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"

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2012.010f-iP***	(to be completed by ICTV officers)

Short title: create a new genus, *Macanavirus*, in the family *Tombusviridae*

Modules attached	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

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

D'Ann Rochon (dann.rochon@agr.gc.ca). On behalf of the Tombusviridae SG

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)	Tombusviridae

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

Date first submitted to ICTV:	8 August 2011
Date of this revision (if different to above):	June 27 2012

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	***2012.010fP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Macanavirus* (new)
Subfamily:	
Family:	***Tombusviridae***
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:**
Furcraea necrotic streak virus	FJ768020

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

Furcraea necrotic streak virus (FNSV) is the only member of the newly proposed Macanavirus genus. Also note that FNSV is not listed in the 2011 ICTV Master Species list

Background information:

FNSV has been known for many years as the agent of the damaging 'macana' disease of fique [fibre crop plants of the genus *Furcraea* (Agavaceae)] in Colombia (Dabek & Castano, 1978). Some preliminary serological and cDNA hybridization studies suggested that it might be a member of the genus *Dianthovirus*, family *Tombusviridae* (Morales et al., 1992). However, dianthoviruses have a bipartite genome and the complete genome of FNSV now determined by the same research group (accession FJ768020) shows it to have a monopartite genome. There is no publication describing the sequence but Dr. Morales has confirmed to the SG the sequence is indeed derived from the isolate described in the 1992 paper. Although the Genbank accession is still labeled as an unclassified dianthovirus, FNSV was listed as a possible member of the genus *Necrovirus* in the *Tombusviridae* chapter of the ICTV 9th Report. This was because comparisons of its replication protein sequence showed that it was more closely related to some necroviruses than to viruses classified in other genera of the family.

As described below, there is a current proposal, expected to be ratified this year, to revise the genus *Necrovirus* and to split it into two genera (*Alpha-* and *Betanecrovirus*) (2011.009a-mP) but both the polymerase sequence and coat protein properties of FNSV place it outside either of these and suggest it is a member of a separate genus (see Module 3 for further details).

Also, last year a proposal was put forth (2011.010a-fP.N.v1) to create the new genus Gallantvirus in the family *Tombusviridae* and to assign Galinsoga mosaic virus (GaMV) currently a species in the genus Carmovirus in the *Tombusviridae* as its type member and to create FNSV as a new species in the genus. This proposal was based on the fact that FNSV and GaMV share similar genome organizations, similar "necrovirus-like" polymerase sequences but the coat proteins have protruding domains, unlike the necroviruses (note that the presence or absence of a coat protein protruding domain is a genus demarcation criteria in the *Tombusviridae*). However, the Study Group was asked to "reconsider whether the two viruses should be placed in the same genus as the phylogenetic trees of the polymerase suggested that two genera could be justified". The Tombusviridae Study Group has considered these comments and has agreed to create two separate genera for FNSV and GaMV.

1MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2012.010gP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Tombusviridae***
Order:	

naming a new genus

Code	***2012.010hP***	(assigned by ICTV officers)

To name the new genus: *Macanavirus*

Assigning the type species and other species to a new genus

Code	***2012.010iP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Furcraea necrotic streak virus
Please enter here the TOTAL number of species (including the type species) that the genus will contain:
1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Genera in the family *Tombusviridae* are distinguished by genome organization and by the properties of the replication protein and the coat protein. Necroviruses have a distinctive type of coat protein without a protruding domain and forming a single lineage but their replication proteins are of two different lineages. There is therefore a current proposal to split the genus *Necrovirus* into two genera, *Alphanecrovirus* and *Betanecrovirus* (2011.009a-mP).

The complete sequence of FNSV shows that this virus is most similar to alphanecroviruses in genome organization and in percent sequence identity in the replication protein and the two small movement protein ORFs (Tables 1-4). This is confirmed by phylogenetic analyses (Figs 3 and 4).

However, unlike necroviruses, the coat protein of FNSV contains a protruding domain (Fig. 1, 2) and is most closely related to the coat proteins of other members of the family with protruding domains in both sequence comparisons (Table 4) and phylogenetic analyses (Fig. 5).

To be consistent with genus demarcation criteria being applied in the family, a new genus is therefore needed to contain FNSV.

Origin of the new genus name:

From the common name of the disease “Macana” that is used for FNSV infected plants in Columbia, South America

Reasons to justify the choice of type species:

This is a monotypic genus

Species demarcation criteria in the new 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.

< 80% amino acid sequence identity in the polymerase; <55% amino acid sequence similarity in the coat protein.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Dabek, A.J. and Castano, J.J. (1978). The occurrence, symptomatology, transmission and virus aetiology of macana disease of fique (*Furcraea* spp.) in Colombia, South America. Phytopath. Z., 92: 57-69

Morales, F.J., Castano, M., Calvert, L.A. and Arroyave, S. (1992). Furcaea necrotic streak virus: and apparent new member of the Dianthovirus group. *J. Phytopath.* **134**: 247-254.

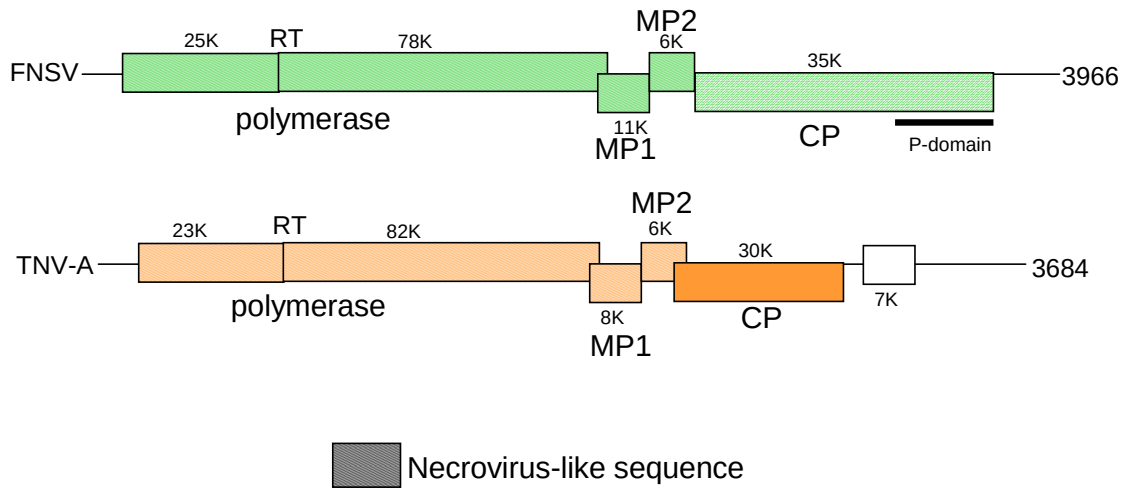

Figure 1. Genome organization of FNSV and comparison to tobacco necrosis virus A (TNV-A), the type member of genus *Necrovirus* (and proposed type member of the new genus Alphanecrovirus). Similar shading patterns indicate significant sequence identity. Note that the coat protein (CP) of FNSV, unlike TNV-A, contains a C-terminal protruding domain which is typical of currently classified viruses in the *Tombusviridae* with the exception of the necroviruses.

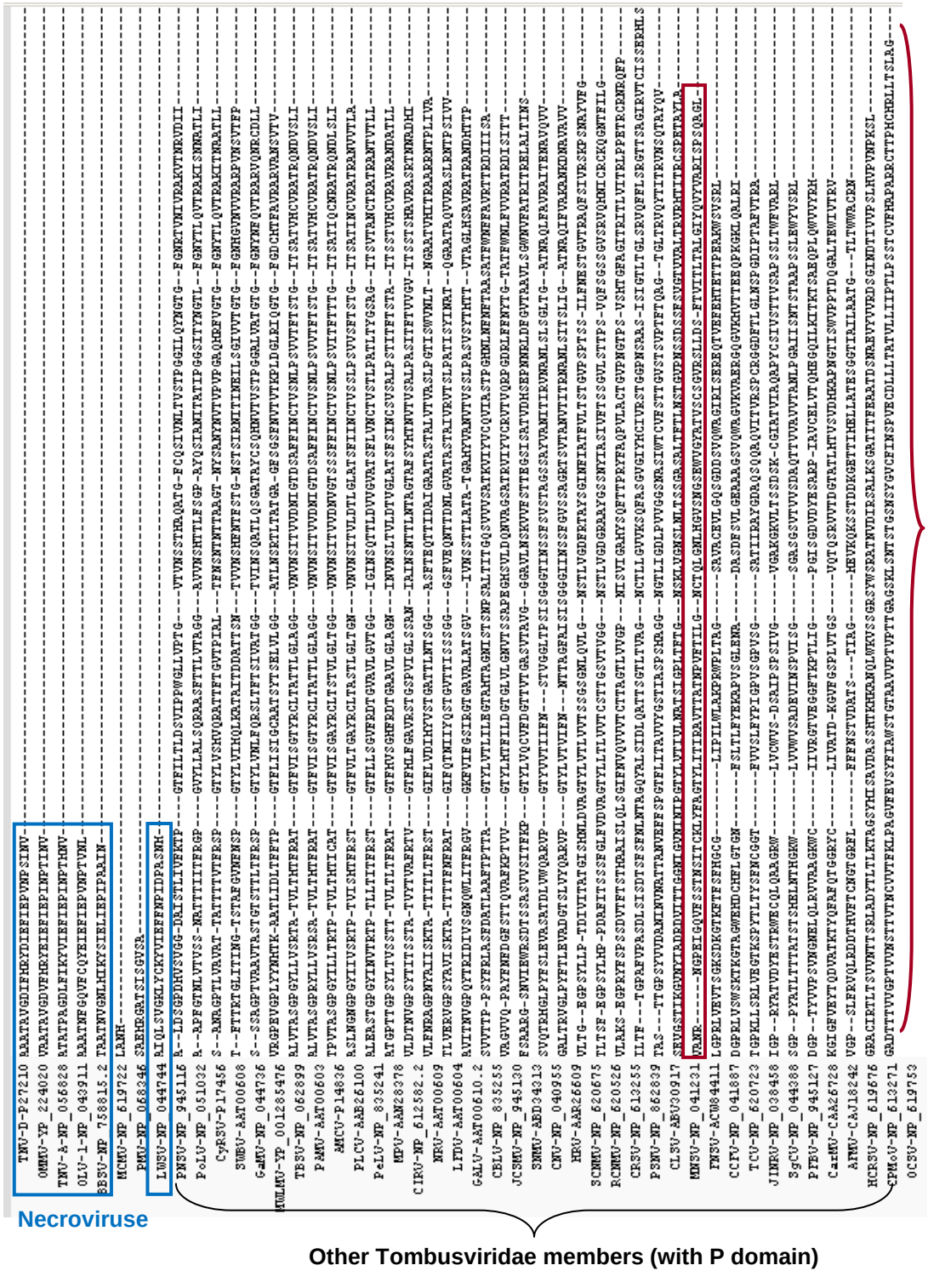

Figure 2. Alignment of the CP sequence of FNSV (boxed in red) with the CPs of the proposed alpha and betanecroviruses (boxed in blue) and remaining members of the *Tombusviridae*. Only the C-terminal region of the CP alignment is shown with the area corresponding to the P-domain being shown in brackets.

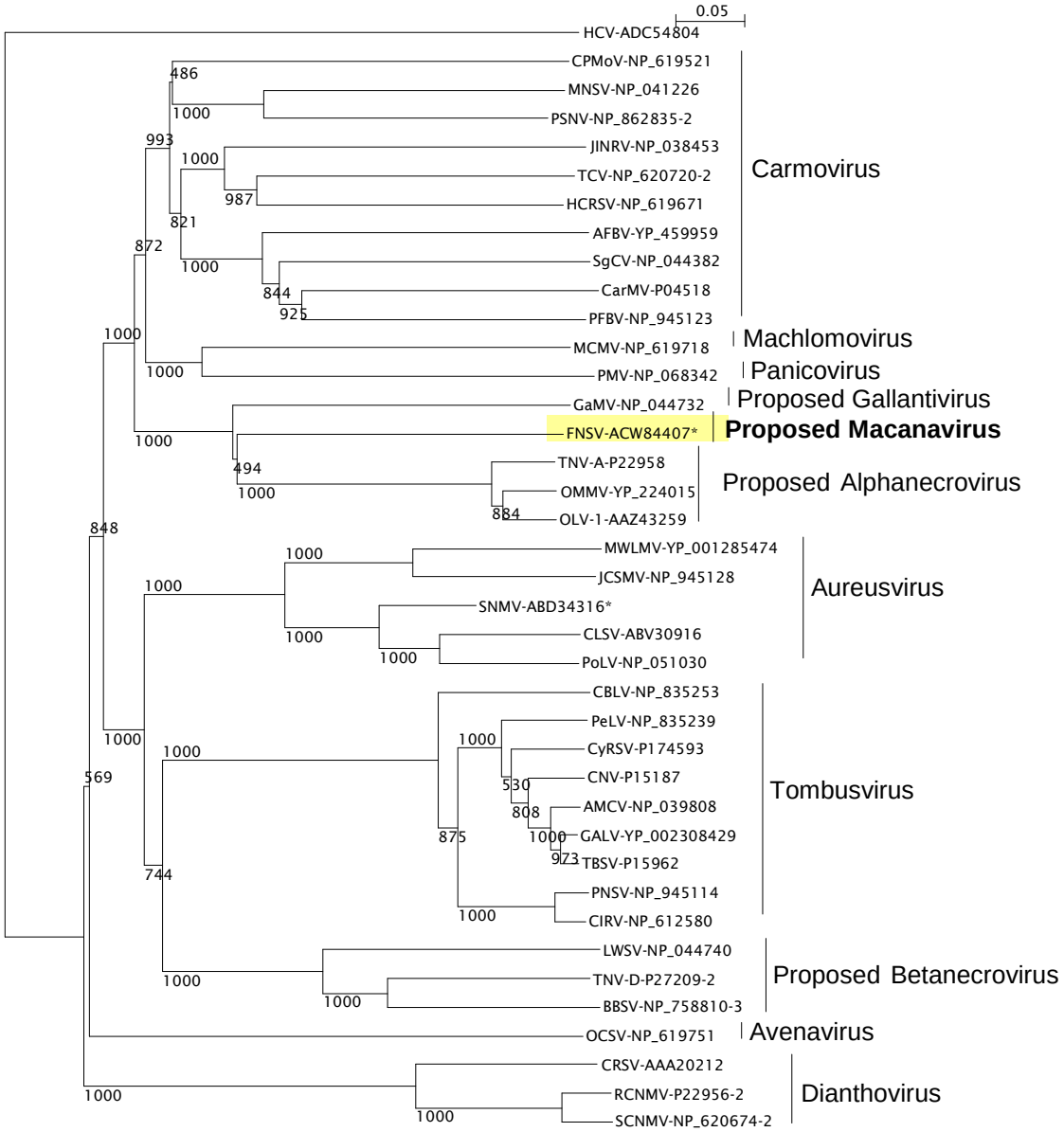

Figure 3. Phylogenetic (distance) tree of the polymerase of *Tombusviridae* members with the position of FNSV highlighted in yellow. Sequences were aligned using the ClustalX 2.1 algorithm and trees were generated by the Neighbor Joining method using 1000 bootstrap replicates. Hepatitis C virus (HCV) polymerase was used as an outgroup.

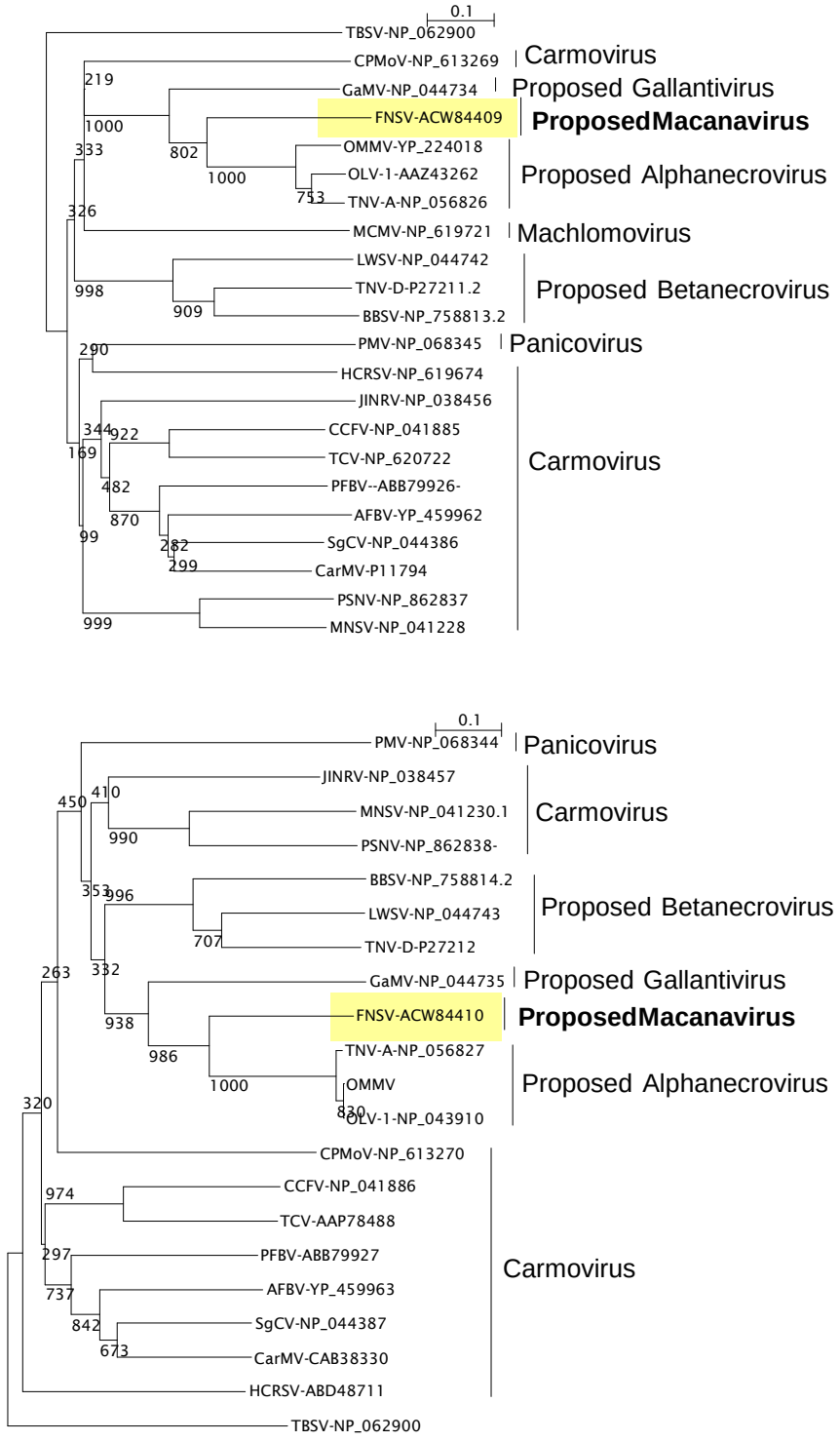

Figure 4. Phylogenetic (distance) tree of the MP1 (top) and MP2 (bottom) sequences of *Tombusviridae* members with the position of the FNSV MPs highlighted in yellow. Sequences were aligned using the ClustalX 2.1 algorithm and trees were generated by the Neighbor Joining method using 1000 bootstrap replicates.

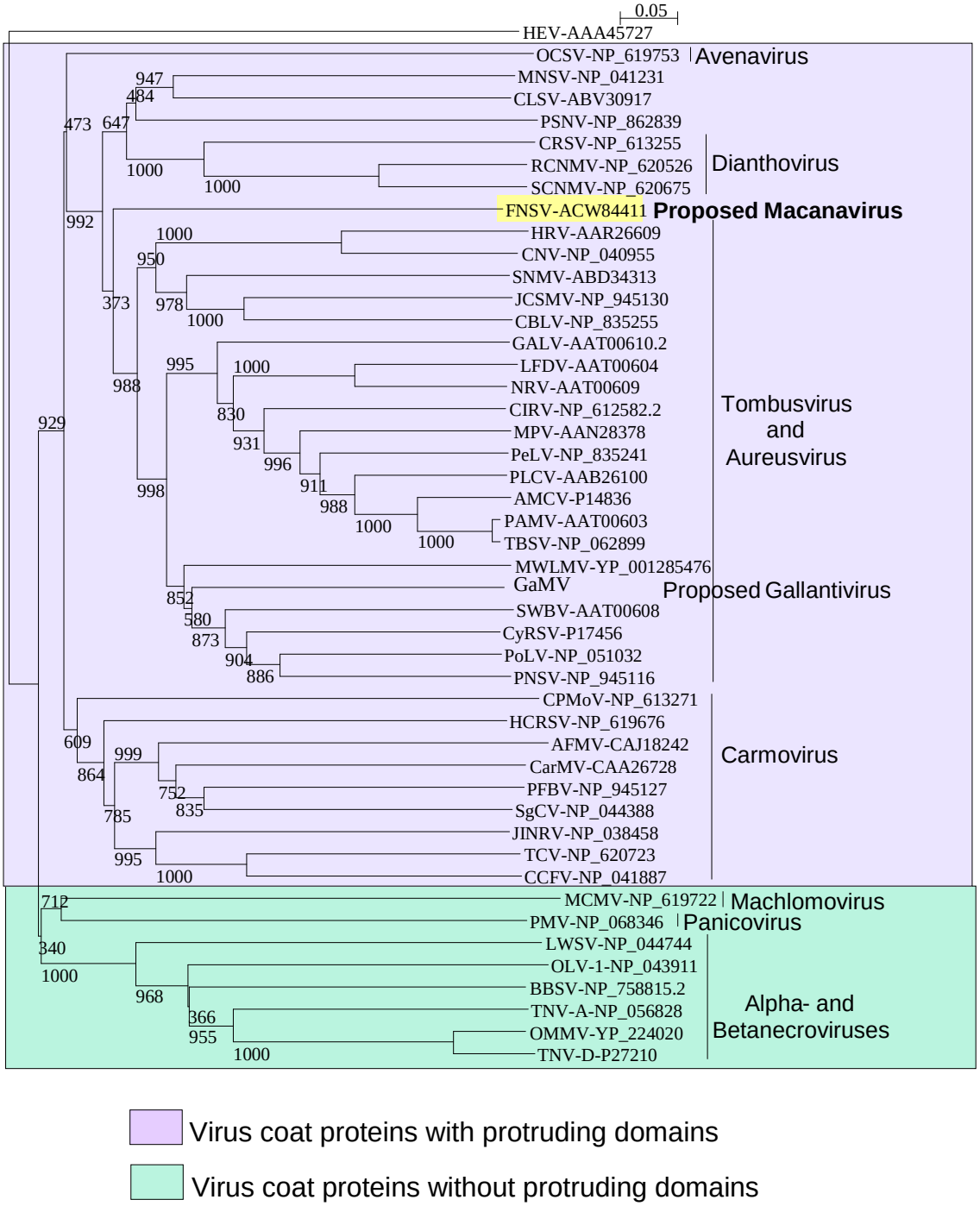

Figure 5. Phylogenetic (distance) tree of CP sequences of *Tombusviridae* members with the position of the FNSV CP highlighted in yellow. Sequences were aligned using the ClustalX 2.1 algorithm and trees were generated by the Neighbor Joining method using 1000 bootstrap replicates. Hepatitis E virus (HEV) coat protein was used as an outgroup.

ABBREVIATIONS USED IN THE PROPOSAL

Tombusviruses

Artichoke mottled crinkle virus	AMCV
Carnation Italian ringspot virus	CIRV
Cucumber Bulgarian latent virus	CBLV
Cucumber necrosis virus	CNV
Cymbidium ringspot virus	CyRSV
Pear latent virus - Italy	PeLV*
Grapevine Algerian latent virus	GALV
Havel river virus	HRV
Lato river virus	LRV
Moroccan pepper virus	*MPV*
Neckar river virus	*NRV*
Pelargonium leaf curl virus	PLCV
Pelargonium necrotic spot virus	PNSV
Petunia asteroid mosaic virus	PAMV
Sikte waterborne virus	SWBV
Tomato bushy stunt virus	TBSV
Limonium flower distortion virus	LFDV

*PeLV is an isolate of *Eggplant mottle crinkle virus*

Dianthoviruses

Carnation ringspot virus	CRSV
Red clover necrotic mosaic virus	RCNMV
Sweet clover necrotic mosaic virus	SCNMV

Aureusviruses

Cucumber leaf spot virus	CLSV
Johnsongrass chlorotic stripe mosaic virus	JCSMV
Maize white line mosaic virus	MWLMV
Pothos latent virus	PoLV
Sesame necrotic mosaic virus (tentative species)	SNMV

Avenavirus

Oat chlorotic stunt virus	OCSV

Carmoviruses

Angelonia flower break virus	AFBV
Cardamine chlorotic fleck virus	CCFV
Carnation mottle virus	CarMV

Cowpea mottle virus	CPMoV
Galinsoga mosaic virus	GaMV
Hibiscus chlorotic ringspot virus	HCRSV
Japanese iris necrotic ring virus	JINRV
Melon necrotic spot virus	MNSV
Pea stem necrosis virus	PSNV
Pelargonium flower break virus	PFBV
Saguaro cactus virus	SgCV
Turnip crinkle virus	TCV

Necroviruses

Beet black scorch virus	BBSV
Leek white stripe virus	LWSV
Olive latent virus 1	OLV-1
Olive mild mosaic virus	OMMV
Tobacco necrosis virus A	TNV-A
Tobacco necrosis virus D	TNV-D

Proposed Macanavirus

Furcraea necrotic streak virus	FNSV

Panicovirus

Panicum mosaic virus	PMV

Machlomovirus

Maize chlorotic mottle virus	MCMV

Proposed Zeavirus

Maize necrotic streak virus	MNeSV

Table 1. Percent amino acid sequence identity between the polymerase of FNSV and those of the proposed alpha- and necrovirus genera and other *Tombusviridae* members

	% aa sequence identity in polymerase		
	Alpha-necrovirus	Beta-necrovirus	Other Tombusviridae
FNSV	52-52	32-42	25-38

Table 1. Percent amino acid sequence identity between the MP1 of FNSV and those of the proposed alpha- and necrovirus genera and other *Tombusviridae* members

	% aa sequence identity in MP1				
	Alpha-necro	Beta-necro	Carmo-	PMV	MCMV
FNSV	47-49	12-20	8-20	8	20

Table 1. Percent amino acid sequence identity between the MP2 of FNSV and those of the proposed alpha- and necrovirus genera and other *Tombusviridae* members

	% aa sequence identity in MP2			
	Alpha-necro	Beta-necro	Carmo-	PMV-
FNSV	57	21-25	7-23	23

Table 1. Percent amino acid sequence identity between the CP of FNSV and those of the proposed alpha- and necrovirus genera and other *Tombusviridae* members

	% aa sequence identity in coat protein								
	Alpha-necro	Beta-necro	PMV	MCMV	Tombus	Aureus	Carmo	OCSV	Diantho
FNSV	13-17	13-18	14	13	25-31	27-32	15-31	20	25-28

Virus coat proteins with protruding domains

Virus coat proteins without protruding domains