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:	***2016.019a,bP***	(to be completed by ICTV officers)

Short title: Create 10 new species in the family *Endornaviridae*
(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** ☐

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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)	Endornaviridae SG

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

Chair and one member of the SG are among the authors of the proposal. Other members of the SG reviewed the proposal and voiced no objections.

Date first submitted to ICTV: July 2016
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	***2016.019aP***	(assigned by ICTV officers)

To create 7 new species in the renamed genus *Alphaendornavirus*

Genus:	***Alphaendornavirus*** (former name *Endornavirus*; see TP 2016.020a-gP)
Subfamily:	
Family:	***Endornaviridae***
Order:	***Unassigned***

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)**
Cucumis melo alphaendornavirus	CmEV CL-01	KT727022.1
Erysiphe cichoracearum alphaendornavirus	EcEV HBJZ1506	KT388110.1
Grapevine endophyte alphaendornavirus	GEEV South Africa	JX678977.1
Hordeum vulgare alphaendornavirus	HvEV Nerz	KT721705.1
Hot pepper alphaendornavirus	HpEV CS	KR080326.1
Lagenaria siceraria alphaendornavirus	LsEV FB	KF562072.1
Rhizoctonia cerealis alphaendornavirus 1	RcEV R0959	KF311065.1

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

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

Endornaviruses are groups of vertically transmitted viruses reported from economically important crops, (e.g. pepper, bean, barley, avocado, melon, etc), wild plants, plant pathogenic fungi, and the oomycete *Phytophthora* sp. (Fukuhara & Gibbs, 2012; Okada et al., 2011, 2013; Roossinck et al., 2011; Sabanadzovic et al., 2016; Villanueva et al., 2012). With the exception of Phaseolus vulgaris endornavirus 1 (PvEV1) and Phaseolus vulgaris endornavirus 2 (PvEV2), all of the other endornaviruses have been isolated from a different host (Okada et al., 2013).

At present, the family *Endornaviridae* contains 12 recognized species, all members of the single genus *Endornavirus*. Currently applied species demarcation criteria for endornavirus species are based upon differences in host-range, genome organization, and nucleotide sequence variations among representative isolates (Fukuhara & Gibbs, 2012).

Search of published literature resulted in a total of 22 well-characterized distinct endornaviruses, all

supported by full genome sequence data. These 10 "extra" viruses clearly differ from each other and from representatives of recognized species and, therefore, potentially represent distinct novel species.

Recent increased scientific interest in these viruses has led to generation of new knowledge and identification of two distinct evolutionary lineages of these viruses. Different evolutionary history is also highlighted by differences in genomes size, genome organization and type of host. Therefore, a sister proposal for the re-organization of this taxon (family *Endornaviridae*) has been prepared and submitted by the same group of authors (please see related proposal 2016.020a-gP on reorganization of the family submitted along with this taxoprop). The proposal for the reorganization of the family includes renaming the extant genus *Endornavirus to Alphaendornavirus* and creation of a new genus named *Betaendornavirus* in order to accommodate species characterized by distinct features.

Here we present a proposal for the recognition of 10 additional novel species in the family *Endornaviridae* and their assignment into the proposed two new genera.

Therefore, taking into account features of viruses representing the putative new species, we propose the creation of **seven** new species in the genus *Alphaendornavirus* and **three** in the genus *Betaendornavirus*.

All proposed new species satisfy species demarcation criteria proposed for members of the genera *Alphaendornavirus* and *Betaendornavirus.* Below is the description of the seven proposed new species in the genus *Alphaendornavirus*.

Criteria for species distinction in the genus *Alphaendornavirus* are:

- Overall nt identity less than 75%.
- Differences in host.

Cucumis melo endornavirus (CmEV)

High molecular weight dsRNA, with an estimated size of 15 kbp, was isolated from a melon (*Cucumis melo* L.) plant of an unknown cultivar and completely sequenced. Nucleotide sequence analyses showed that this dsRNA is associated with an endornavirus referred to as Cucumis melo endornavirus isolate CL01(CmEV-CL01) (Sabanadzovic et al., 2016). The monocistronic genome of CmEV-CL01 consists of 15,078 nucleotides (nt) and terminates with a stretch of 10 cytosine residues on its 3' terminus. Putative CmEV-CL01 encoded polyprotein consists of 4,939 amino acids (aa) and has a unique genome organization characterized by the presence of the following domains: viral helicase Superfamily 1 (Hel-1), three glucosyltransferases (doublet of putative capsular polysaccharide synthesis proteins and a putative C 28 Glycosyltransferase), and an RNA-dependent RNA polymerase (RdRp) (Fig. 1). Such glycome-rich organization makes CmEV unique among known endornaviruses. Phylogenetic analyses of viral RdRp domains showed that CmEV belongs to a specific lineage of plant-infecting endornaviruses within the genus *Alphaendornavirus* in the family *Endornaviridae* (see Fig 2). A survey of different melons belonging to 25 genotypes revealed common presence of CmEV among melon germplasm accession (>87% of tested samples). Unexpectedly, CmEV has been detected in plants belonging to three different genera in the family Cucurbitaceae which makes host range of this virus rather unusual for endornaviruses and suggests a long history of virus-cucurbit association (Sabanadzovic et al., 2016). Based upon differences in genome organization of CmEV-CL01, its limited nt and aa homology with other known endornaviruses and distinct evolutionary history, we propose to assign this virus to a new species, named *Cucumis melo alphaendornavirus.*

Erysiphe cichoracearum endornavirus (EcEV)

A double-stranded RNA of approximately 12 kbp was recovered and sequenced from isolate HBJZ1506 of the phytopathogenic fungus *Erysiphe cichoracearum* infecting *Calendula officinalis* in Hubei Province in China (Du et al., 2016). Nucleotide sequencing showed that it represents a genome of a new virus, provisionally named Erysiphe cichoracearum endornavirus (EcEV). The EcEV-HBJZ genome comprises 11,908 nucleotides (nt) and contains a 11,859 nt-long open reading frame (ORF) coding for a polypeptide that is 61 % identical to that of a putative endornavirus named grapevine endophyte endornavirus (GEEV). EcEV-encoded putative polyprotein contains an RNA-dependent RNA polymerase (RdRp) domain and an RNA helicase domain, both similar to that of counterparts present in approved endornaviruses. In phylogenetic analyses of amino acid sequences of the RdRp region, EcEV clustered with alphaendornaviruses and formed a well-supported monophyletic branch with GEEV. The whole putative polyprotein of EcEV-HBJZ1506 exhibited 60 % aa sequence identity to that of GEEV. These results suggest that the virus from HBJZ1506 represents a novel species of endornaviruses, for which the name *Erysiphe cichoracearum alphaendornavirus* is proposed.

Grapevine endophyte endornavirus (GEEV)

Double-stranded RNA resembling endornaviruses was extracted from phloem tissue of a diseased *Vitis vinifera* cv. Shiraz vine, reverse-transcribed and sequenced using a short read Illumina approach. The short reads were trimmed, filtered for quality and de novo assembled. RACE-PCR was used to confirm the 5' and 3' ends. The complete genome of a virus, referred to as grapevine endophyte endornavirus (GEEV), is 12,154 bp long and contains a single ORF whose product has a predicted molecular mass of 452.7 kDa. Predicted protein domains include a Hel-1 in the central part of the polyprotein and an RdRp near the C terminus. Phylogenetic analysis performed on aa sequences of viral RdRp domains showed that GEEV share common evolutionary lineage with EcEV within the clade embracing alphaendornaviruses. As expected, in pairwise comparisons, GEEV resulted most closely related to EcEV, sharing 60 % common nucleotides (Espach et al., 2012). In summary, the endornavirus sequenced from grapevine is prototype of a novel species for which the name *Grapevine endophyte alphaendornavirus* is proposed.

Hot pepper endornavirus (HpEV)

The complete genome of a putative new endornavirus infecting hot peppers (*Capsicum annuum*), denominated hot pepper endornavirus (HPEV), was determined to be 14,729 nt in size, including 12 cytosines (Cs) at the 3' end (Lim et al., 2015). The HPEV has the highest nucleotide sequence similarity (94 % query cover and 72 % identity) to bell pepper endornavirus (BPEV) isolated from the cultivar Yolo Wonder in the USA (GenBank accession no. JN019858). The single, large open reading frame identified in the HPEV genome encodes a 4,884-aa-long polyprotein that contains four putative functional domains: a viral methyltransferase (MTR), a Hel-1, a glycosyltransferase, and an RdRp. A phylogenetic tree based on whole polyprotein sequences confirmed the close evolutionary relationship of HPEV and BPEV. The hot pepper-infecting virus also has a nick at nt position 975. Taken together, these results suggest that HpEV belongs to a new species in the genus *Alphaendornavirus* (family *Endornaviridae*), for which the name *Hot pepper alphaendornavirus* is proposed.

Hordeum vulgare endornavirus (HvEV)

The complete genome sequence of an endornavirus was determined from paired Illumina MySeq

reads derived from reverse-transcribed dsRNAs isolated from variety Nertz of barley (*Hordeum vulgare*). The genome of a putative new endornavirus, referred to as Hordeum vulgare endornavirus (HvEV), is 14,243 nt long, with short 5' and 3' non-coding regions (Candresse et al., 2016). The monocistronic genome encodes a single large protein of 4,663 amino acids in length, containing three conserved domains that are common in other endornaviruses: a MTR, a Hel-1 and an RdRp (Fig. 1). Their order and relative positions in the polyprotein is similar to that in other endornaviruses. However, no UDP-glycosyltransferase motif observed in many, but not all, endornaviral genomes could be identified in HvEV-encoded polyprotein. Pairwise comparison of complete aa sequences showed that HvEV is highly divergent from other recognized endornaviruses. The two most closely related viruses, BPEV and PvEV2, shared only 19.3-19.5 % aa sequence identity with HvEV. A phylogenetic analysis confirms common evolutionary history with members of recognized species in the genus *Alphaendornavirus* (Fig. 2). Based upon distinct features of HvEV, we propose creation of a novel species in the genus *Alphaendornavirus* to accommodate isolates of this virus. The proposed species name is *Hordeum vilgare alphaendornavirus.*

Lagenaria siceraria endornavirus (LsEV)

Double stranded-RNA (dsRNA) analysis of hard shell ornamental gourd (*Lagenaria siceraria*) samples affected with severe yellowing symptoms collected in southern California revealed the presence of high molecular weight molecules with sizes similar to that of endornaviruses. Complete sequencing revealed that genome of putative new endornavirus, tentatively named Lagenaria siceraria endornavirus isolate California (LsEV-CA), was 15,088 bp in length, and contained one large ORF encoding a 576 kDa polyprotein (Kwon et al., 2014). The predicted protein contained several domains identified with searches in Protein Family Databank (Pfam): a Hel-1 domain, followed by two glycosyltransferase motifs and an RdRp (Fig. 1). Phylogenetic analyses of viral RdRP domain indicated that LsEV is related to several plant infecting endornaviruses including another cucurbit infecting endornavirus (e.g, cucumis melo endornavirus) (Fig. 2). Nevertheless, overall nt identity with CmEV resulted to be far below species demarcation level suggesting that the virus from ornamental gourd represents a new species in the genus *Alphaendornavirus*. Survey results as well as greenhouse-based studies indicate that LsEV-CA is likely not associated with the gourd-yellows syndrome originally observed in the field. The name for a new proposed species is *Lagenaria siceraria alphaendornavirus*.

Rhizoctonia cerealis endornavirus 1 (RcEV1)

A novel endornavirus, tentatively named Rhizoctonia cerealis endornavirus 1 (RcEV1), has recently been characterized from a Chinese isolate (R0959) of the fungus *Rhizoctonia cerealis*, the cause of sharp eyespot disease of wheat (Li et al., 2014). This is the first report of an endornavirus in this plant pathogenic fungus. Sequence analysis showed that the genome of RcEV1 is 17,486 bp long, making it second largest genome among sequenced endornaviruses. It contains a single open reading frame (ORF) potentially coding for a protein of 5,747 amino acids. The predicted protein contains conserved motifs of putative viral MTR, Hel-1, and RdRp (Li et al., 2014) (Fig. 1). Phylogenetic analyses clearly show that RcEV1 domains have distinct evolutionary history from counterparts in other endornaviruses (Fig. 2). Nucleotide sequence identities with other endornaviruses are far below species demarcation criterion proposed for alphaendornaviruses. Therefore, we propose creation of a new species, named *Rhizoctonia cerealis alphaendornavirus 1*, in the genus *Alphaendornavirus*.

In summary, we propose creation **of seven novel species in the genus *Alphaendornavirus*** in order to accommodate new endornaviruses with similar, but distinct characteristics (CmEV, EcEV, GEEV, HpEV, HvEV, LsEV and RcEV1).

These viruses, considered representatives of new species in the genus, have been reported from distinct plant and fungal hosts, have genome size of c. 12-17.6 kb that code for glucosyltransferase, all belong to the same lineage as OsEV within the family *Endornaviridae* and share less than 75% overall nt identity with any other endornavirus.

An updated list of species in the genus *Alphaendornavirus* is presented in Table 1

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	***2016.019bP***	(assigned by ICTV officers)

To create 3 new species within:

Genus:	***Betaendornavirus***
Subfamily:	***NA***
Family:	***Endornaviridae***
Order:	***Unassigned***

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)**
Alternaria brassicicola betaendornavirus 1	AbEV 817-14 Hunan	KP239989.1
Gremmeniella abietina betaendornavirus 1	GaBRV-XL AU58	DQ399289.1
Tuber aestivum betaendornavirus	TaEV Jaszag	HQ380014.1

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

Criteria for species distinction in the genus *Betaendornavirus* are:

- Overall nt identity less than 75%.
- Differences in host.

Additionally, viruses belonging recognized species in the genus *Betaendornavirus* have the following features:

- Genome of approximately 9-11.5 kb in size.
- Presence of easily identifiable viral MTR domain.
- Infect ascomycete fungi.

The brief description of three viruses representing the new species proposed in the genus *Betaendornavirus*:

Alternaria brassicicola endornavirus 1 (AbEV1)

A dsRNA molecule of 10,290 nt, resembling those associated with the viruses belonging to the family *Endornaviridae*, was isolated from *Alternaria brassicicola* strain 817-14 isolated from rapeseed leaves collected from Hunan Province in China (Shang et al. 2015). Genome sequencing and analyses revealed genome organization typical for endornaviruses,

characterized by the presence of a single large open reading frame coding for a polyprotein of 3,400 aa. The virus was tentatively named as Alternaria brassicicola endornavirus 1 (AbeV1). The polyprotein contained conserved viral MTR, viral Hel-1, and RdRp as well as, a cysteine-rich region (CRR) located between the MTR and Hel-1 domains (Fig. 1). Pairwise comparisons with recognized and putative endornaviruses, revealed limited identities with closest relatives (i.e. only 14.7% with Tuber aestivum endornavirus). Phylogenetic analysis based on the RdRp sequence, strongly suggested that AbEV1 is distinct from other known endornaviruses (Fig.2) and should be considered a representative of a novel species in the genus, designated as *Alternaria brassicicola betaendornavirus 1*.

Gremmeniella abietina RNA virus XL (GaBRV-XL)

A 11 kbp dsRNA was isolated from two isolates (AU58 and E46) of *Gremmeniella abietina* type B (Tuomivirta et al., 2009). Complete sequencing of these two molecules revealed that they differed by one nt in size (10,375 and 10,374 bp, respectively) and 3% nt content, therefore representing isolates of the same virus, named Gremmeniella abietina RNA virus XL1 and XL2 (in general GaBRV-XL). Computer analyses showed that GaBRV-XL genome is monocistronic. Large ORF encoded a putative protein of 3,429 aa in length and encompassed more than 99% of the genome. Polyprotein contained identifiable motifs of viral MTR, two helicases belonging to different superfamilies (DEAD-like and Hel-1) as well as RdRp (Fig. 1). Additionally, a CRR with several CxCC signatures have been found between the MTR and DEAD-like helicase domains in the GaBRV-XL-encoded polypeptide. Phylogenetic analyses conducted on the putative MTR, DEAD box helicase, viral RNA helicase 1 and RdRp regions suggest that GaBRV-XL is related to but distinct from known betaendornaviruses (Fig. 2). Therefore, we propose creation of new species in the genus *Betaendornavirus*, denominated *Gremmeniella abietina betaendornavirus 1* to accommodate isolates of this virus.

Tuber aestivum endornavirus (TaEV)

The presence of putative novel endornavirus, denominated Tuber aestivum endornavirus (TaEV), from an ectomycorrhizal fungus was reported by a German group of scientists using the black truffle ascocarp collected in Hungary as source for dsRNA isolation. A 10 kbp dsRNA molecule was used for random primed RT-PCR protocol (Stielow et al., 2011). The complete genome of TaEV resulted 9,760 bp in length, containing a large ORF accounting for almost 99% of the whole molecule. TaEV genome terminated with a stretch of 12 Cs at the 3' terminus. The large polyprotein contained domains of viral MTR, a DEXDc element of the DEAD-like helicase superfamily, and the RdRp (Fig.1). A phylogenetic tree constructed on viral RdRp placed TaEV in the group of "short" endornaviruses along with SsEV1, EcEV GaBRV-XL (Fig. 2). Overall nt identity with the closest relative (GABRV-XL) was estimated at 45.4%, which is far below species demarcation criterion proposed for the genus *Betaendornavirus*. Therefore, we propose creation of a novel species in the genus referred to as *Tuber aestivum betaendornavirus* typified by TaEV isolate Jaszag from Hungary (Stielow et al., 2011).

In summary, we propose creation of 3 (three) novel species in the genus *Betaendornavirus* in order to accommodate new endornaviruses with characteristics of betaendornaviruses (e.g. AbEV1, GaBRV-XL and TaEV). These viruses, considered representatives of new species in the genus, were reported from distinct hosts belonging to Ascomycetes, have genome size of c. 10 kb with clear presence of MTR domain, belong to the same lineage as SsEV1 within the family *Endornaviridae* and share less than 75% overall nt identity.

An updated list of species in the genus *Betaendornavirus* is presented in Table 1

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Candresse T, Marais A, Sorrentino R, Faure C, Theil S, Cadot V, Rolland M, Villemot J, Rabenstain F (2016) Complete genomic sequence of barley (*Hordeum vulgare*) endornavirus (HvEV) determined by next-generation sequencing. Arch Virol 161:741-743

Du Z, Lin W, Qiu P, Liu X, Guo L, Wu K, Zhang S, Wu Z. (2016) Complete sequence of a double-stranded RNA from the phytopathogenic fungus *Erysiphe cichoracearum* that might represent a novel endornavirus. Arch Virol 161(8):2343-2346

Espach Y, Maree HJ, Burger JT (2012) Complete genome of a novel endornavirus assembled from next-generation sequence data. J Virol 86(23):13142

Fukuhara, T., Gibbs, M. J. (2012) Family *Endornaviridae*. In: (A. M. Q. King, M. J. Adams, E. B. Carstens & E. J. Lefkowitz Eds) Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses, pp. 519–521.. Tokyo: Elsevier Academic Press.

Kwon, S.-J., Tan, S., Vidalakis, G., (2014) Complete genome sequence and genome organization of an endornavirus from bottle gourd (*Lagenaria siceraria*) in California, U.S.A. Virus Genes 49, 163-168.

Li W, Zhang T, Sun H, Deng Y, Zhang A, Chen H, Wang K (2014) Complete genome sequence of a novel endornavirus in the wheat sharp eyespot pathogen *Rhizoctonia cerealis*. Arch virol 159(5):1213-6.

Lim S, Kim KH, Zhao F, Yoo RH, Igori D, Lee S-H, Moon JS (2015) Complete genome sequence of a novel endornavirus isolated from hot pepper. Arch Virol 160:3153–3156

Okada R, Kiyota E, Sabanadzovic S, Moriyama H, Fukuhara T, Saha P, Roossinck MJ, Severin A, Valverde RA (2011) Bell pepper endornavirus: molecular and biological properties, and occurrence in the genus Capsicum. J Gen Virol 92:2664–2673

Okada R, Yong CK, Valverde RA, Sabanadzovic S, Aoki N, Hotate S, Kiyota E, Moriyama H, Fukuhara T (2013) Molecular characterization of two evolutionarily distinct endornaviruses coinfecting common bean (*Phaseolus vulgaris*). J Gen Virol 94:220–229

Roossinck MJ, Sabanadzovic S, Okada R, Valverde RA (2011) The remarkable evolutionary history of endornaviruses. J Gen Virol 92:2674–2678

Sabanadzovic S, Wintermantel WM, Valverde RA, McCreight JD, Aboughanem-Sabanadzovic N (2016) Cucumis melo endornavirus: genome organization, host range and co-divergence with the host. Virus Research 214:49-58.

Shang, H-H, J Zhong, R-J Zhang, C-Y Chen, B-D Gao, H-J Zhu (2015). Genome sequence of a novel endornavirus from the phytopathogenic fungus *Alternaria brassicicola*. Arch. Virol. 160:1827–1830.

Stielow B, Klenk HP, Menzel W (2011) Complete genome sequence of the first endornavirus from the ascocarp of the ectomycorrhizal fungus *Tuber aestivum* Vittad. Arch Virol

References:

156:343–345

Tuomivirta TT, Kaitera J, Hantula J (2009) A novel putative virus of *Gremmeniella abietina* type B (Ascomycota: Helotiaceae) has a composite genome with endornavirus affinities. J Gen Virol 90:2299–2305

Villanueva F, Sabanadzovic S, Valverde RA, Navas-Castillo J (2012) Complete genome sequence of a double-stranded RNA virus from avocado. J Virol 86(2):1282–1283

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.

Table 1. Proposed new structure of the family *Endornaviridae*

Family *Endornaviridae*	
Genus *Alphaendornavirus* (18 species)	**Genus *Betaendornavirus*** (4 species)
Oryza sativa alphaendornavirus *	***Sclerotinia sclerotiorum betaendornavirus 1****
Basella alba alphaendornavirus 1	*Alternaria brassicicola betaendornavirus 1*
Bell pepper alphaendornavirus	*Gremmeniella abietina betaendornavirus 1*
Cucumis melo alphaendornavirus	*Tuber aestivum betaendornavirus*
Erysiphe cichoracearum alphaendornavirus	
Grapevine endophyte alphaendornavirus	
Helicobasidium mompa alphaendornavirus 1	
Hordeum vulgare alphaendornavirus	
Hot pepper alphaendornavirus	
Lagenaria siceraria alphaendornavirus	
Oryza rufipogon alphaendornavirus	
Persea americana alphaendornavirus 1	
Phaseolus vulgaris alphaendornavirus 1	
Phaseolus vulgaris alphaendornavirus 2	
Phytophthora alphaendornavirus 1	
Rhizoctonia cerealis alphaendornavirus 1	
Vicia faba alphaendornavirus	
Yerba mate alphaendornavirus	

*** - type species in the genus**

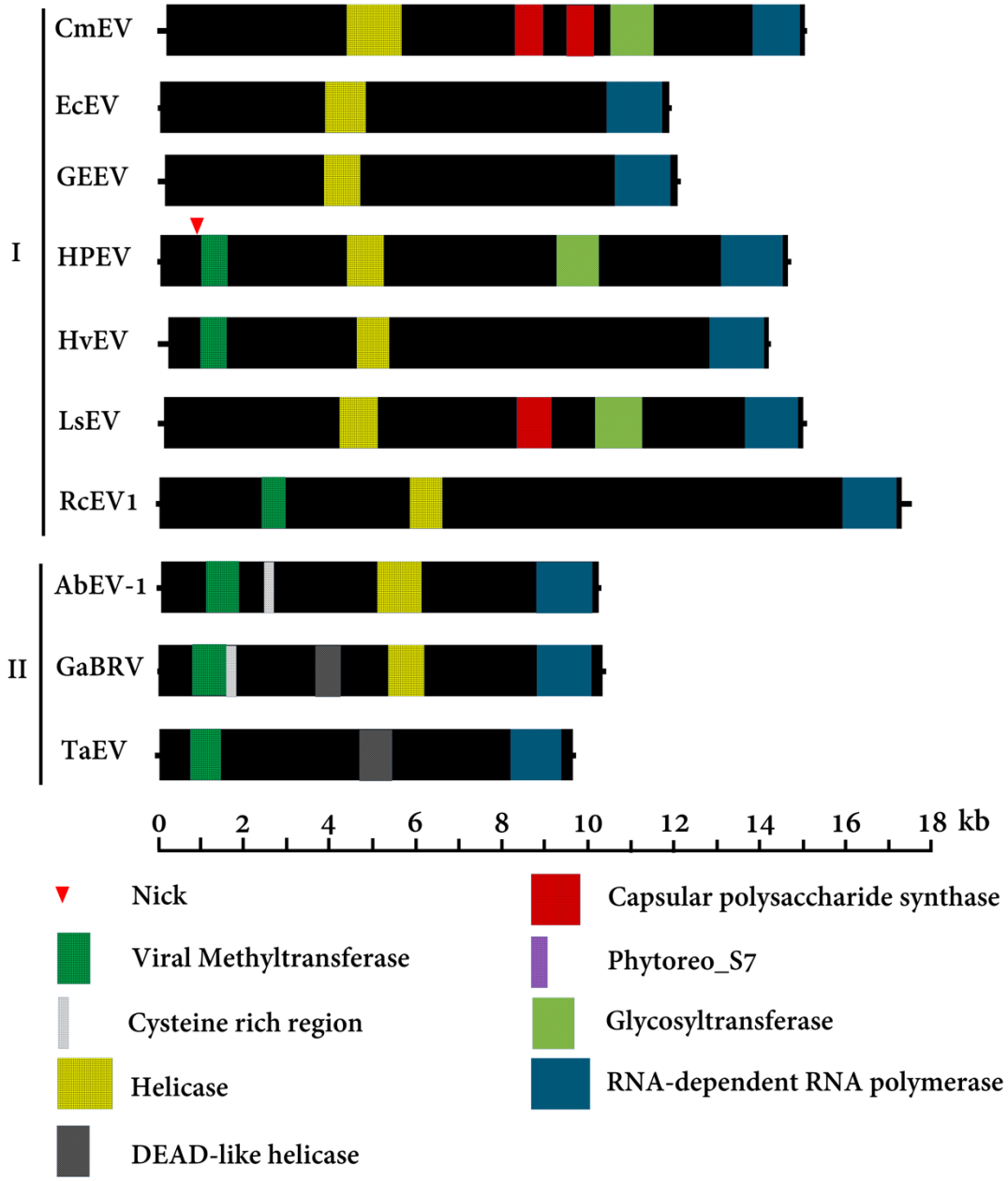
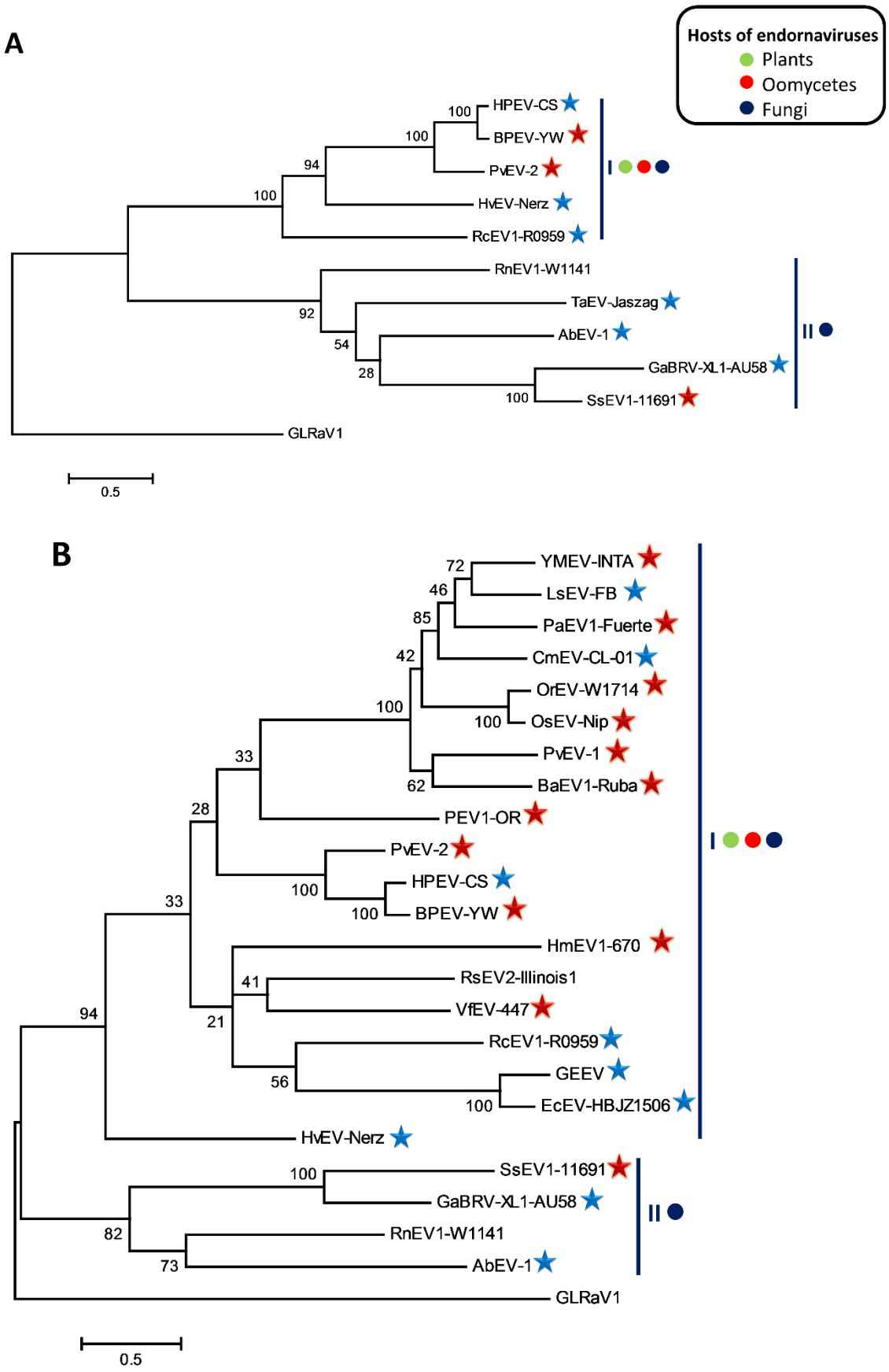


Fig. 1. Schematic representation of the genome organization for viruses representing proposed novel species in the genera *Alphaendornavir*us (labeled as "I") and *Betaendornavirus* (labeled as "II"). Conserved domains are represented by colored boxes. The presence of a site-specific nick has not been studied in most of these species.


A
Hosts of endornaviruses
Plants
Oomycetes
Fungi
HPEV-CS
BPEV-YW
PvEV-2
HvEV-Nerz
RcEV1-R0959
RnEV1-W1141
TaEV-Jaszag
AbEV-1
GaBRV-XL1-AU58
SsEV1-11691
GLRaV1
100
100
94
100
92
54
28
100
I
II
0.5
B
YMEV-INTA
LsEV-FB
PaEV1-Fuerte
CmEV-CL-01
OrEV-W1714
OsEV-Nip
PvEV-1
BaEV1-Ruba
PEV1-OR
PvEV-2
HPEV-CS
BPEV-YW
HmEV1-670
RsEV2-Illinois1
VfEV-447
RcEV1-R0959
GEEV
EcEV-HBJZ1506
HvEV-Nerz
SsEV1-11691
GaBRV-XL1-AU58
RnEV1-W1141
AbEV-1
GLRaV1
72
46
85
42
100
100
33
62
28
100
100
33
41
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94
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100
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I
II
0.5

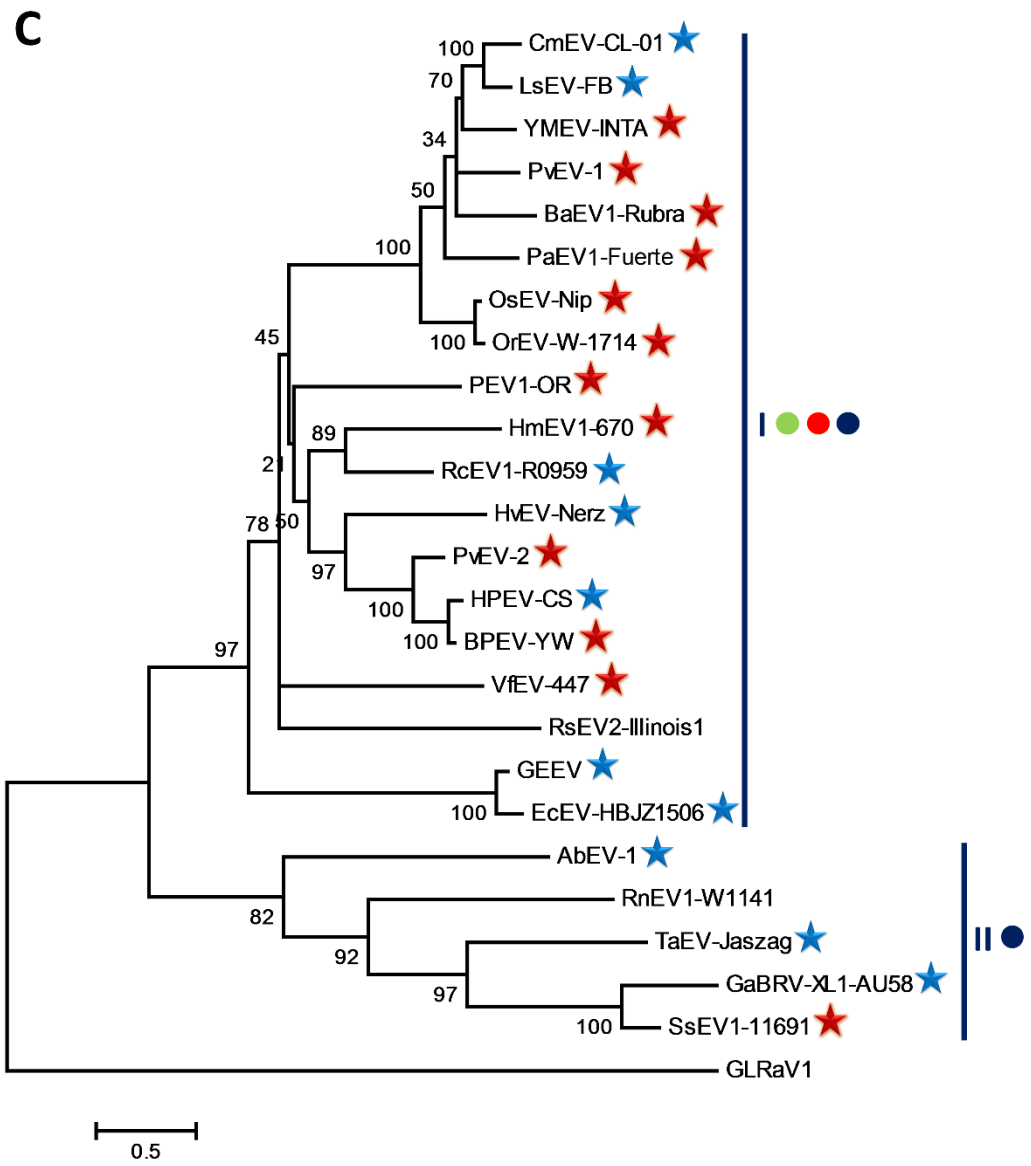

Figure 2. Maximum likelihood phylogenetic trees constructed with **(A)** the methyltransferase (MTR), **(B)** the helicase (Hel), and **(C)** the RNA-dependent RNA polymerase (RdRp) domains of endornaviruses. The best-fit substitution models were chosen and maximum likelihood phylogenetic trees constructed using MEGA7 software (Kumar et al., 2016). The Le and Gascuel with gamma-distributed site rates and invariant sites (LG+G+I) was used. Numbers on the nodes represent bootstrap support from 100 replicates. Currently recognized *Endornaviridae* members are marked with **red asterisks**, while those proposed for recognition in this TP are labeled with **blue asterisks**. Legend: Roman numerals I and II indicate genera *Alphaendornavirus* and *Betaendornavirus*, respectively. Names, acronyms and GenBank accession numbers for viruses used to construct trees are: Alternaria brassicicola endornavirus 1 (AbEV-1, KP239989.1), Basella alba endornavirus 1 (BaEV1, AB844264.1), bell pepper endornavirus (BPEV, JN019858.1), Cucumis melo endornavirus (CmEV, KT727022.1), Erysiphe cichoracearum endornavirus (EcEV, KT388110.1), Gremmeniella abietina type B RNA virus XL (GaBRV-XL, YP_529670.1), grapevine endophyte endornavirus (GEEV, JX678977.1), Helicobasidium mompa

endornavirus 1 (HmEV-1, AB218287.1**),** Hordeum vulgare endornavirus (HvEV, KT721705.1), hot pepper endornavirus (HpEV, KR080326.1), Lagenaria siceraria endornavirus (LsEV, KF562072.1), Oryza rufipogon endornavirus (OrEV, YP_438202.1), Oryza sativa endornavirus (OsEV, YP_438200.1**),** Persea americana endornavirus 1 (PaEV1**,** YP_005086952.1**),** Phaseolus vulgaris endornavirus 1 (PvEV-1, AB719397.1) Phaseolus vulgaris endornavirus 2 **(**AB719398.1**),** Phytophthora endornavirus 1 (PEV1, YP_241110.1), Rhizoctonia cerealis endornavirus 1 (RcEV1, KF311065.1), Sclerotinia sclerotiorum endornavirus 1 (SsEV-1, KJ123645.1), Tuber aestivum endornavirus (TaEV, YP_004123950.1), Vicia faba endornavirus (VfEV, YP_438201.1), yerba mate endornavirus (YmEV, KJ634409.1). The closterovirus grapevine leafroll associated virus 1 (GLRaV-1, JQ023131.1) was used as an outgroup. Roman numerals I and II indicate genera *Alphaendornavirus* and *Betaendornavirus*, respectively.