



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**

<b>Code assigned:</b>	<b>2014.007aP</b>	(to be completed by ICTV officers)			
<b>Short title:</b> One new species, <i>Thin paspalum asymptomatic virus</i> , in the genus <i>Panicovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

**Author(s) with e-mail address(es) of the proposer:**

Kay Scheets kay.scheets@okstate.edu

**List the ICTV study group(s) that have seen this proposal:**

A list of study groups and contacts is provided at <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Tombusviridae and Umbravirus Study Group
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**ICTV-EC or Study Group comments and response of the proposer:**

The decision to accept this proposal was unanimous.

Date first submitted to ICTV:

Date of this revision (if different to above):

June 18, 2014

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	<b>2014.007aP</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Panicovirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<b><i>Tombusviridae</i></b>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate:</b>	<b>GenBank sequence accession number(s)</b>
<i>Thin paspalum asymptomatic virus</i>	05TGP00369 (2005 strain)	JX848617

**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

- Source data and biological properties of Thin paspalum asymptomatic virus (TPAV) are summarized as follows:
  - The virus was obtained via a metagenomic survey of a natural prairie, and RT-PCR sequencing of isolated dsRNA identified it as being closely related to Panicum mosaic virus (PMV) (Scheets, 2013).
  - TPAV has the same genome organization as PMV and cocksfoot mild mosaic virus (CMMV), the only other panicovirus, including the genus-specific p15 ORF (Fig. 1) and a noncanonical start codon for the movement protein 2 (MP2) ORF (Fig. 2). Phylogenetic analyses of RNA dependent RNA polymerase (RdRp) and coat protein (CP) also support its placement in the genus *Panicovirus*, family *Tombusviridae* (Figs. 3-6). See Table 2 for virus abbreviations and GenBank numbers.
  - Virus and RNA are both mechanically transmissible.
  - Transcripts from full length cDNA are systemically infectious to the source host *Paspalum setaceum* (thin paspalum), green millet, and foxtail millet but do not infect switchgrass, seven other grasses, or *Nicotiana benthamiana*.
  - TPAV infections are asymptomatic in the three susceptible grasses, while PMV produces symptoms in green millet and foxtail millet as well as its source host switchgrass.
  - Gel analysis indicates that virion RNA and CP migrate at the locations expected from their sizes (Scheets, 2013).

Two strains of TPAV have been completely sequenced (2005 [JX848617] and 2010 [JX848616]), and sequence comparisons to PMV and CMMV as well as biological

characteristics support the inclusion of TPAV in the panicovirus genus. Characteristics that distinguish TPAV as a new species include host range, symptom differences, and sequence differences, with the most divergent being ORF1 which shows noticeable size and identity differences for the encoded replicase-associated protein (RAP) (Fig. 1 & Table 1). The replicase of TPAV shows 70% and 53% amino acid identity to PMV and CMMV, respectively, while TPAV CP has 72% and 40% identity. There are no species demarcation criteria for the panicovirus genus, but with this proposal we now suggest demarcation criteria of <75% amino acid sequence identity for polymerase and <75% identity for CP.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Scheets, K., 2013. Infectious transcripts of an asymptomatic panicovirus identified from a metagenomic survey. *Virus Res.* 176:161-168

**Annex:**

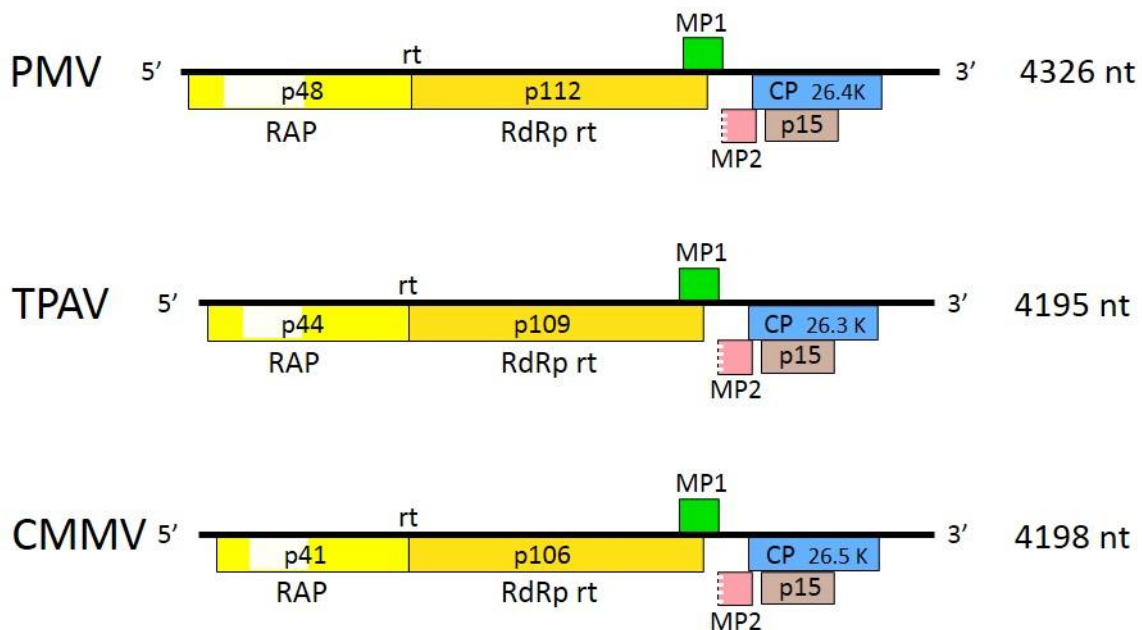


Figure 1. Genome organization of panicum mosaic virus (PMV; type member), thin paspalum asymptomatic virus (TPAV) and cocksfoot mild mosaic virus (CMMV). Color-coding indicates significant protein sequence similarity (34-97%) while white sections in replicase associated proteins (RAPs) have less similarity (14-27%). Dashed lines for movement protein (MP) 2 indicates noncanonical start codons. Coat protein (CP); RNA dependent RNA polymerase readthrough (RdRp rt)



Figure 2. MP2 noncanonical start codon (green) contexts for panicoviruses. MP1 sequences are above the nt sequences.

Table 1. Comparison of sequence identities of proteins encoded by TPAV to proteins encoded by other panicoviruses. RdRp corresponds to the RAP plus RdRp readthrough (rt) region.

<u>Protein</u>	<u>% identity* to TPAV</u>	
	<b>PMV</b>	<b>CMMV</b>
RAP	50	31
RdRp	70	52
RdRp rt	86	66
p8 (MP1)	73	38
p6.8 (MP2)	95	55
CP	72	40
p15	61	33

\* % amino acid sequence identity determined using ClustalW

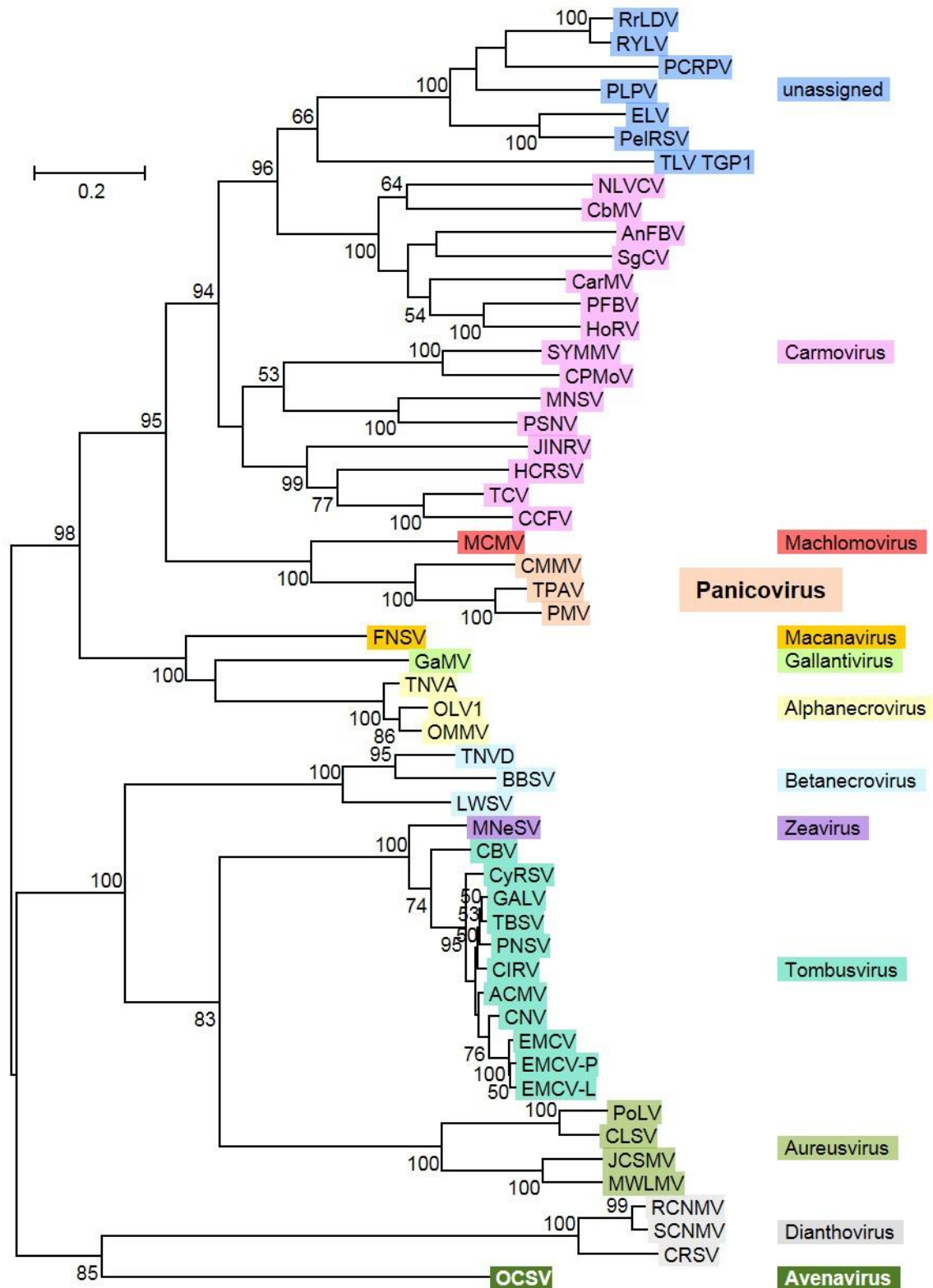


Figure 3. Phylogenetic (distance) analysis of the RdRps of Tombusviridae members. TPAV clusters with panicoviruses (tan). Alignments were made using Clustal Omega while trees were generated with the Maximum Likelihood algorithm using 1000 bootstrap replicates (showing values >50%). See Table 2 for abbreviations and GenBank numbers.



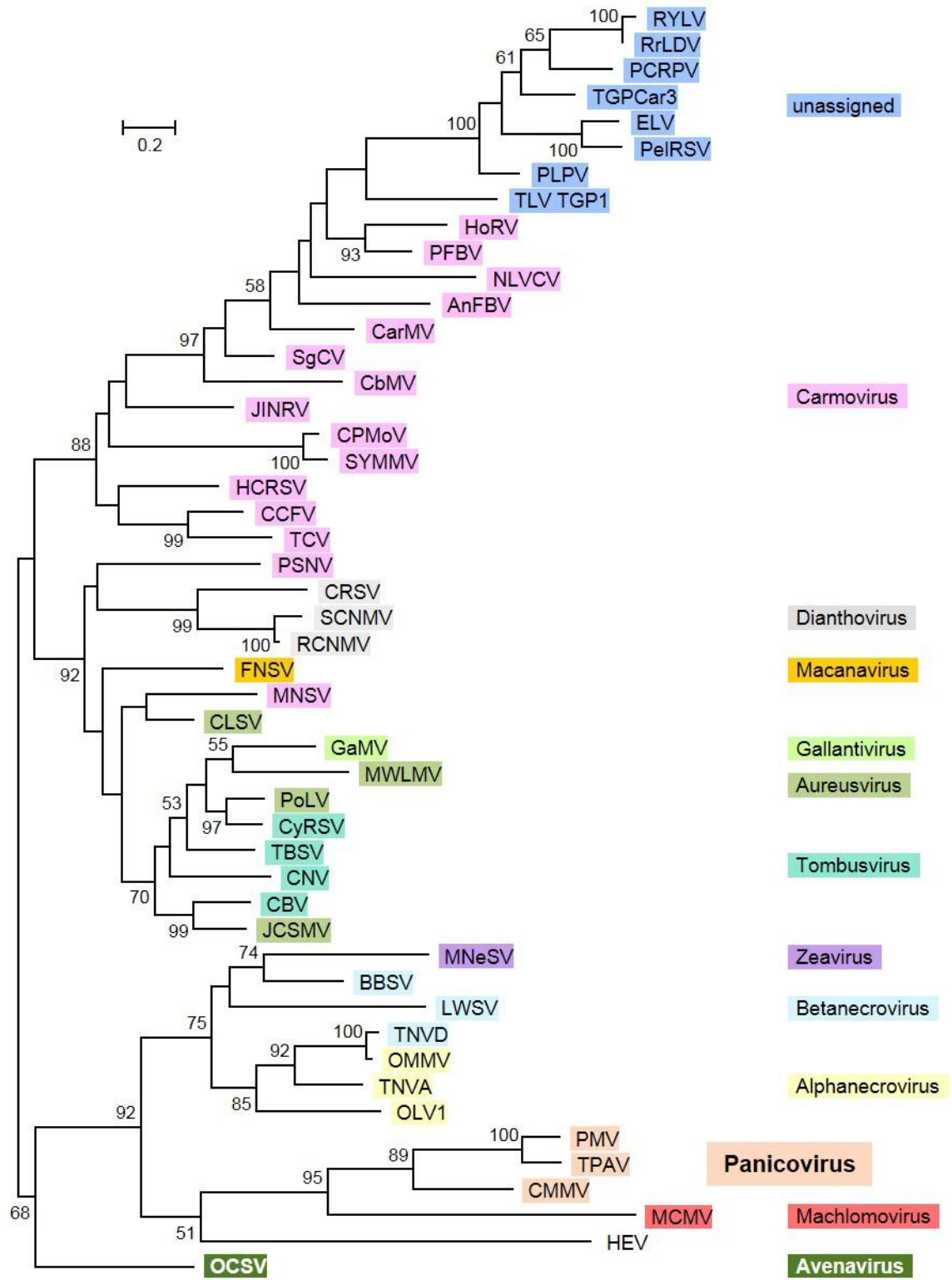


Figure 4. Phylogenetic (distance) analysis of the coat proteins of Tombusviridae members. Only four tombusviruses were included. TPAV clusters with panicoviruses (tan). Alignments were made by Clustal Omega while trees were generated with the Maximum Likelihood algorithm using 1000 bootstrap replicates (showing values >50%). See Table 2 for abbreviations and GenBank numbers.

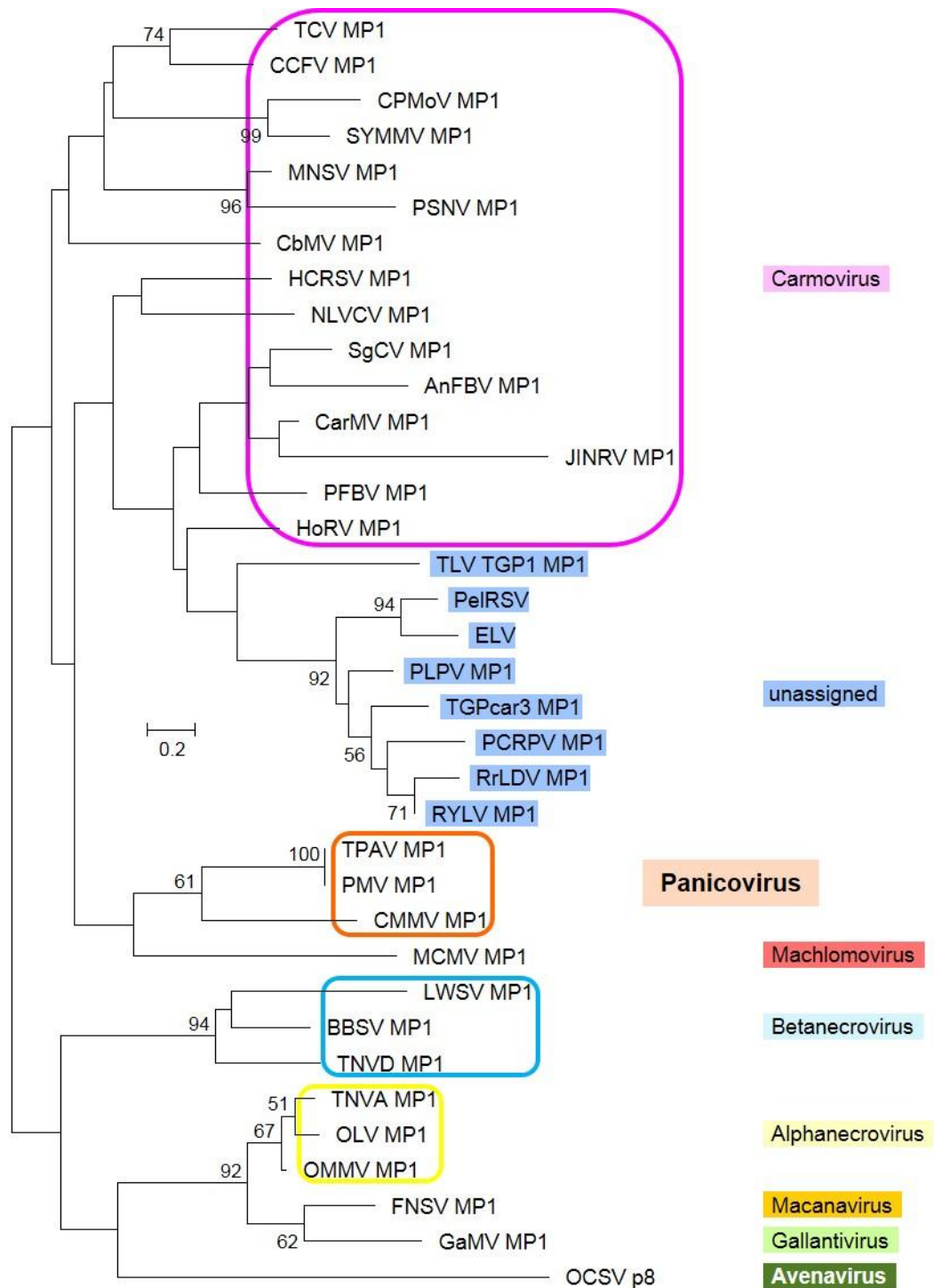


Figure 5. Phylogenetic (distance) analysis of the MP1 proteins of Tombusviridae members. TPAV clusters with panicoviruses (tan). Alignments were made by Clustal Omega while trees were generated with the Maximum Likelihood algorithm using 1000 bootstrap replicates of all sites (showing values >50%). See Table 2 for abbreviations and GenBank numbers.

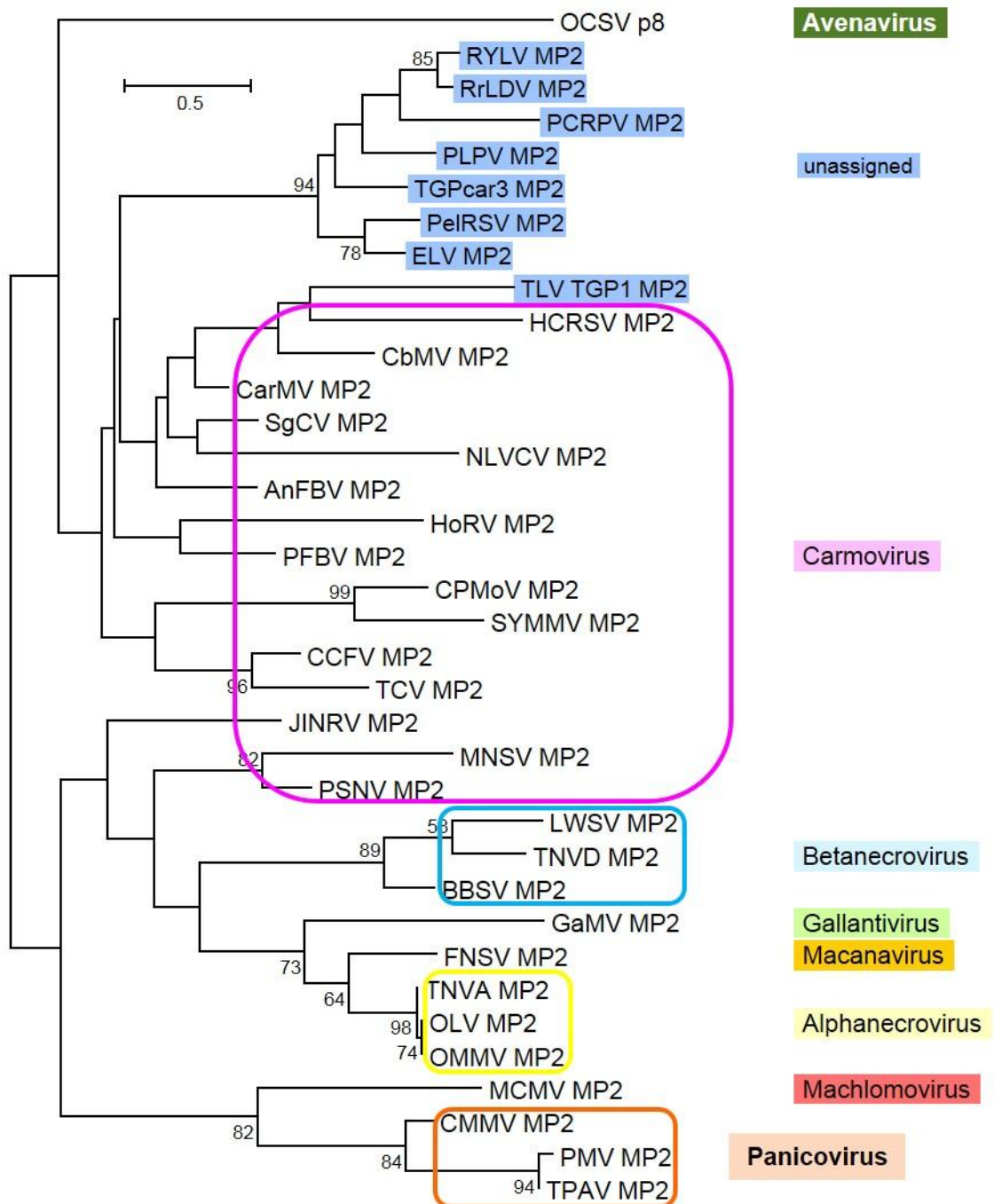


Figure 6. Phylogenetic (distance) analysis of the MP2 of Tombusviridae members. TPAV clusters with panicoviruses (tan). Alignments were made by Clustal Omega while trees were generated with the Maximum Likelihood algorithm using 1000 bootstrap replicates of all sites (showing values >50%). See Table 2 for abbreviations and GenBank numbers.



**Table 2. ABBREVIATIONS USED IN THE PROPOSAL**

	<b>Alphanecrovirus</b>	
OLV1	<i>Olive latent virus 1</i>	X85989
OMMV	<i>Olive mild mosaic virus</i>	AY616760
TNVA	<i>Tobacco necrosis virus A</i>	M33002
	<b>Aureusvirus</b>	
CLSV	<i>Cucumber leaf spot virus</i>	EU127904
JCSMV	<i>Johnsongrass chlorotic stripe mosaic virus</i>	AJ557804
MWLMV	<i>Maize white line mosaic virus</i>	EF589670
PoLV	<i>Pothos latent virus</i>	X87115
	<b>Avenavirus</b>	
OCSV	<i>Oat chlorotic stunt virus</i>	X83964
	<b>Betanecrovirus</b>	
BBSV	<i>Beet black scorch virus</i>	AF452884
LWSV	<i>Leek white stripe virus</i>	X94560
TNVD	<i>Tobacco necrosis virus D</i>	U62546
	<b>Carmovirus</b>	
AnFBV	<i>Angelonia flower break virus</i>	DQ219415
CbMV	<i>Calibrachoa mottle virus</i>	GQ244431
CCFV	<i>Cardamine chlorotic fleck virus</i>	L16015
CarMV	<i>Carnation mottle virus</i>	X02986
CPMV	<i>Cowpea mottle virus</i>	U20976
HCRSV	<i>Hibiscus chlorotic ringspot virus</i>	X86448
HoRSV	<i>Honeysuckle ringspot virus</i>	HQ677625
JINRV	<i>Japanese iris necrotic ring virus</i>	D86123
MNSV	<i>Melon necrotic spot virus</i>	M29671
NLVCV	<i>Nootka lupine vein clearing virus</i>	EF207438
PSNV	<i>Pea stem necrosis virus</i>	AB086951
PFBV	<i>Pelargonium flower break virus</i>	AJ514833
SgCV	<i>Saguaro cactus virus</i>	U72332
SYMMV	<i>Soybean yellow mottle mosaic virus</i>	FJ457015
TCV	<i>Turnip crinkle virus</i>	M22445
	<b>Dianthovirus</b>	
CRSV	<i>Carnation ringspot virus</i>	L18870, M8858
RCNMV	<i>Red clover necrotic mosaic virus</i>	J04357, X08021
SCNMV	<i>Sweet clover necrotic mosaic virus</i>	L07884, S4602
	<b>Gallantivirus</b>	
GaMV	<i>Galinsoga mosaic virus</i>	Y13463
	<b>Macanavirus</b>	
FNSV	<i>Furcraea necrotic streak virus</i>	FJ768020

continued

	<b>Machlomovirus</b>	
MCMV	<i>Maize chlorotic mottle virus</i>	X14736
	<b>Panicovirus</b>	
CMMV	<i>Cocksfoot mild mosaic virus</i>	EU081018
PMV	<i>Panicum mosaic virus</i>	U55002
TPAV	<i>Thin paspalum asymptomatic virus</i> (this proposal)	JX848617
	<b>Tombusvirus</b>	
AMCV	<i>Artichoke mottled crinkle virus</i>	X62493
CIRV	<i>Carnation Italian ringspot virus</i>	X85215
CBV	<i>Cucumber Bulgarian virus</i>	AY163842
CNV	<i>Cucumber necrosis virus</i>	M25270
CyRSV	<i>Cymbidium ringspot virus</i>	X15511
EMCV	<i>Eggplant mottled crinkle virus</i>	JQ864181
EMCV-P	<i>Eggplant mottled crinkle virus-P</i> (pear latent virus)	AY100482
EMCV-L	<i>Eggplant mottled crinkle virus-L</i> (lisianthus necrosis virus)	DQ011234
GALV	<i>Grapevine Algerian latent virus</i>	AY830918
PNSV	<i>Pelargonium necrotic spot virus</i>	AJ607402
TBSV	<i>Tomato bushy stunt virus</i>	M21958
	<b>Zeavirus</b>	
MNeSV	<i>Maize necrotic streak virus</i>	AF266518
	<b>unassigned Tombusviridae</b>	
PLPV	<i>Pelargonium line pattern virus</i>	AY613852
	<b>unassigned viruses</b>	
ELV	elderberry latent virus	AY038066
PCRVP	pelargonium chlorotic ring pattern virus	AY038069
PeIRSV	pelargonium ringspot virus	AY038068
RrLDV	rosa rugosa leaf distortion virus	KC166238
RYLV	rose yellow leaf virus	KC166239
TLV TGP1	trailing lespedeza virus TGP 1 (TGP carmovirus 1)	HM640935
	<b>other virus sequences</b>	
HEV	<i>Hepatitis E virus</i> CP	AAA45727
TGPCar3	TGP carmovirus 3	JF437874