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:	***2010.015aP***	(to be completed by ICTV officers)

Short title: A new species in the genus Emaravirus
(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:

G.P. Martelli (martelli@agr.uniba.it) and H.P. Muehlbach (muehlbach@botanik.uni-hamburg.de)

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)	

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

Date first submitted to ICTV:
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	***2010.015aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Emaravirus***
Subfamily:	
Family:	***Unassigned***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Fig mosaic virus	AM94171 (RNA-1); FM864225 (RNA-2); FM991954 (RNA-3); FM992851 (RNA-4)

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

Mosaic, a long-known disease of fig (*Ficus carica*), was first reported form California (Condit and Horne, 1933) and is now known to occur in virtually all countries where fig is grown. Mosaic-diseased trees can be infected by a number of different viruses, one of which, however, is consistently present in symptomatic plants and has recently been identified as the putative agent of the disease. This virus (FMV) has properties largely conforming to those characterizing the newly described monotypic genus *Emaravirus*.

(i) Virus particles: enveloped, round to ovoid 90-200 nm in diameter, occasionally elongated bacilliform up to or above 1 µm in length.

(ii) dsRNAs: multiple dsRNA species ranging from 0.6 kbp to approximately 7 kbp in size.

(iii) Protein size (deduced from sequence): Nucleocapsid, 35 kDa; glycoprotein precursor, 73 kDa.

(iv) Nucleic acid: four segment of negative-stranded ssRNA, 7,093 (RNA-1), 2,252 (RNA-2), 1,490 (RNA-3) and 1, 472 (RNA-4) nt in size. No poly(A) tail present. The first 13 nt of the 5' UTRs of each segment have an identical sequence, the same as the last 13 nt of the 3' UTRs.

(v) Genome: Multipartite, each segment containing a single ORF that encodes, in order, the polymerase (264 kDa), a putative glycoprotein (73 kDa), the putative nucleocapsid (35 kDa),

and a 40.5 kDa protein with unknown function (Fig. 1).

(vi) Phylogenetic relationships: Based on RNA-1 and RNA-2 sequences, FMV groups consistently with *European mountain ash ringspot-associated virus* (EMARaV, the type species of the genus *Emaravirus)* in a cluster of their own, close to clades comprising members of the genera *Tospovirus* and *Orthobunyavirus.* In trees constructed with the amino acid sequence of RNA-3, FMV, EMARaV, Maize red stripe virus (MRSV) and Pigeonpea sterility mosaic virus (PPSMV), two related viruses not yet approved as species, group together in a cluster close to that of the genus *Tospovirus* (Fig. 2)

(vii) Serology: No ultimate information (preliminary data indicate that FMV may not be serologically related with EMARaV)

(viii) Mechanical transmission: unsuccessful

(ix) Seed transmission: not found

(x) Vector transmission: Transmitted by the eriophyid mite *Aceria ficus*, with a semi-persistent modality

(xi) Cytopathology: Virus particles apparently acquire their envelope from the endoplamic reticulum and accumulate in discrete clusters in parenchyma cells.

(xii) Natural host range: Apparently restricted to *Ficus carica*.

Currently available data, especially at the molecular level, indicate that FMV is a distinct species in the genus *Emaravirus*

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Appiano A., Conti M., Zini N., 1995. Cytopathological study of the double-membrane bodies occurring in fig plants affected by fig mosaic. Acta Horticulturae 386: 585-592

Benthack W., Mielke N., Buttner C., Muehlbach H.P., 2005. Double stranded RNA patterns and partial sequence data indicate plant virus infection associated with ringspot disease of European mountain ash (Sorbus aucuparia L.). Archives of Virology 150: 37-52

Castellano M.A., Gattoni G., Minafra A. , Conti M., Martelli G.P., 2007. Fig mosaic in Mexico and South Africa. Journal of Plant Pathology 89: 441-443.

Condit I.J., Horne W.T., 1933. A mosaic of the fig in Californis. Phytopathology 23: 887-896.

Elbeaino, T., Digiaro, M., Alabdullah A., De Stradis A., Minafra A., Mielke N., Castellano, M.A., Martelli G.P., 2009a. A multipartite single-stranded negative-sense RNA virus is the putative agent of fig mosaic disease. Journal of General Virology 90: 1281-1288.

Elbeaino T., Digiaro M., Martelli G.P., 2009b. Complete nucleotide sequence of four RNA segments of fig mosaic virus. Archives of Virology 154: 1719-1727.

Flock R.A., Wallace J.M., 1955. Transmission of fig mosaic by the eriophyid mite Aceria ficus. Phytopathology 45: 52-54.

Martelli G.P., Castellano M.A., Lafortezza, R., 1993. An ultrastructural study of fig mosaic. Phytopathologia Mediterranea 32: 33-43.

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.) . Journal of General Virology 88: 1337-1346.

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.

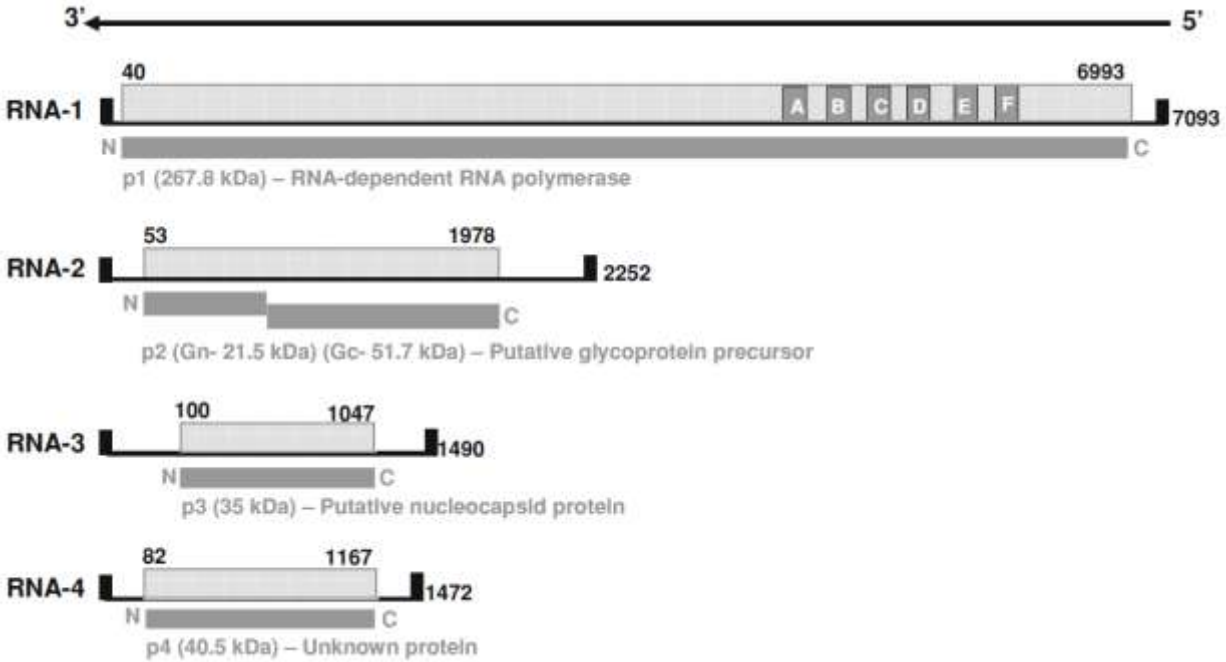
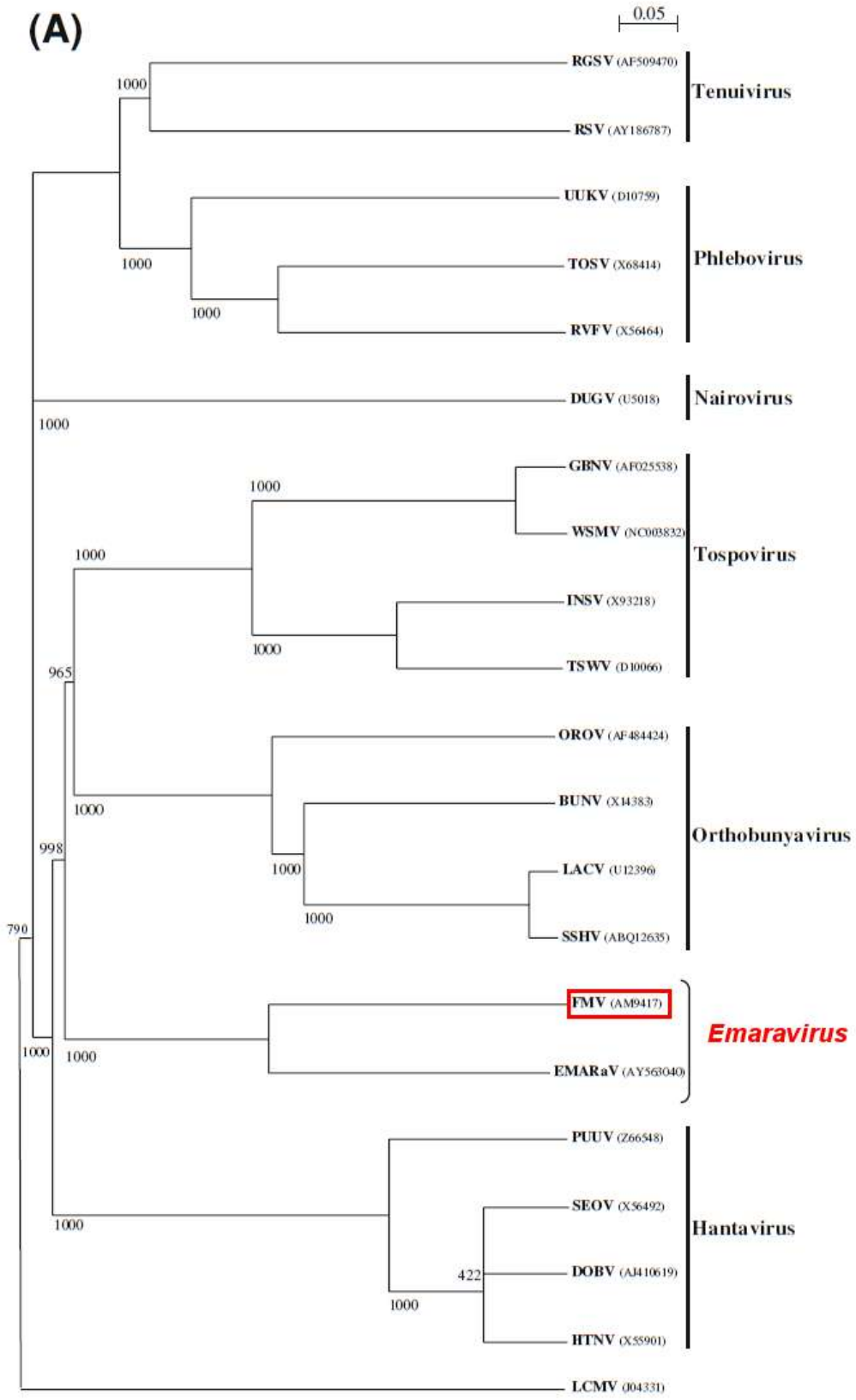
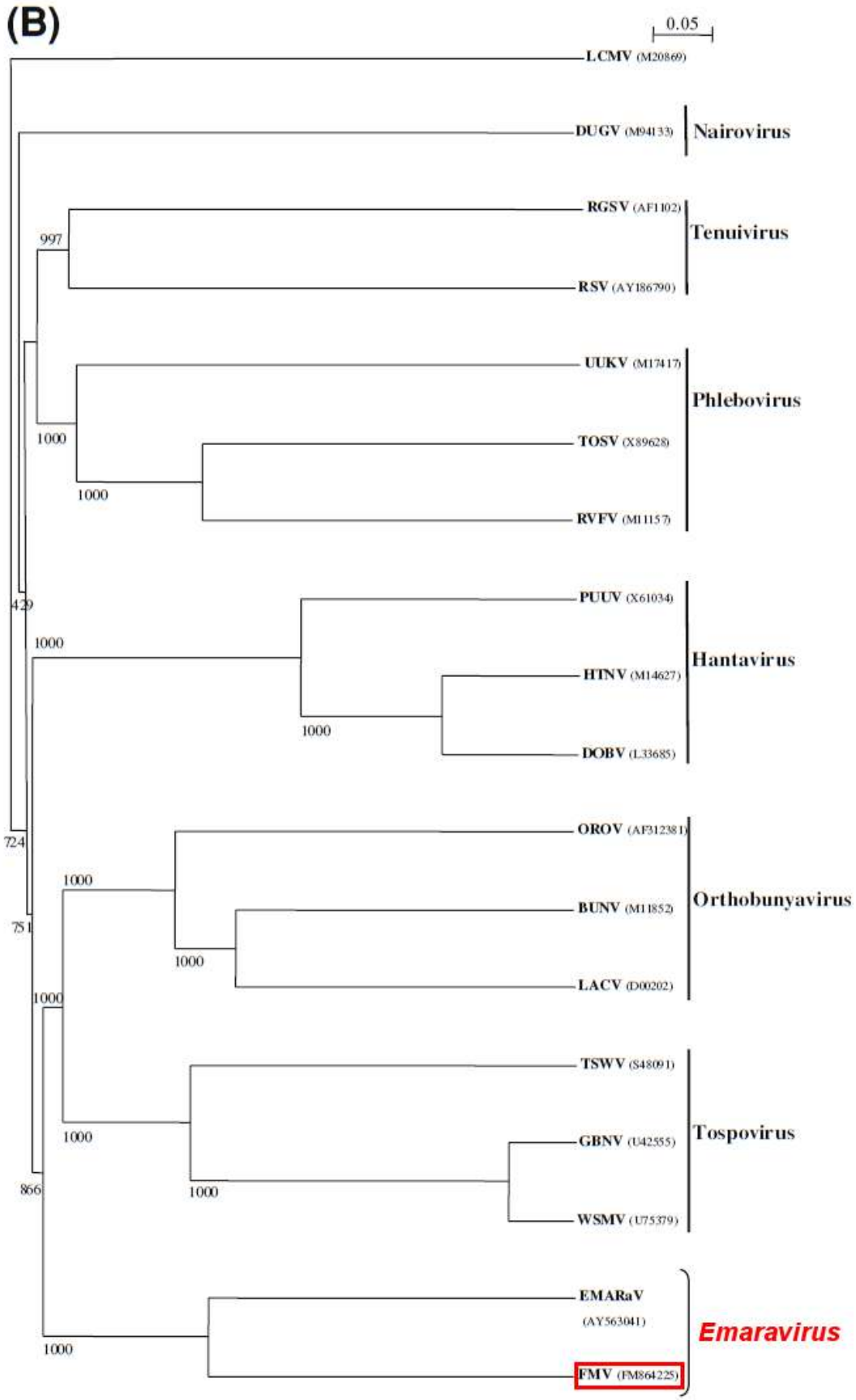


Fig. 1. Organization of the four FMV genomic RNA segments (from Elbeaino *et al*., 2009b). The terminal 13 nucleotides conserved at the 5' and 3' termini are indicated as black boxes on each segment. Letters (A-F) represent thte conserved motifs on the RdRp (RNA-1) gene. Expression products of each RNA (p1 to p4) are represented as dark gray boxes. The protein function and estimated molecular weight of each segment are reported. Figure not drawn to scale.

Fig. 2. Phylogenetic trees constructed with the complete amino acid sequences from RNA-1 (a), RNA-2 (b) and RNA-3 (c) of FMV, EMARaV, PPSMV, MRSV and the corresponding proteins of members of the family *Bunyaviridae* and the genus *Tenuivirus* (from Elbeaino *et al*., 2009b)

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DUGV (M94133)
Nairovirus
RGSV (AF1102)
Tenuivirus
RSV (AY186790)
997
UUKV (M17417)
Phlebovirus
1000
TOSV (X89628)
1000
RVFV (M11157)
429
PUUV (X61034)
1000
HTNV (M14627)
Hantavirus
1000
DOBV (L33685)
724
OROV (AF312381)
1000
BUNV (M11852)
Orthobunyavirus
751
1000
LACV (D00202)
1000
TSWV (S48091)
1000
GBNV (U42555)
Tospovirus
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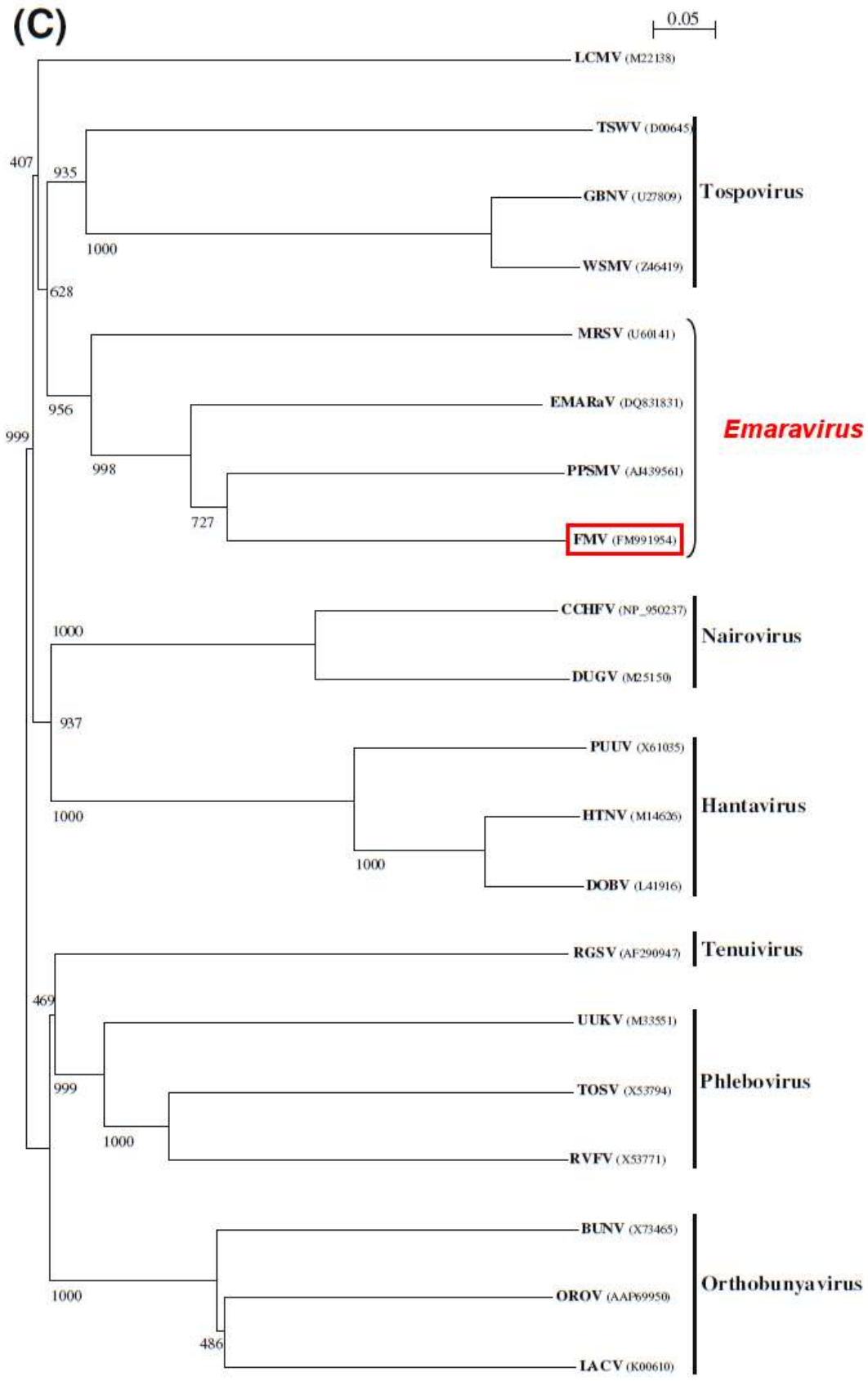
WSMV (U75379)
EMARaV
(AY563041)
Emaravirus
1000
FMV (FM864225)


(C)
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TSWV (D00645)
GBNV (U27809)
WSMV (Z46419)
Tospovirus
MRSV (U60141)
EMARaV (DQ831831)
PPSMV (AJ439561)
FMV (FM991954)
Emaravirus
CCHFV (NP_950237)
DUGV (M25150)
Nairovirus
PUUV (X61035)
HTNV (M14626)
DOBV (L41916)
Hantavirus
RGSV (AF290947)
Tenuivirus
UUKV (M33551)
TOSV (X53794)
RVFV (X53771)
Phlebovirus
BUNV (X73465)
OROV (AAP69950)
IACV (K00610)
Orthobunyavirus
407
935
1000
628
956
999
998
727
1000
937
1000
1000
469
999
1000
1000
486