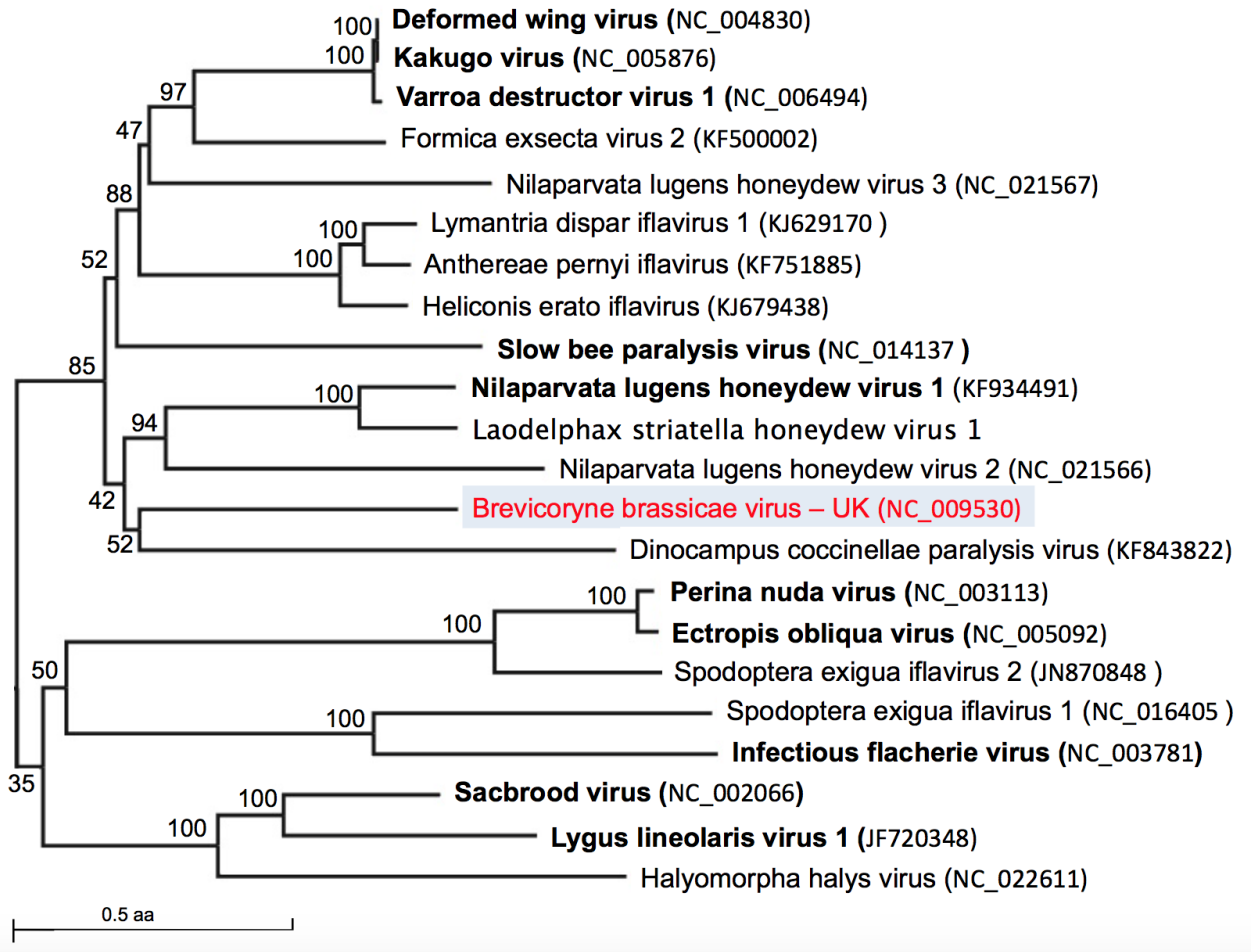

Figure 3. Phylogram of the recognized and putative members of the genus *Iflavirus* and BrBV. Full-length polyprotein sequences of the *Iflavirus* isolates were used. Members of the genus *Iflavirus* recognized by the ICTV, 2014 report are shown in bold. Rooted phylogenetic tree was produced using the Neighbor-joining method and evaluated with bootstrap analysis, 1000

replicates, percentage of bootstrap support if each branch is indicated at the node. Branch length indicates evolutionary distance; scale bar shows 0.5 amino acid substitutions per site.