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: ***2015.021aP*** (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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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)	Endornavirus study group.

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

None

Date first submitted to ICTV: June 15, 2015
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	***2015.021aP***	(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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Yerba mate endornavirus 1	INTA	KJ634409

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)

Endornavirus 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, 2012).

Background and properties

The endornavirus from yerba mate, tentatively designated Yerba mate endornavirus (YmEV) was identified and properties described in 2014 (Debat et al. 2014). The publication of this virus represents the first report of a virus infecting the subtropical tree crop yerba mate (*Ilex paraguariensis* St. Hil.). YmEV consist in a linear dsRNA viral genome of 1,3954 nt long, containing a single 1,3743 nt ORF. YmEV presents a 149 nt 5´UTR and a 61 nt 3´UTR (Figure 1). The predicted ORF encodes a 4581 aa polypeptide with a UDP-glucose glycosyl-transferase, a capsular polysaccharide synthesis protein and a RNA dependent RNA polymerase domain.

While most endornaviruses have been described to present a helicase domain (HEL), we failed to recognize a putative HEL-like encoding region in the YmEV genome. We hypothesize that if YmEV harbors a functional HEL domain, it has exceedingly diverged to be recognized by our criteria (Roossinck et al., 2011). The RdRp domain of YmEV had the closest homology to the RdRp domain of the unclassified virus Lagenaria siceraria endornavirus (LgEV), sharing 67.1

% similarity at the aa level. When compared with other species and unclassified viruses, the percentage of identity of the YmEV domains suggests that YmEV is more closely related to plant endornaviruses and that whilst the length of the polypeptide is relatively conserved, global sequence identity is low (Table 1). Multiple MUSCLE amino acid alignments of the RdRp domain, followed by a Bayesian phylogenetic tree indicate that YmEV is more closely and robustly related to the proposed new species Persea americana endornavirus 1 (see separate proposal for this virus), the unclassified virus LgEV, and *Oryza sativa endornavirus*. (Villanueva et al., 2012; Song et al., 2013; Espach et al., 2012), (Table 1, Fig. 2,). The presence of YmEV in yerba mate was not accompanied by any apparent typical viral symptoms.

The unique genomic organization, host, phylogeny, the 54.6 % nucleotide sequence identity with the closest endornavirus species (*Oryza sativa endornavirus*) suggest that YmEV represents a novel species of the genus *Endornavirus* for which the name Yerba mate endornavirus 1 (YmEV1**)** is proposed.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

-Fukuhara T. and Gibbs M.J. Family Endornaviridae In "Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses". Andrew MQ King, ed. Elsevier, pp519-521 (2012).
-Debat H.J., M. Grabiele, P. Aguilera, R. Bubillo, P.D. Zapata, D.A. Marti, and D.A. Ducasse, Virus Genes. doi: 10.1007/s11262-014-1096-2 (2014).
-Roossinck M. J., S. Sabanadzovic, R. Okada, and R. A. Valverde, J. Gen. Virol. 92, 2674 (2011).
-Villanueva, S. Sabanadzovic, R. A. Valverde, and J. Navas-Castillo, J. Virol. 86, 1282 (2012).
-D. Song, W. K. Cho, S.-H. Park, Y. Jo, and K.-H. Kim, PLoS ONE 8, e64270 (2013).
-Y. Espach, H. J. Maree, and J. T. Burger, J. Virol. 86, 13142 (2012).

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.

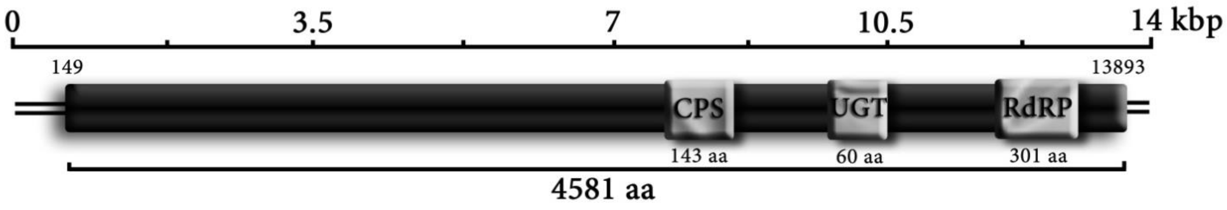

Figure 1. The Yerba mate endornavirus 1 single linear dsRNA is 13954 nt long, contains a single 1,3743 nt ORF, and a 149 nt 5´UTR and a 61 nt 3´UTR. The predicted ORF encodes a 4581 aa polypeptide. Pfam searches identified a CPS domain between 2778-2920 aa, a UGT domain between 3359-3418 aa and a RdPR domain between 4182-4480 aa. doi: 10.1007/s11262-014-1096-2

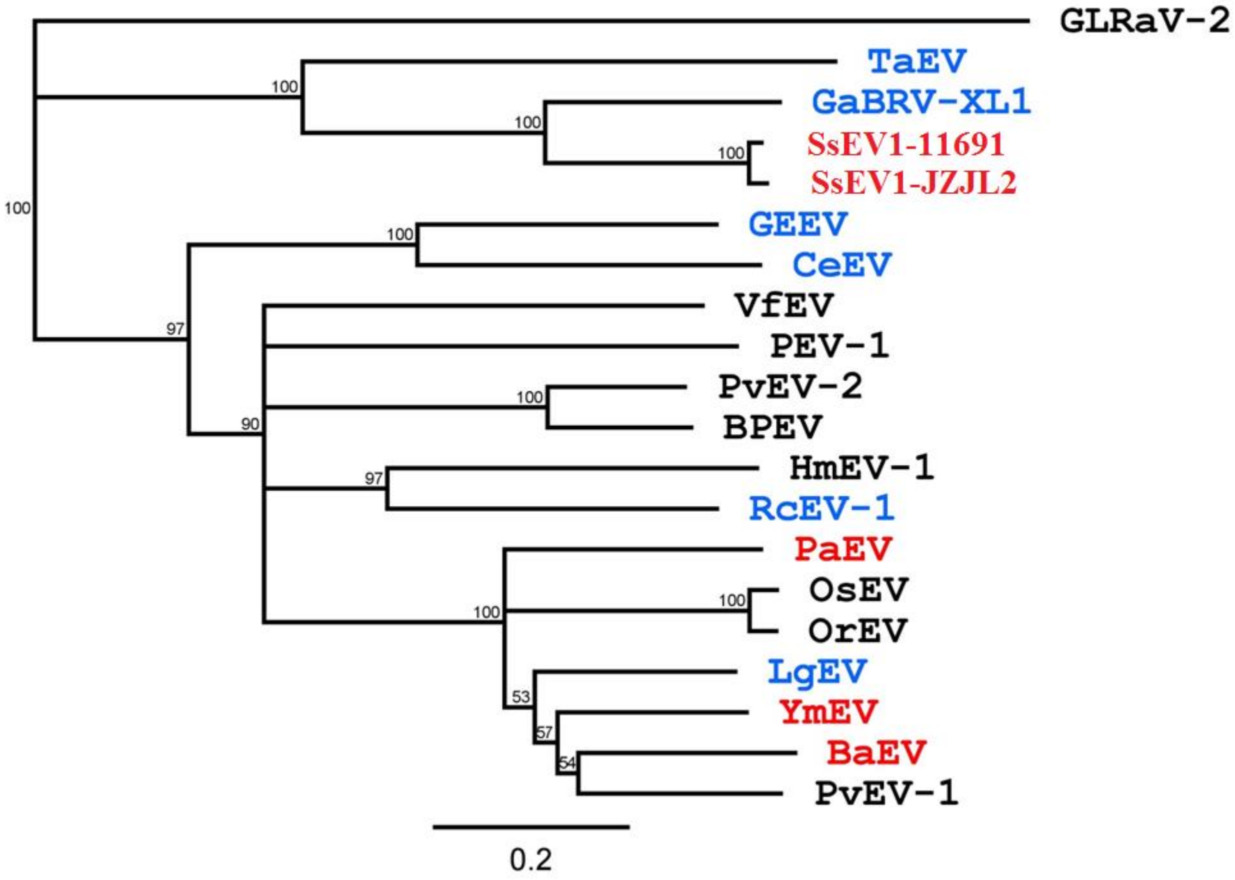

Figure 2. Neighbor-joining phylogenic tree of the RdRp region of endornaviruses (accepted species in **black**, species proposed in this or accompanying proposals in **red** and unclassified viruses in **blue**). Values at the nodes indicate bootstrap support values obtained for 1,000 replicates (only more than 50% bootstrap values are shown). LgEV: Lagenaria siceraria endornavirus; OsEV: *Oryza sativa endornavirus*; OrEV: *Oryza rufipogon endornavirus*; PaEV: Persea americana endornavirus 1; PvEV-1: *Phaseolus vulgaris endornavirus 1*; PvEV-2: *Phaseolus vulgaris endornavirus 2*; BaEV: Basella alba endornavirus 1; PEV-1: *Phytophthora endornavirus* 1; BPEV: *Bell pepper endornavirus*; HmEV-1: *Helicobasidium mompa endornavirus 1*; VfEV: *Vicia fava endornavirus*; CeEV: Chalara elegans endornavirus; GEEV: Grapevine endophyte endornavirus; GaBRV-XL1: Gremmeniella abietina type B RNA virus -XL1; TaEV: Tuber aestivum endornavirus; SsEV1-11691: Sclerotinia sclerotiorum endornavirus 1 strain 11691; SsEV1-JZJL2; Sclerotinia sclerotiorum endornavirus 1 strain JZJL2; RcEV-1: Rhizoctonia cerealis endornavirus 1; YmEV: Yerba mate endornavirus 1. GLRaV-2: *Grapevine leafroll-associated virus*-2 was used as outgroup.

Table 1. Amino acid sequence identity percentage of Yerba mate endornavirus 1 predicted polypeptide and conserved domains compared with other endornavirus species (**black** font), proposed new species (**red** font, this or accompanying proposals) and unclassified viruses (**blue** font). Poly, Polypeptide; CPS, capsular polysaccharide synthase protein; UGT, UDP-glucose glycosyl-transferase; RdRp, RNA-dependent RNA polymerase; ND, not detected; P, Plant; F, Fungus; O, Oomycete

Endornavirus	Host	CPS	UGT	RdRp	Poly	Complete nt sequence	Accession no.
Lagenaria siceraria endornavirus	P	44.4 %	ND	67.1 %	36.0 %	54.9 %	AHK22715.1
Basella alba endornavirus 1	P	40.6 %	30.0 %	66.8 %	33.4 %	54.7 %	AB844265.1
Oryza sativa endornavirus	P	32.9 %	38.3 %	61.5 %	34.4 %	54.6 %	YP_438200.1
Oryza rufipogon endornavirus	P	34.3 %	40.0 %	61.8 %	33.8 %	53.7 %	YP_438202.1
Persea americana endornavirus 1	P	44.8 %	30.0 %	63.1 %	38.8 %	56.1 %	YP_005086952.1
Phaseolus vulgaris endornavirus 1	P	40.6 %	38.3 %	62.5 %	33.9 %	53.9 %	BAM68539.1
Bell pepper endornavirus	P	ND	14.5 %	41.9 %	18.3 %	51 %	BAK52155.1
Phaseolus vulgaris endornavirus 2	P	ND	12.3 %	42.2 %	18.0 %	50.1 %	BAM68540.1
Vicia faba endornavirus	P	ND	ND	39.9 %	16.6 %	49.7 %	YP_438201.1
Phytophthora endornavirus 1	O	ND	11.5 %	42.2 %	17.9 %	50.3 %	YP_241110.1
Helicobasidium mompa endornavirus 1	F	ND	11.0 %	38.0 %	16.2 %	49.4 %	YP_003280846.1
Gremmeniella abietina type B RNAvirus Xl1	F	ND	ND	25.7 %	15.2 %	50.3 %	YP_529670.1
Tuber aestivum endornavirus	F	ND	ND	23.0 %	13.9 %	50.2 %	YP_004123950.1
Chalara elegans endornavirus	F	ND	18.5 %	31.5 %	17.2 %	48.6 %	ADN43901.1
Grapevine endophyte endornavirus	P	ND	ND	33.2 %	17.4 %	49.6 %	YP_007003829.1
Rhizoctonia cerealis endornavirus 1	F	ND	ND	40.9 %	17.0 %	50.3 %	YP_008719905.1
Sclerotinia sclerotiorum endornavirus 1-JZJL2	F	ND	ND	23.4 %	14.4 %	50.7 %	YP_008169851.1
Sclerotinia sclerotiorum endornavirus 1-11691	F	ND	ND	23.4 %	14.5 %	50.9 %	YP_009022070