This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.021-025P***	(to be completed by ICTV officers)

Short title: Creation of genus Emaravirus for the new species European mountain ash ringspot-associated virus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply): **1** ☐ **2** ☐ **3** ☐ **4** ☒ **5** ☒ **6** ☐ **7** ☐

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

MODULE 4: **NEW GENUS** (if more than one genus is to be created, please complete additional copies of this section)

Code	***2008.021P***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	-
Family:	***Unassigned (ssRNA –ve)***
Order:	-

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	***2008.022P***	(assigned by ICTV officers)

To name the new genus: *Emaravirus*

Code	***2008.023P***	(assigned by ICTV officers)

To assign the following as species in the new genus:
You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

European mountain ash ringspot-associated virus **(new species)**

Code	***2008.024P***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:

European mountain ash ringspot-associated virus

Argument to justify the creation of a new genus:

See below on the creation of the species

Origin of the new genus name:

Sigla from the name of the (only) species ***E****uropean* ***m****ountain* ***a****sh* ***r****ingspot-associated* ***virus***

Argument to justify the choice of type species:

It is the only species

Species demarcation criteria in the genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable: only one species

MODULE 5: **NEW SPECIES**

Code	***2008.025P***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Emaravirus***
Subfamily:	-
Family:	-
Order:	-

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

European mountain ash ringspot-associated virus

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

The so called 'Ringspot disease' of European mountain ash (*Sorbus aucuparia* L.) is characterized by leaves showing chlorotic ringspots and mottling as well as a slow decay of diseased trees (Kegler, 1960). In leaf sections, virus-like membrane-bound bodies of 80-100 nm in diameter, resembling tospoviral particles, were detected only in affected *S. aucuparia*

Argument to justify the creation of the new species:

L. (Ebrahim Nesbath & Izadpanah, 1992). Nevertheless, a tospovirus-infection could not be approved by immunodetection. Later, the characteristic leaf symptoms were shown to be graft transmissible (Fuehrling & Buettner, 1995), supporting the hypothesis of a viral infection. By isolating high molecular, virus specific dsRNA from 'Ringspot disease' affected trees and subsequent cloning, we could identify a novel plant virus exhibiting a multipartite genome of four ssRNAs and which we named European mountain ash ringspot-associated virus (EMARAV) (Benthack et al., 2005; Mielke & Muehlbach, 2007). Each of the four RNAs contains one open reading frame of the same orientation, encoding the viral RdRp (RNA 1, 7.040 nt), a putative glycoprotein precursor with a molecular weight of 75 kDa (RNA 2, 2.335 nt), a 35 kDa nucleocapsid (N-) protein (RNA 3, 1.560 nt) and a 27 kDa protein of still unknown function (RNA 4, 1.348 nt). The RdRp sequence exhibits all conserved domains (premotif A, motifs A-E) and a putative endonucleolytic centre, which is typical for ss(-)RNA viruses using the mechanism of 'cap-snatching'. Database analyses revealed highest similarity of EMARAV RdRp to replicases of members of the family *Bunyaviridae*, especially with the genera *Tospovirus* and *Orthobunyavirus*, and the unassigned genus *Tenuivirus* (Fig. 1). As it is typical for ss(-)RNA viruses, the RNA termini are complementary and the conserved ultimate 13 nucleotides show high similarity with the ends of orthobunyaviruses and hantaviruses (Table 1). All other EMARAV proteins are unrelated to bunyaviral peptides. However, the deduced aa-sequence of the 35 kDa N-protein, which can be enriched by gradient centrifugation (Mielke & Muehlbach, 2007, Mielke et al. 2008), revealed a certain similarity to the N-proteins of two other unclassified RNA viruses with a multipartite genome, *Pigeonpea sterility mosaic virus* (PPSMV) and High Plains virus (HPV) (Fig. 2). RdRp sequences of these two viruses are not yet available. Furthermore, one terminus of the N-protein encoding RNA of HPV corresponds extensively to the conserved termini of the EMARAV genome (Table 1). Unfortunately, no other end of PPSMV and HPV RNA is published.

EMARAV is clearly a distinct virus species representing a new genus of ssRNA- viruses. While very distant relationships to members of the family *Bunyaviridae* and the genus *Tenuivirus* can be established using the RdRp sequence, there are no other substantial similarities and genome organisation differs from both these taxa. PPSMV and HPV may prove to be members of this new genus but more information about their genomes will be required before this can be verified.

References:

Benthack, W., Mielke, N., Buettner, C. & Muehlbach, H.-P. (2005). Double-stranded RNA pattern and partial sequence data indicate plant virus infection associated with ringspot disease of European mountain ash (Sorbus aucuparia L.). Arch Virol 150, 37–52.

Ebrahim-Nesbat, F. & Izadpanah, K. (1992). Viruslike particles associated with ringfleck mosaic of mountain ash and a mosaic disease of raspberry in the Bavarian Forest. Eur J Forest Pathol 22, 1–10.

Fuehrling, M. & Buettner, C. (1995). Transmission experiments of viruses to woody seedlings (Quercus robur L. and Sorbus aucuparia L.) by grafting and mechanical

References:

inoculation. Eur J Forest Pathol 25, 129–135.

Kegler, H. (1960). Das Ringfleckenmosaik der Eberesche (*Sorbus aucuparia* L.). Phytopathol Z 37, 214–216 (in German).

Mielke, N & Muehlbach, H-P (2007). A novel, multipartite, negative-strand RNA virus is associated with the ringspot disease of European mountain ash (*Sorbus aucuparia* L.). J Gen Virol 88, 1337–1346.

N. Mielke, N, Weber, M, Khan, S and Muehlbach, H-P (2008). Detection of European mountain ash ringspot-associated virus (EMARAV) in *Sorbus aucuparia* L. by a specific antiserum and reverse transcription-PCR. Forest Path, accepted.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

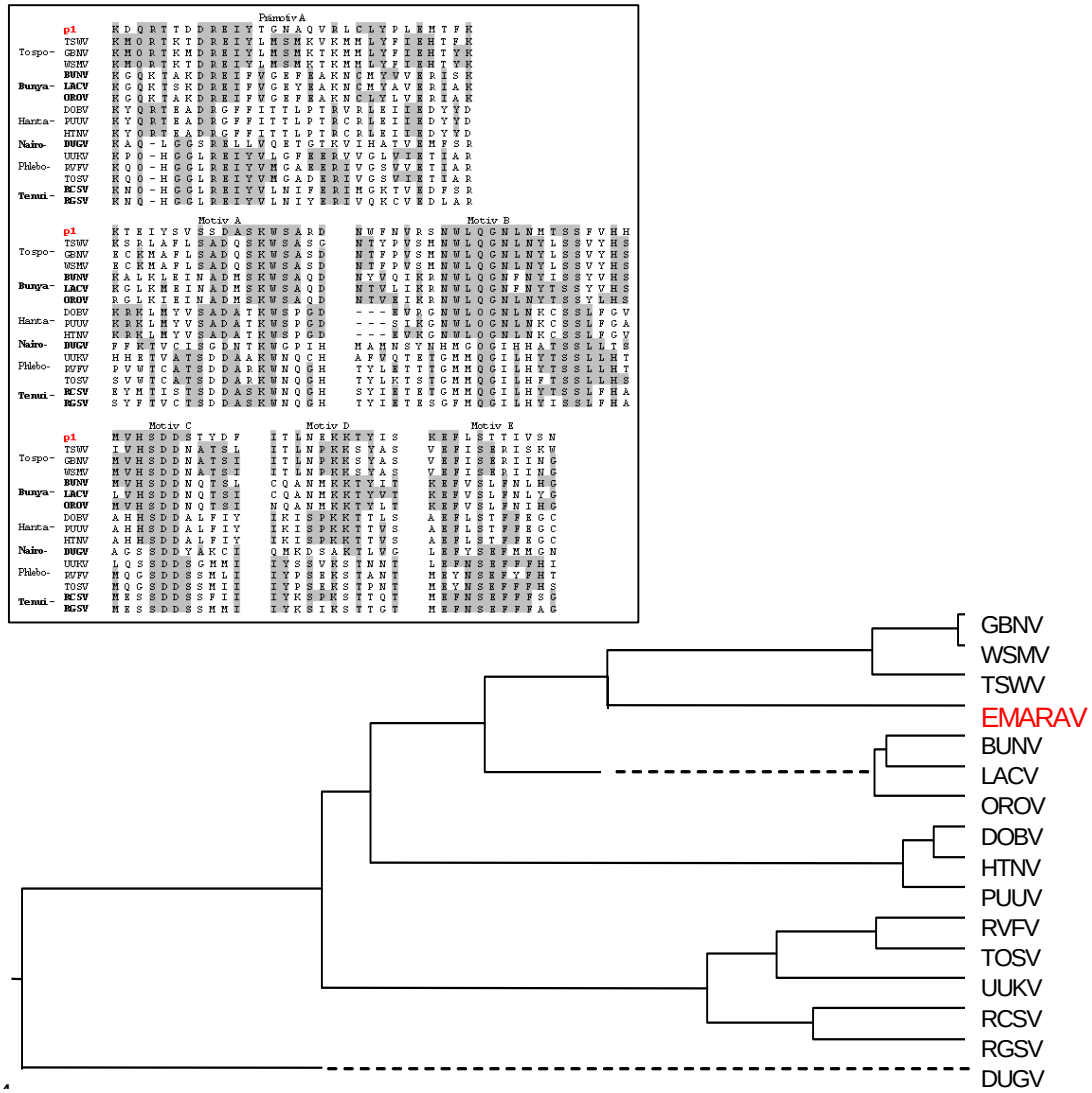

Fig. 1: Amino acid identity between conserved RdRp motifs A–E and premotif A of EMARAV and 15 members of the family *Bunyaviridae* and the genus *Tenuivirus*. Identical amino acids are marked grey. TSWV, *Tomato spotted wilt virus*, *Tospovirus*; GBNV, *Groundnut bud necrosis virus*, *Tospovirus*; WSMV, *Watermelon silver mottle virus*, *Tospovirus*; BUNV, *Bunyamwera virus*, *Orthobunyavirus*; LACV, *La Crosse virus*, *Orthobunyavirus*; OROV, *Oropouche virus*, *Orthobunyavirus*; DOBV, *Dobrava virus*, *Hantavirus*; PUUV, *Puumala virus*, *Hantavirus*; HTNV, *Hantaan virus*, *Hantavirus*; DUGV, *Dugby virus*, *Nairovirus*; UUKV, *Uukuniemi virus, Phlebovirus*; *RVFV, Rift Valley fever virus, Phlebovirus*; *TOSV, Toscana virus, Phlebovirus*; *RCSV, Rice stripe virus, Tenuivirus*; *RGSV, Rice grassy stunt virus, Tenuivirus.*

Table 1: Comparison of the conserved termini of RNA 1 of EMARAV with the different genera of the family *Bunyaviridae*, the genus *Tenuivirus* and HPV. Identical nucleotides are marked in red.

	5'-Terminus	*3'-Terminus*
EMARAV RNA 1	AGU AGU GUU CU...	...AGG GAG UUC ACU ACU
Orthobunyavirus	AGU AGU GUG CU...	...AG UAC ACU ACU
Hantavirus	U AGU AGU AUG CU...	...AG UCU ACU ACU A
Tospovirus	AGA GCA AU...	...AU UGC UCU
Nairovirus	UCU CAA AG...	...CU UUG AGA
Phlebovirus	ACA CAA AG...	...CU UUG UGU
Tenuivirus	ACA CAA AG...	...CU AUG UGU
HPV, N protein encoding RNA		...UGG GAG CAC ACU ACU

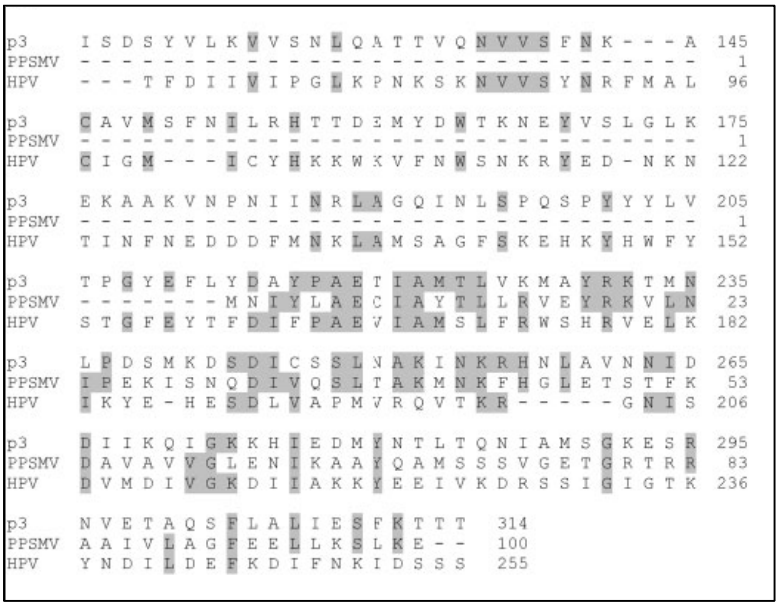

Fig. 2: Comparison of the amino acid sequences of the N-proteins of High Plains virus (HPV), *Pigeonpea sterility mosaic virus* (PPSMV) and EMARAV (p3). Identical amino acids are marked in grey.