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:	***2015.020aP***	(to be completed by ICTV officers)

Short title: To create a new species in the genus *Endornavirus*

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

Author(s):

Valverde, R. A.
Navas-Castillo, J.

Corresponding author with e-mail address:

Valverde, R. A. (rvalverde@agcenter.lsu.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)	The Endornavirus study group (two members only)

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

None

Date first submitted to ICTV: June 15, 2015
Date of this revision (if different to above):

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	***2015.020aP***	(assigned by ICTV officers)

To create a new species within:

Fill in all that apply.

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

- 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)**
Persea americana endornavirus 1	Fuerte	JN880414

Reasons to justify the creation and assignment of the new species:

Endornaviruses have been reported to infect economically important crops, such as broad bean, common bean, pepper, rice, some plant pathogenic fungi, and the oomycete *Phytophthora* sp. Currently endornavirus species are distinguished on the basis of their host, genome size and organization, and nucleotide sequence variations. The nucleotide sequences of different endornavirus species ranges from 30% to 75% identity (Fukuhara & Gibbs, 2012).

Recently, we found a 13.4 kbp dsRNA molecule in several plants of the avocado (*Persea americana*) cultivar Fuerte. Sequencing the dsRNA yielded a virus genome with properties similar to those of members of the genus *Endornavirus* (family *Endornaviridae*). An isolate of the putative virus (from avocado cv. Fuerte), tentatively named Persea americana endornavirus (PaEV), was sequenced and its sequence analyzed and compared with sequences of other endornavirus species and tentative species. PaEV was transmitted at 100% rate when 45 seedlings obtained from an infected avocado tree were tested. A BLAST search using amino acid sequences of PaEV revealed conserved domains of a putative RNA helicase-1 (HEL), capsular polysaccharide synthase (CPS), UDP-glucose-glycosyltransferase (GTB), and an RNA-dependent RNA polymerase (RdRp) typical of endornaviruses **(Fig. 1).** A unique molecular feature of members of the family *Endornaviridae* is the presence of a site-specific nick near the 5' region of the coding strand of the RNA molecule. Sequence analyses of RACE-generated clones indicated the presence of putative nicks in the coding strand at nucleotides 630 and 860. Phylogenetic analyses of the RdRp domain showed that PaEV clustered with other members of the family *Endornaviridae* (**Fig. 2)**. When the complete aa sequence of PaEV was compared with other endornaviruses, proposed new endornavirus species and unclassified viruses, the closest viruses were Yerba mate endornavirus 1 (YmEV1) (this proposed new species is presented in a separate proposal), an unclassified virus from *Lagenaria siceraria*, *Oryza sativa endornavirus*, and *Oryza rufipogon endornavirus*, with a maximum identity of 62 % with YmEV1 **(Table 1)**. Similar results were obtained when the complete nucleotide sequence of PaEV was compared with the viruses listed above **(Table 1).**

The biological and molecular properties of PaEV, including 66 % nucleotide sequence identity with the most closely related endornavirus species (*Oryza sativa endornavirus*), support creating a new species of the genus *Endornavirus* and the name Persea americana endornavirus 1 (PaEV1) is proposed.

MODULE 10: **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.

Villanueva, F., Sabanadzovic, S., Valverde, R. A., and Navas-Castillo, J. 2012. Complete genome sequence of a double-stranded RNA virus from avocado. Journal of Virology 86:1282-1283.

Annex

Table 1. Percent aminoacid sequence identity of Persea americana endornavirus 1 RdRp domain and complete polyprotein (ORF) compared with species (**black** font) and proposed new species (**red** font, this or accompanying proposal) and unclassified viruses (**blue** font). The percentage of the overall nucleotide sequence identify with some viruses is also presented. See Fig. 2 legend for virus GenBank accession numbers. ND=Not determined

Virus name	ORF	RdRp	Complete nucleotide sequence
Yerba mate endornavirus 1	37	62	67
Lagenaria siceraria endornavirus	32	60	67
Oryza sativa endornavirus	30	59	64
Oryza rufipogon endornavirus	30	58	66
Basella alba endornavirus 1	30	57	67
Phaseolus vulgaris endornavirus 1	30	57	65
Bell pepper endornavirus	13	38	ND
Phaseolus vulgaris endornavirus 2	13	38	ND
Vicia faba endornavirus	10	31	ND
Chalara elegans endornavirus	11	27	ND
Grapevine endophyte endornavirus	10	30	ND

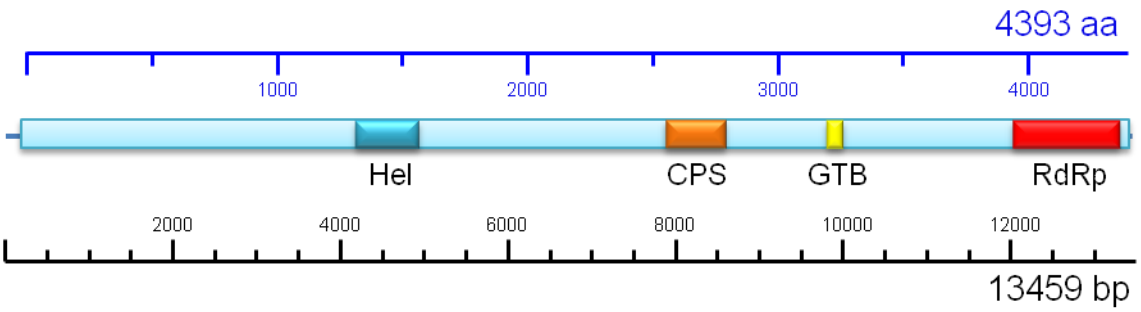

Fig. 1. Schematic representation of the genome organization of Persea americana endornavirus 1. The box represents the large ORF. HEL: helicase 1; CPS: Capsular polysaccharide synthesis protein; GTB: UDP-glucose glycosil-transferase; RdRp: RNA-dependent RNA polymerase.

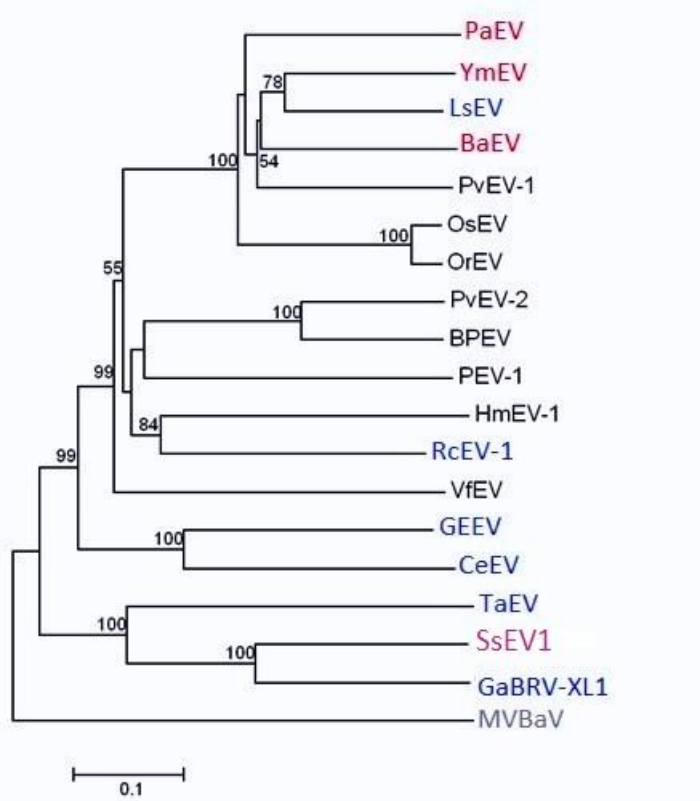

Fig. 2. Neighbor joining phylogenetic tree obtained from the translated sequences of the RdRp region of available complete endornavirus genomes (accepted species in **black**, proposed species in this or accompanying proposals in **red** and unclassified viruses in **blue**). Virus acronyms are: Persea americana endornavirus 1 (PaEV1, AEX28369), Yerba mate endornavirus 1 (YmEV1, KJ634409), Lagenaria siceraria endornavirus (LsEV, KF562072), Basella alba endornavirus 1 (BaEV1, AB844264), *Phaseolus vulgaris endornavirus 1* (PvEV1, BAM68539), *Lagenaria siceraria endornavirus* (OsEV, BAA06862), *Oryza rufipogon endornavirus* (OrEV, YP_438202), *Phaseolus vulgaris endornavirus 2* (PvEV2, BAM68540), *Bell pepper endornavirus* (BPEV, AEK22062), *Phytophtora endornavirus 1* (PEV1, CAI47561), *Helicobasidium mompa endornavirus 1* (HmEV1, BAE94538), Rhizoctonia cerealis endornavirus 1 (RcEV-1, AGY34962), *Vicia faba endornavirus* (VfEV, CAA04392), Grapevine endophyte endornavirus (GEEV, AFV91541), Chalara elegans endornavirus (CeEV, ADN43901), Tuber aestivum endornavirus (TaEV, ADU64759), Sclerotinia sclerotiorum endornavirus 1 (SsEV1, AGP03024), Gremmeniella abietina type B RNA virus XL1 (GaBRV-XL1, ABD73305). *Mint vein banding associated virus* (MVBaV, AY548173) was used as outgroup. Bootstrap values higher than 50 are represented above the nodes. The scale bar indicates the number of substitutions per amino acid position.