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:	***2012.014aP***	(to be completed by ICTV officers)

Short title: To create a new species in the genus *Endornavirus*, family *Endornaviridae*
(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:

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Sabanadzovic Sead (ss501@msstate.edu)
On behalf of the *Endornaviridae* Study Group

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)	*Endornaviridae*

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

Date first submitted to ICTV:
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	***2012.014aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Endornavirus***
Subfamily:	
Family:	***Endornaviridae***
Order:	

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:**
Bell pepper endornavirus	JN019858

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

Current species demarcation criteria in the genus (9th Report ICTV)
At present, species are distinguished on the basis of their host-range and sequence differences. Each recognized endornavirus species was isolated from a different host species. The genomic nucleotide sequences of different endornavirus species are only 30% to 75% identical (Fukuhara & Gibbs, 2011).

Background on *Bell pepper endornavirus* (BPEV)

This virus was described in 1990 (Valverde et al., 1990) and partial sequences were reported in 2008 (Valverde & Gutierrez, 2008). The full sequence of two isolates of the virus, one from the United States isolated from bell pepper cv. Yolo Wonder (Accession number JN019858, BPEV-YW) and another from Japan isolated from bell pepper cv. Kyousuzu (Accession number AB597230, BPEV-KS) were recently published (Okada et al., 2011). The same paper reports in-depth molecular analyses as well as some biological properties of the virus. Variants of the virus occur in other Capsicum species (Okada et al., 2011)

Properties of BPEV
The virus consists of naked linear dsRNA of 14,727 nt, transmitted only vertically, and does not appear to cause symptoms. A single open reading frame was found in the plus strand of BPEV starting at nt 226 and ending at nt 14,670, which could encode a polyprotein of 4,815 aa of an estimated Mr of 545 kDa. The genome size and protein coding strategy are typical of endornaviruses (Figure 1). In agreement with general endornavirus features, BPEV contains a

nick in the positive-strand RNA molecule. Conserved domains of BPEV are: viral methyltransferase (MTR), viral RNA helicase 1 (Hel-1), UDP-glycosyltranferase (UGT) and viral RNA-dependent RNA polymerase (RdRp) domains. This arrangement of conserved domains is unique and diverse from all extant endornavirus species (Figure 1). Moreover, BPEV is the first plant endornavirus containing the putative MTR domain similar to the putative endornavirus GaBRV-XL, infecting the fungus, *Gremmeniella abietina* type B. The conserved order of MTR, Hel-1 and RdRp domains also supports that BPEV shares a common evolutionary ancestor with positive ssRNA viruses in alpha-like virus supergroup.
A phylogenetic tree prepared on the RdRp sequences of two BPEV isolates and other endornviruses shows that BPEV is closest to Phytophthora endornavirus 1 forming a separate clade within the genus endornavirus as shown in Figure 2. Using conserved domains sequences the percentage of identity with other members (and putative members) of this genus ranges from 11-42 % (Table 1).

The biological properties, host range, unique genomic organization, and phylogeny support that the dsRNA isolated from the bell pepper cultivars represent a novel species of the genus *Endornavirus* for which the name ***Bell pepper endornavirus*** **(BPEV)** is proposed.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Fukuhara, T. & Gibbs, M. J. 2012. Family Endornaviridae. In Virus Taxonomy: Classification and Nomenclature of Viruses Ninth Report of the International Committee on Taxonomy of Viruses. Edited by Andrew M.Q. King, Michael J. Adams, Eric B. Carstens, and Elliot J. Lefkowitz. pp 519-521. Elsevier/Academic Press.

Okada, R., Kiyota, E., Sabanadzovic, S., Moriyama,H., Fukuhara, T., Saha, P., Roossinck. M. J., Severin, A., & Valverde, R. A. 2011. Bell pepper endornavirus: molecular and biological properties and occurrence in the genus *Capsicum*. Journal of General Virology 92:2664-2673.

Roossinck, M. J., Sabanadzovic, S., Okada, R., & Valverde, R. A. 2011. The remarkable evolutionary history of endornaviruses. Journal of General Virology 92:2674-2678.

Valverde, R. A. & Gutierrez, D. L. 2007. Transmission of a dsRNA in bell pepper and evidence that it consists of the genome of an endornavirus. Virus Genes 35:399-403.

Valverde, R. A., Nameth, S. T., Abdallha, A. O., Desjardins, P. R., & Dodds, J. A. 1990. Indigenous double-stranded RNA from pepper (*Capsicum annuum*). Plant Science 67:195-201.

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.

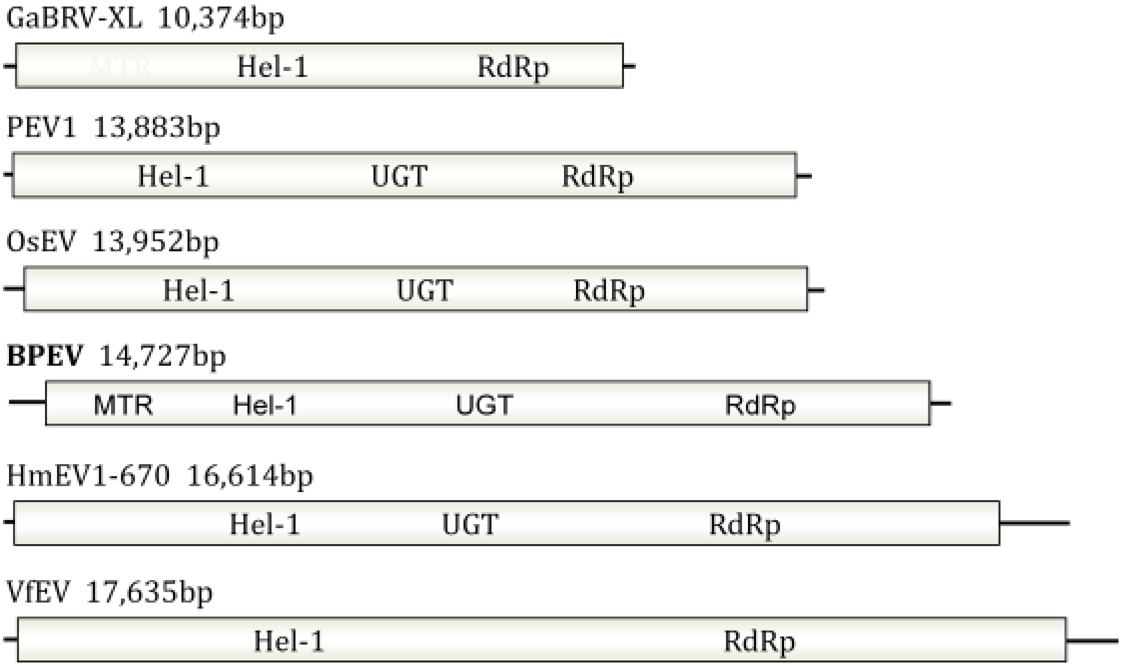

Figure 1. Schematic representation of the genome organization of Bell pepper endornavirus (BPEV) and four endornaviruses. *Gremmeniella abietina* type B RNA virus (GaBRV-XL), *Phytophthora endornavirus* 1 (PEV1), *Oryza sativa endornavirus* (OsEV), *Helicobasidium mompa* endornavirus 1-670 (HmEV1-670), and *Vicia fava endornavirus* (VfEV).

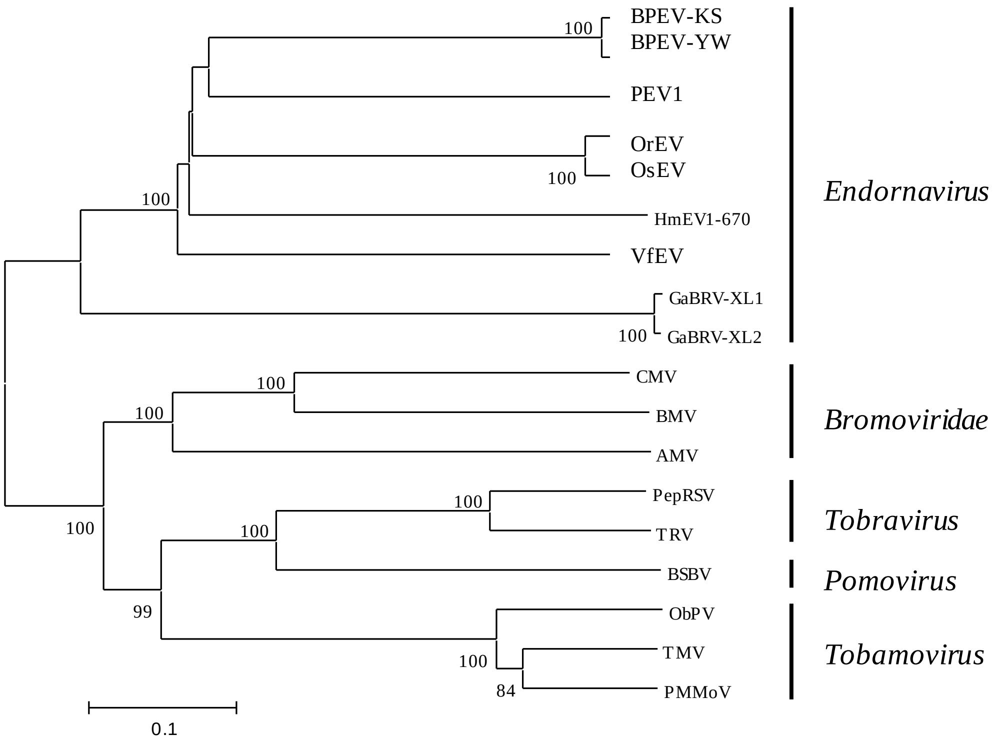

Figure 2. Neighbor-joining phylogenetic tree of the RdRp- like regions encoded by two isolates of Bell pepper endornavirus, one from Japan (BPEV-KS) and the isolate from the United States (BPEV-YW), several endornaviruses and some plant ssRNA viruses. Bootstrap values (1000 replicates) of over 50 % are indicated on the branches. Acronyms, virus names and corresponding GenBank accession number in parenthesis are: PEV1, *Phytophthora endornavirus* 1 (CAI47561); OsEV, *Oryza sativa endornavirus* (BAA06862); OrEV, *Oryza rufipogon endornavirus* (YP_438202); VfEV, *Vicia faba endornavirus* (CAA04392); HmEV1-670, *Helicobasidium mompa* endornavirus 1-670 (BAE94538); GaBRV-XL1, *Gremmeniella abietina* type B RNA virus XL1 (ABD73305); GaBRV-XL2, *Gremmeniella abietina* type B RNA virus XL2 (ABD73306); CMV, *Cucumber mosaic virus* (BAA21693); BMV, *Brome mosaic virus* (CAA41361); AMV, *Alfalfa mosaic virus* (AAA46289); PepRSV, *Pepper ringspot virus* (AAA47081); TRV, *Tobacco rattle virus* (BAA00110); BSBV, *Beet soil-borne virus* (CAB10764); ObPV, *Obuda pepper virus* (BAA02700); TMV, *Tobacco mosaic virus* (Swiss-Prot: P03586); PMMoV, *Pepper mild mottle.*

Table 1. Comparisons of conserved domains of Bell pepper endornavirus with the orthologs in other endornaviruses and a putative endornavirus. Shown numbers are percentages of identity and similarity

	MTR		Hel-1		UGT		RdRp	
	Identity		Identity		Identity		Identity	
GaBRV-XL	15.2		18.7		NP		26.0	
PEV1	NP		29.5		11.0		42.0	
OsEV	NP		32.2		12.0		39.2	
HmEV	NP		28.4		14.0		42.1	
VfEV	NP		34.2		NP		41.9	

GaBRV-XL): *Gremmeniella abietina* type B RNA virus
PEV1: *Phytophthora endornavirus* 1
OsEV): *Oryza sativa endornavirus*
HmEV1-670), *Helicobasidium mompa* endornavirus 1-670 and
VfEV: *Vicia fava endornavirus*
MTR: Methyltransferase
Hel-1: Helicase 1
UGT: UDP-glycosyltranferase
RdRp: RNA-dependent RNA polymerase
NP: Domain not present