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

Code assigned:	*2011.010a-eP*	(to be completed by ICTV officers)

Short title: create new genus, *Gallantivirus*, 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 26 2012

MODULE 3: **NEW GENUS**

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

Code	*2011.010aP*	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	*Tombusviridae*
Order:	

naming a new genus

Code	*2011.010bP*	(assigned by ICTV officers)

To name the new genus: *Gallantivirus*

Assigning the type species and other species to a new genus

Code	*2011.010cP*	(assigned by ICTV officers)

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

Galinsoga mosaic 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 *Galinsoga mosaic virus* (GaMV) shows that this virus is 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 GaMVcontains a protruding domain (Fig. 1, 2) and it is most similar 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 GaMV.

Origin of the new genus name:

Derived from "Gallant soldier", the vernacular English name of *Galinsoga parviflora*, the host of the type species of the genus

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 7: **REMOVE and MOVE**

Part (a) taxon/taxa to be removed or moved

Code	*2011.010dP*	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Galinsoga mosaic virus

The present taxonomic position of these taxon/taxa:

Genus:	*Carmovirus*	
Subfamily:		Fill in all that apply.
Family:	*Tombusviridae*	
Order:		

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:

Virus is being proposed to represent a new genus (this proposal)

Part (b) re-assign to a higher taxon

Code	*2011.010a-eP*	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	*Gallantivirus* (new genus)
Subfamily:	
Family:	*Tombusviridae*
Order:	

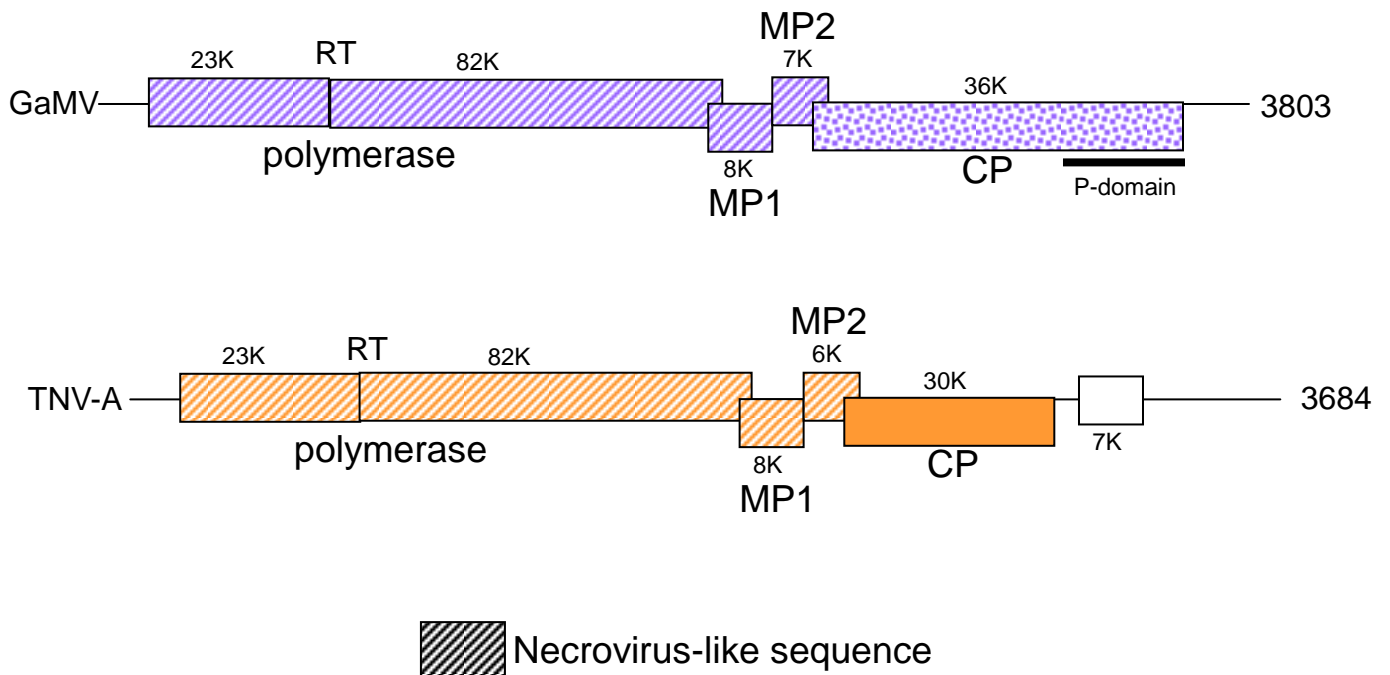**Reasons to justify the re-assignment:**
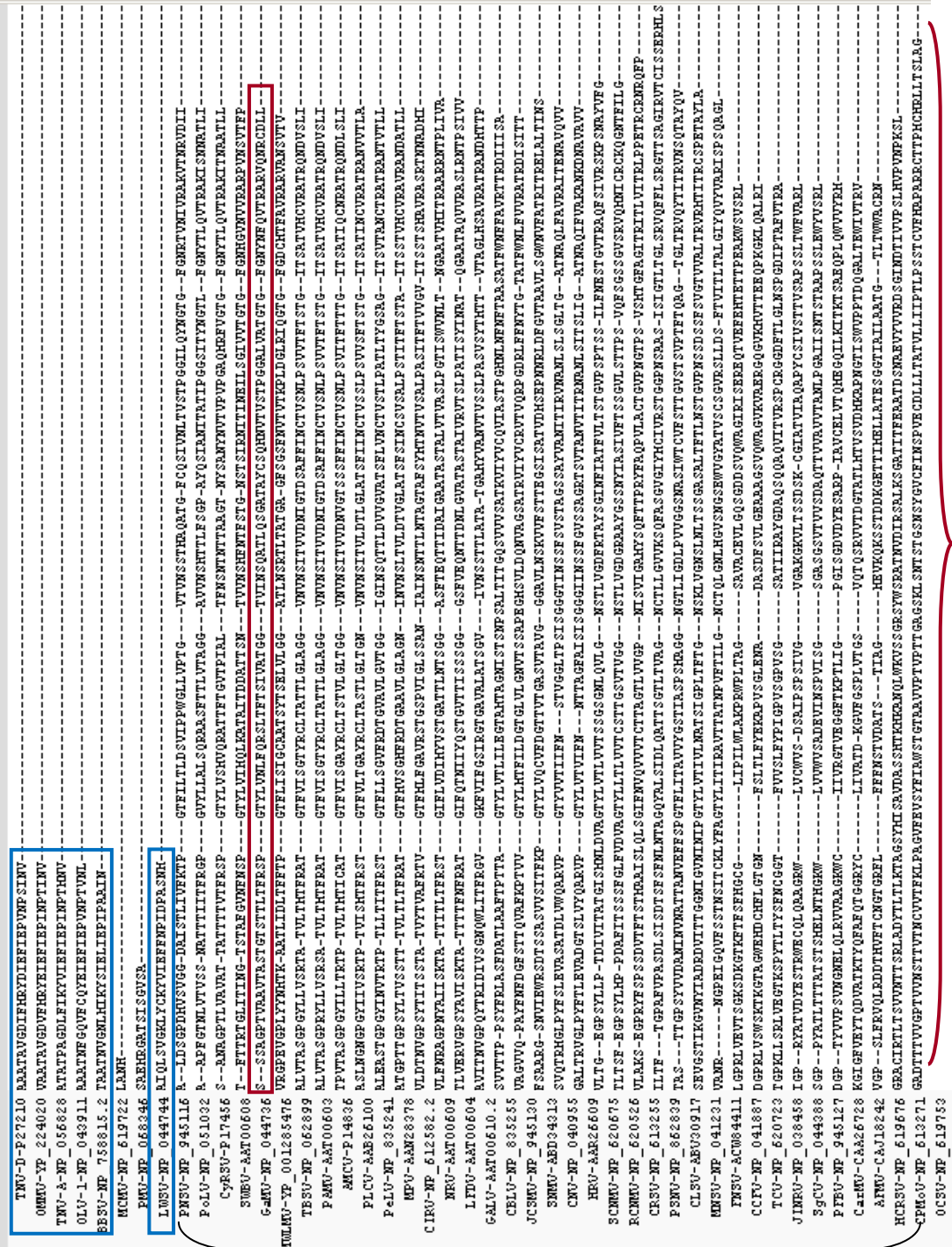
See Modules 3 and 9

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

Necroviruse

Other Tombusviridae members (with P domain)

Coat protein protru...

Figure 2. Alignment of the CP sequence of GaMV (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.
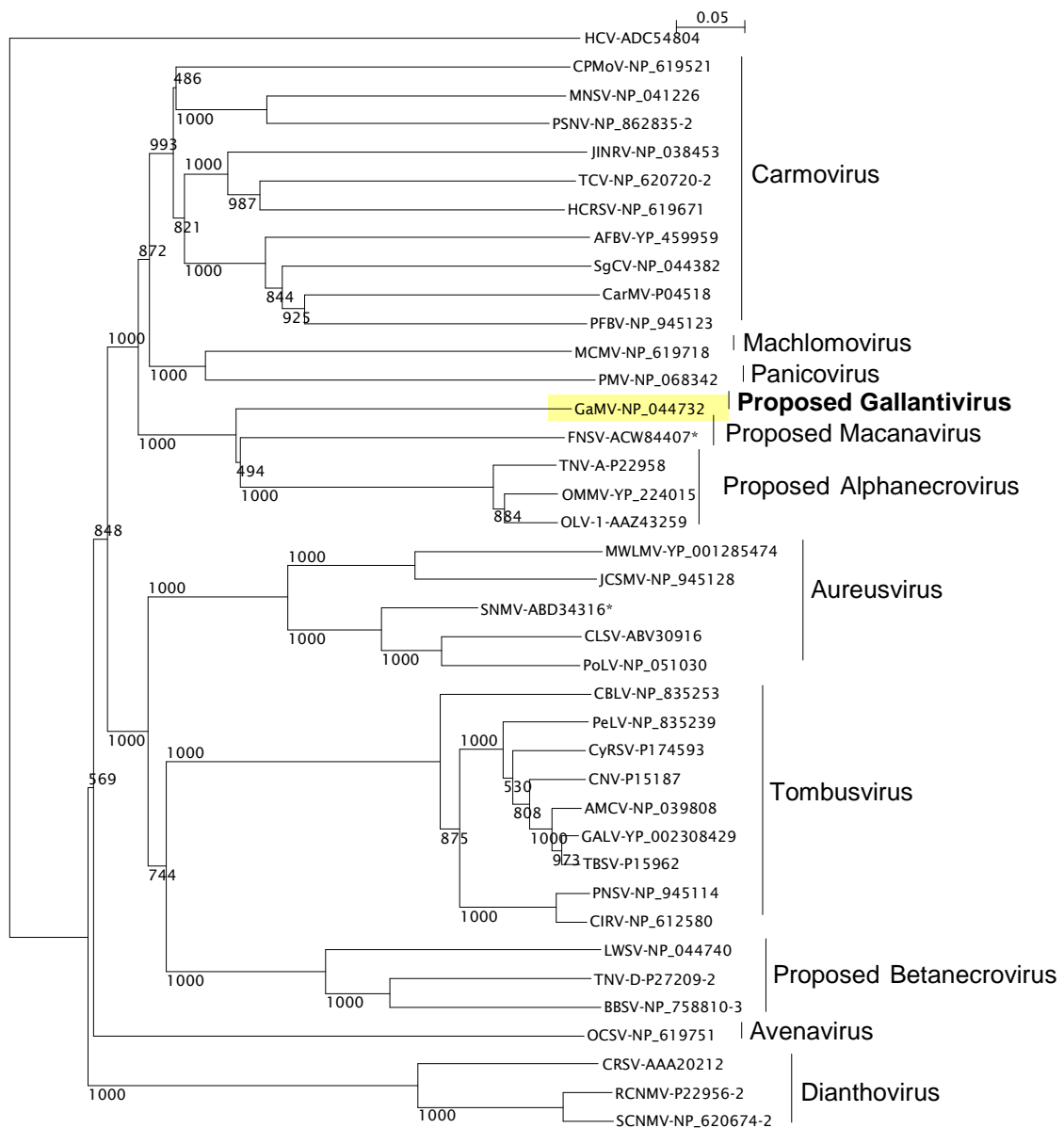
Figure 3. Phylogenetic (distance) tree of the polymerase of *Tombusviridae* members with the position of GaMV highlighted in yellow. Sequences were aligned using the ClustalX 2.1 algorithm and trees were generated by the Neighbor Joining method using 1000 bootstrap replicates. Hepatitis C virus (HCV) polymerase was used as an outgroup.
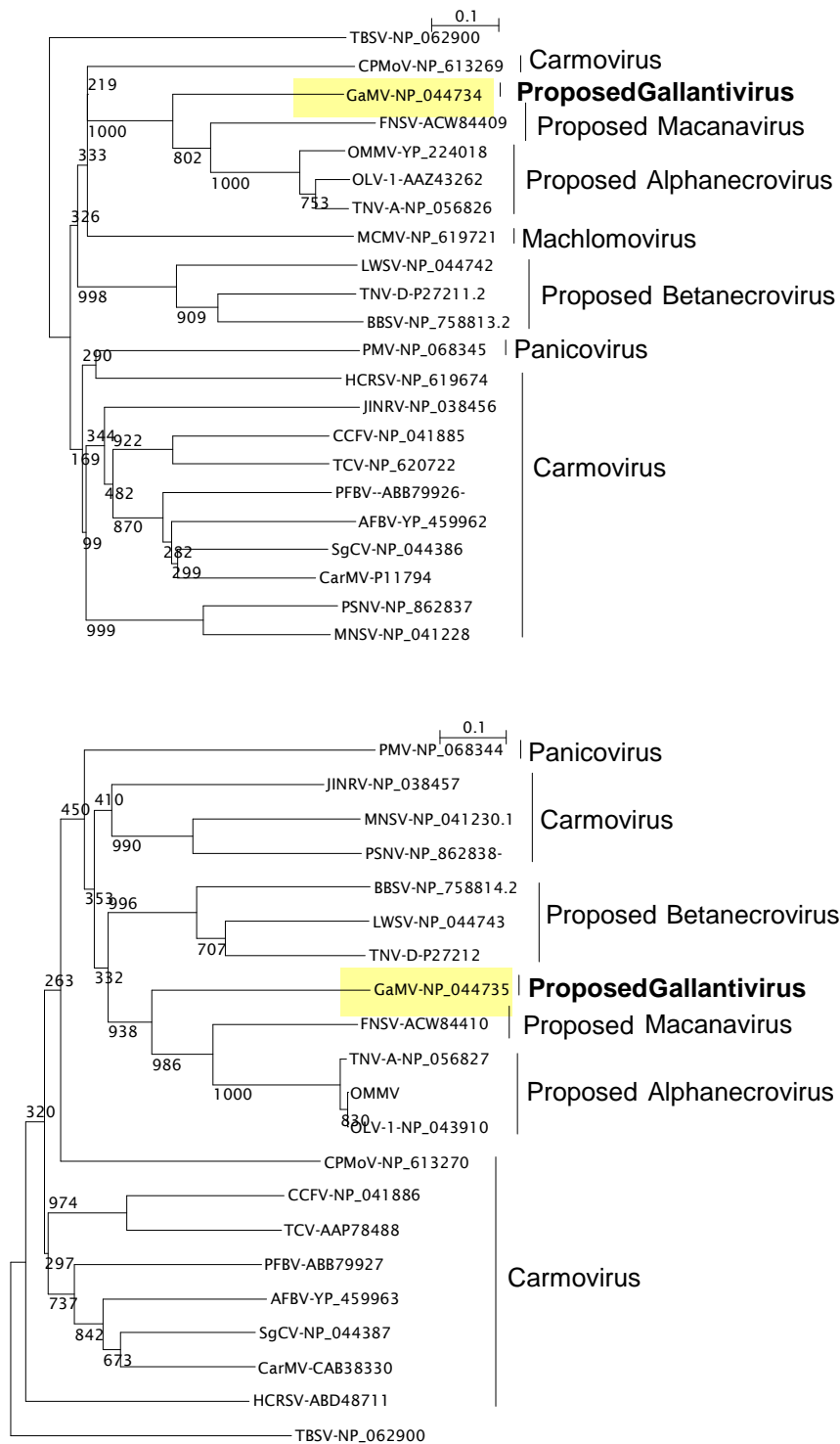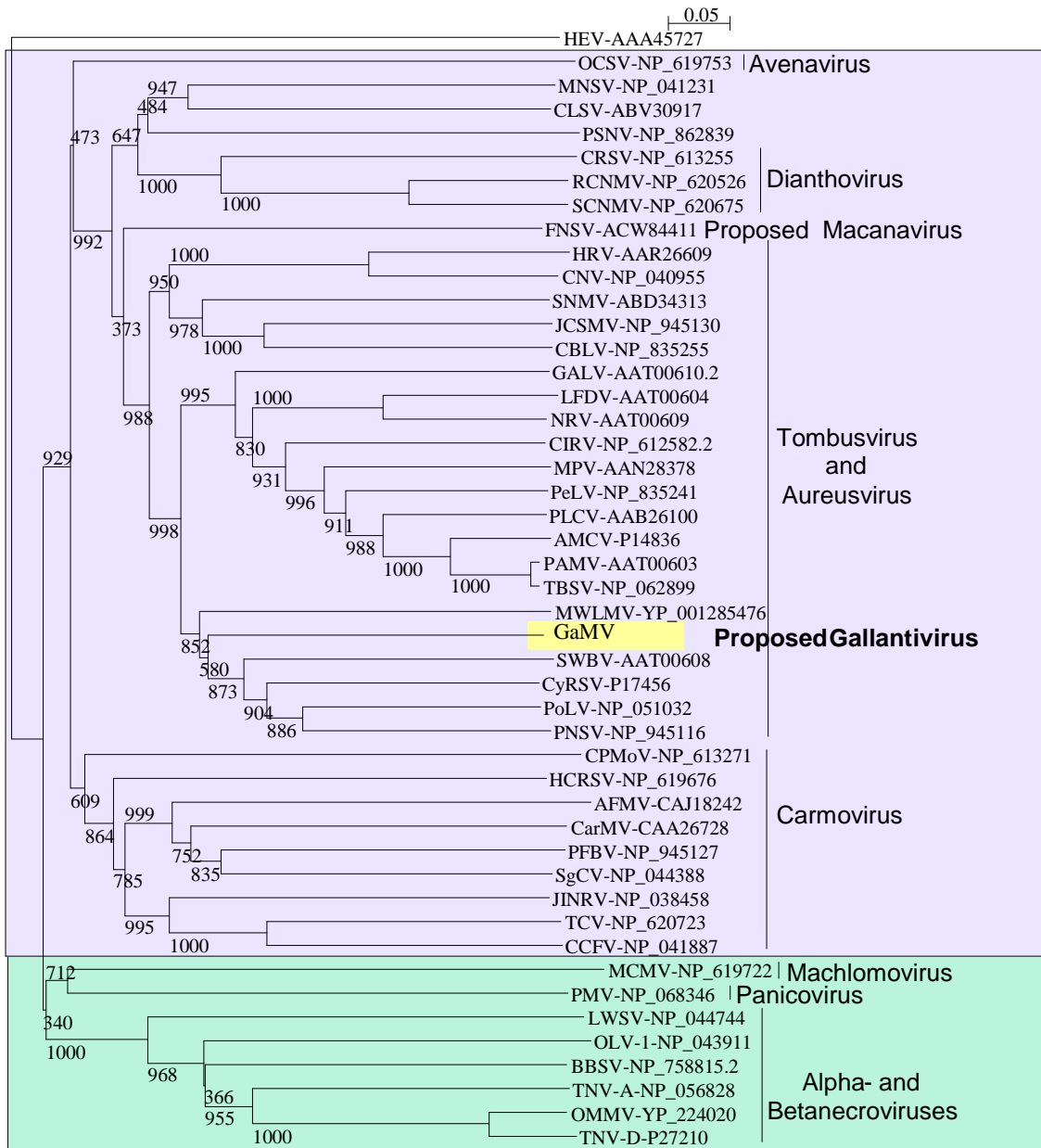
Figure 4. Phylogenetic (distance) tree of the MP1 (top) and MP2 (bottom) sequences of *Tombusviridae* members with the position of the GaMV MPs highlighted in yellow. Sequences were aligned using the ClustalX 2.1 algorithm and trees were generated by the Neighbor Joining method using 1000 bootstrap replicates.

Figure 5. Phylogenetic (distance) tree of CP sequences of *Tombusviridae* members with the position of the GaMV 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.

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

	% aa sequence identity in polymerase			
	GaMV	Alpha-necrovirus	Beta-necrovirus	Other Tombusviridae
GaMV	-	51	30-33	24-39

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

	% aa sequence identity in MP1					
	GaMV	Alpha-necro	Beta-necro	Carmo-	PMV	MCMV
GaMV	-	37-42	8-22	8-22	14	17

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

	% aa sequence identity in MP2			
	GaMV	Alpha-necro	Beta-necro	Carmo-	PMV-
GaMV	-	37	19-25	10-24	6

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

	% aa sequence identity in coat protein									
	GaMV	Alpha-necro	Beta-necro	PMV	MCMV	Tombus	Aureus	Carmo	OCSV	Diantho
GaMV	-	14-15	11-19	15	14	31-49	33-50	14-30	24	22-25

☐ Virus coat proteins with protruding domains

☐ Virus coat proteins without protruding domains

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