

Template for Taxonomic Proposal to the ICTV Executive Committee

Creating Species in an existing genus

Code † **2006.021P** To designate the following as species in the genus:

Endornavirus

belonging to the family° : *Endornaviridae*

Helicobasidium mompa endornavirus 1

Phytophthora endornavirus 1

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Order

Family *Endornaviridae*

Genus *Endornavirus*

Type Species *Oryza sativa endornavirus*

Species in the Genus

Oryza rufipogon endornavirus

Oryza sativa endornavirus

Phaseolus vulgaris endornavirus

Vicia faba endornavirus

New Taxonomic Order

Order

Family *Endornaviridae*

Genus *Endornavirus*

Type Species *Oryza sativa endornavirus*

Species in the Genus

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Phaseolus vulgaris endornavirus

Vicia faba endornavirus

Helicobasidium mompa endornavirus 1

Phytophthora endornavirus 1

ICTV-EC comments and response of the SG

The original proposal was for 8 new species but the ICTV-EC commented that there appeared to be insufficient sequence data to create some of these species and invited a revised proposal. This revised version is just for those (2) species for which there are complete sequences. We shall regard the other viruses as tentative species for the time being.

Species demarcation criteria in the genus

In the eighth report of ICTV, four species, *Oryza rufipogon endornavirus* (OrEV), *Oryza sativa endornavirus* (OsEV), *Phaseolus vulgaris endornavirus* (PvEV), and *Vicia faba endornavirus* (VfEV), were listed in the genus *Endornavirus*. The two rice endornaviruses are the most closely related, with almost 80% amino acid sequence identity in their entire open reading frames (ORFs) (Moriyama et al., 1999) while the others are most distantly related. No investigation of endornavirus species demarcation nor speciation has been made. Therefore, we have adopted a conservative arbitrary threshold for species demarcation of 80% amino acid sequence identity.

Argumentation to justify the designation of new species in the genus

Endornavirus genomes have a common structure. They consist of a single large dsRNA 14 to 17 kbp long with a site-specific nick within 3kbp of the 5' end of the coding strand. Endornavirus genomes are the longest known monopartite dsRNA genomes. They encode a single long ORF, which encodes conserved motifs for an RNA dependent RNA polymerase (RdRp) and an RNA helicase. The locations of the motifs are conserved as shown by alignments.

Recently, two reports describing new endornavirus-like dsRNA agents have been published (Hacker et al., 2005; Osaki et al., 2006). The published information on these dsRNA agents shows that they have the characteristics typical of endornaviruses. They have a single dsRNA genome of 13,883 and 16,614 bp respectively, with a site-specific nick in the 5' region, and this dsRNA encodes a single long ORF. BLAST searches indicate that the most similar sequences are those of known endornaviruses and that the proteins encoded by the dsRNAs include RdRp and RNA helicase regions related to those of endornaviruses. Fig. 1 shows a comparison of the genome structures of two known plant endornaviruses, OsEV and VfEV, and these two new species, one isolated from a fungus and the other isolated from a protist. Alignments of the proteins encoded by the two new dsRNA species show that they are distinct from the proteins of recognized endornaviruses, having less than 35% identity across the entire sequence. The names *Helicobasidium mompa endornavirus 1* (HmEV1) and *Phytophthora endornavirus 1* (PEV1) have been proposed in the published descriptions of these agents and we support these proposed names, since they are consistent with the naming formula used for the recognized endornaviruses. We believe that HmEV1 and PEV1 should be classified as new virus species in the genus *Endornavirus*.

We carried out a phylogenetic analysis using amino acid sequences of the RdRp region (about 480 amino acid residues). The two new endornavirus-like dsRNAs formed a monophyletic group with the four known endornaviruses, supported by a high bootstrap score (Fig. 2). The two proposed new species are quite distantly related to one another and to the recognised species and therefore clearly satisfy the criteria to be considered as independent species.

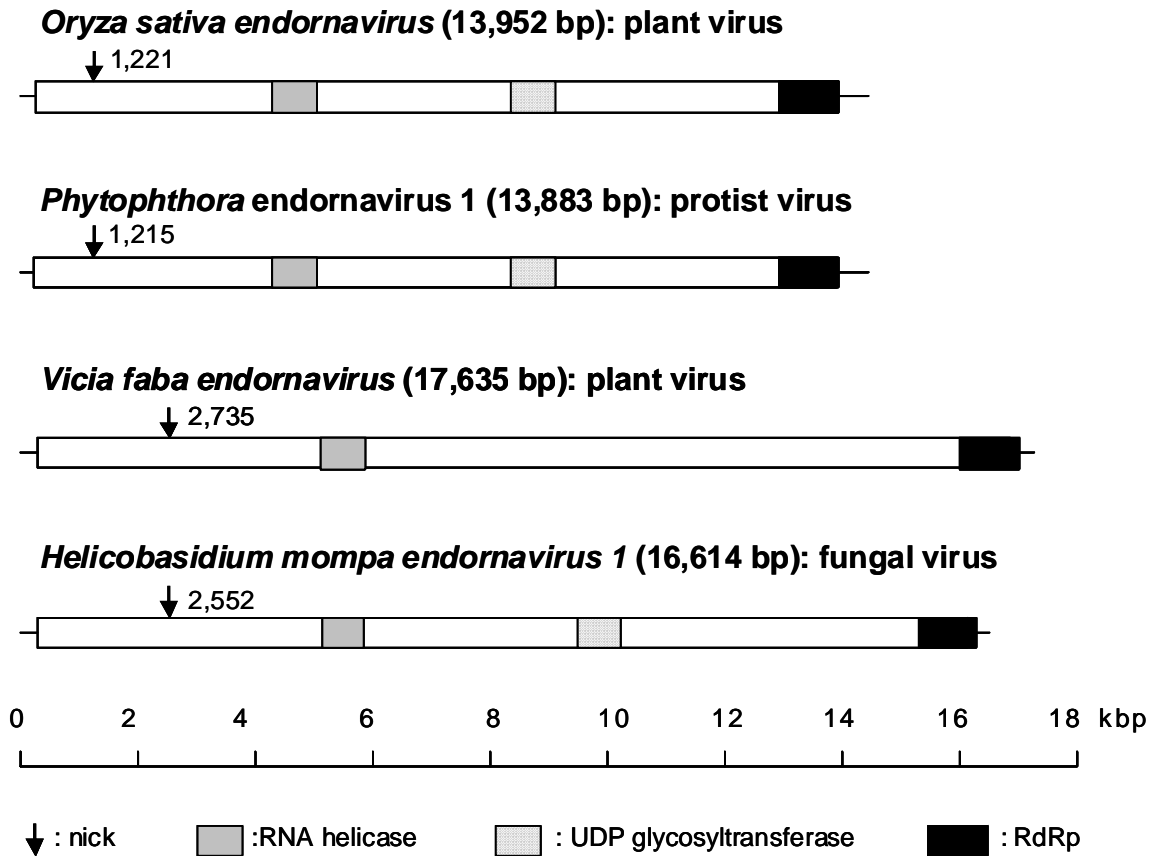


Fig. 1. Comparison of the genome organizations of four endornaviruses: *Oryza sativa* endornavirus (OsEV), *Phytophthora* endornavirus 1 (PEV1), *Vicia faba* endornavirus (VfEV), and *Helicobasidium mompa* endornavirus 1 (HmEV1).

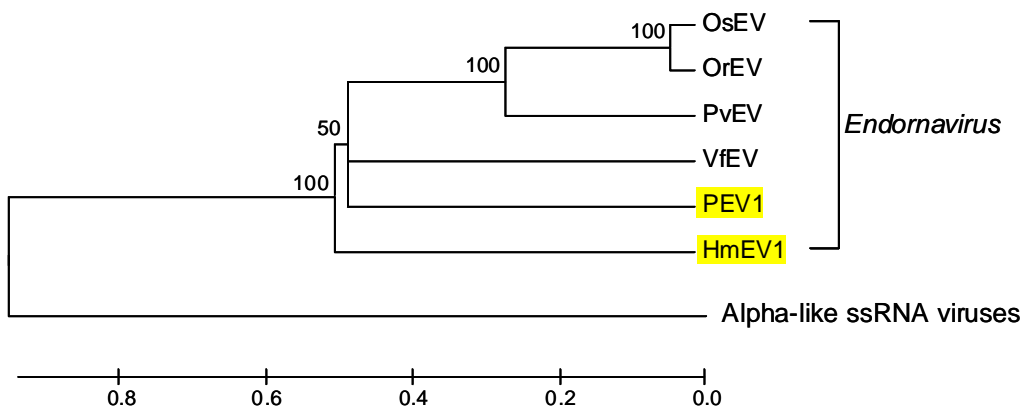


Fig. 2. A dendrogram of endornavirus sequences calculated from about 480 amino acids including the RdRp regions using the NJ method (MEGA ver. 4). The RdRp regions of 16 alpha-like ssRNA viruses were used as the outgroup. A bootstrap test was performed with 100 resamplings.

Table 1. Amino acid sequence identities from an alignment of about 480 amino acid residues including the conserved RdRp regions from endornaviruses.

	OsEV	OrEV	PvEV	VfEV	PEV1	HmEV1
OsEV		92	57	36	38	36
OrEV	98		57	36	38	35
PvEV	74	74		34	37	36
VfEV	54	54	51		35	32
PEV1	57	57	58	55		34
HmEV1	52	51	53	50	54	

Percentages of amino acid identities (top right triangle) and similarities (bottom left triangle) were calculated with the GeneDoc program.

List of created Species in the genus

Helicobasidium mompa endornavirus 1
AB218287 (HmEV1)

Phytophthora endornavirus 1
AJ877914 (PEV1)

References

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- Moriyama, H., Horiuchi, H., Koga, R. and Fukuhara, T. (1999). Molecular characterization of two endogenous double-stranded RNAs in rice and their inheritance by interspecific hybrids. *J. Biol. Chem.* 274, 6882-6888.
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- Pfeiffer, P. (1998). Nucleotide sequence, genetic organization and expression strategy of the double-stranded RNA associated with the '447' cytoplasmic male sterility in *Vicia faba*. *J. Gen. Virol.* 79, 2349-2358.