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:	***2015.007a-rP***	(to be completed by ICTV officers)

Short title: Divide the genus *Carmovirus* into three new genera: *Alphacarmovirus*, *Betacarmovirus*, and *Gammacarmovirus.*

(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☐	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☒	**9** ☐	**10** ☒

Author(s):

Kay Scheets, K Andrew White, Luisa Rubino, Giovanni Martelli, D'Ann Rochon

Corresponding author with e-mail address:

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 http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Tombusviridae

ICTV Study Group comments (if any) and response of the proposer:

The study group is in favor of this division of the current carmovirus genus.

Date first submitted to ICTV: June 3, 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.007aP***	(assigned by ICTV officers)

To create a new genus within:

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.007bP***	(assigned by ICTV officers)

To name the new genus: *Alphacarmovirus*

Assigning the type species and other species to a new genus

Code	***2015.007cP***	(assigned by ICTV officers)

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

Carnation mottle virus	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

7

Reasons to justify the creation of a new genus:

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

Background for revision of genus *Carmovirus*

In 1987 the carmovirus group contained seven members. Since then the group has been changed to a genus and two members (*Galinsoga mosaic virus* and *Glycine mottle virus*) have been removed while 14 have been added, which now makes it the largest genus in the family. The Tombusviridae study group (SG) had noted an increased complexity of phylogenetic trees several years ago, and at the prompting of the executive committee (EC) (see below) propose to divide the current genus into three new genera.

EC comments from proposal 2014.006aP.A.v2.Tombusviridae_4sp.pdf [Scheets et al. 2014]:
"In the taxonomy code, the definition of a genus (or of any taxonomic taxon) stipulates that it should be monophyletic to indicate a common evolutionary origin. While mosaic evolution is acknowledged to complicate classification in many virus family (including the tombusviridae), the study group should decide which protein is the most valid to determine evolutionary relationships for this family and consider a classification scheme supported by phylogenetic trees for this protein. The problem with the proposed pelarspovirus genus is that it does not separate clearly from the carmovirus genus into two separate monophyletic branches for any of the proteins considered. It was also noted that the current genus carmovirus is not monophyletic for any of the proteins considered. This suggests that the taxonomy of the family (especially of species related to the genus carmovirus) may need to be reconsidered."

Revision of genera demarcation criteria

The following criteria demarcating tombusvirid genera are listed in the 9th Report of the International Committee on Taxonomy of Viruses [Rochon et al., 2011].

- Structural criteria: spherical virions with either a smooth or granular appearance.
- Genomic criteria: genome organization, number of genome segments, size of genome.
- Polymerase criteria: gene interrupted by a termination codon or a -1 ribosomal frameshifting element that is periodically read through.

The SG proposes modifying the genus demarcation criteria by including "number of subgenomic RNAs (sgRNAs)" within Genomic criteria and "differential branching of phylogenetic trees based on complete RNA dependent RNA polymerase (RdRp)" under Polymerase criteria. Accumulation of data on the sequences and molecular biology of tombusvirids now indicates that a significant number of viruses **initiate translation and expression of three or more proteins from a single subgenomic RNA**, and this criteria differentiates monophyletic lineages of the viral polymerase for some viruses with similar genome organizations. The recent addition of genus *Umbravirus* to the family [Rochon et al., 2014], whose members do not encode CPs, greatly decreases the relevance of CP phylogenetic trees for assigning taxonomical placement of new family members. As was previously noted, the phylogenetic trees based on RdRps most closely show monophyletic lineages for genera compared to trees for other virally-encoded proteins [Rochon et al., 2011], and the SG endorses the use of RdRps as the main protein for generating phylogenetic trees that define genera. The SG thinks that whole genome sequence comparisons [Bao et al., 2014] may provide useful information about the relationships of viral species within the family, but should not be used to define tombusvirid genera. These new criteria would not change the current organization of tombusvirid genera except for genus *Carmovirus* and supports the formation of a new genus *Pelarspovirus* (separate proposal) from five unassigned tombusvirids.

Revised genus demarcation criteria in the family *Tombusviridae*

- Structural criteria: spherical virions with either a smooth or granular appearance.
- Genomic criteria: genome organization, number of genome segments, size of genome, number of subgenomic RNAs.
- Polymerase criteria: gene interrupted by a termination codon or a -1 ribosomal frameshifting element that is periodically read through; differential branching of phylogenetic trees based on complete RdRp.

Viruses currently placed in carmovirus genus

The carmovirus genus contains 19 species: *Angelonia flower break virus* (AnFBV), *Calibrachoa mottle virus* (CbMV), *Carnation mottle virus* (CarMV), *Honeysuckle ringspot virus* (HoRV), *Nootka lupine vein clearing virus* (NLVCV), *Pelargonium flower break virus* (PFBV), *Saguaro cactus virus* (SgCV), *Cardamine chlorotic fleck virus* (CCFV), *Hibiscus chlorotic ringspot virus*, (HCRSV) *Japanese iris necrotic ring virus* (JINRV), *Turnip crinkle virus* (TCV), *Cowpea mottle virus* (CPMoV), *Melon necrotic spot virus* (MNSV), *Soybean yellow mottle mosaic virus* (SYMMV), *Pea stem necrosis virus* (PSNV), *Ahlum waterborne virus* (AWV), *Bean mild mosaic virus* (BMMV), *Cucumber soil-borne virus* (CSBV), and *Weddel waterborne virus* (WWV). Virions are 32-35 nm spheres with a granular appearance due to the C-terminal protruding domain of their coat proteins which range in size from ~37-42 kDa. Complete sequences of 15 viruses are known. All sequenced carmoviruses encode a 5´ ORF1 encoding the amino end of the RdRp which is expressed via readthrough of the ORF1 leaky stop codon [Rochon et al., 2011] (Fig. 1). Following the RdRp are two small ORFs encoding movement proteins (MP1 and MP2) that are expressed from the larger of two subgenomic RNAs (sgRNAs) while the smaller sgRNA expresses the CP ORF. CPMoV and SYMMV contain ORFs immediately following the MP2 stop codon that potentially encode 28 or 25 kDa proteins, respectively [Nam 2009; You et al., 1995] while

HCRSV contains a 5´ ORF overprinted within ORF1 encoding a 23 kDa protein [Huang et al., 2000] as well as an overlapping ORF with a CUG start codon that slightly precedes the CP AUG in a different reading frame to express a 27 kDa protein [Koh et al., 2006].

Phylogenetic analyses

Phylogenetic analyses were performed for RdRp, MP1, MP2, and CP of sequenced tombusvirids encoding CPs [Scheets et al., 2015]. Umbraviruses were omitted from the analyses since their polymerases branch in a separate clade from all CP-coding tombusvirids [Rochon et al., 2014]. Two alignment methods (MUSCLE and ClustalOmega) with two statistical approaches (maximum likelihood or neighbor-joining) using two or three treatments of gaps and missing data were used to generate up to 10 trees for each protein ([Scheets et al., 2015] for ClustalOmega trees and data not shown). Not all combinations of treatments were capable of analyzing MP1 and MP2 due to their generally low similarities. None of the trees for RdRp, MP1, MP2, and CP produced monophyletic branches containing all 15 carmoviruses (Figs. 2-7, [Scheets et al., 2015] and data not shown). For the 10 RdRp trees, a consistent pattern of grouping seven (AnFBV, CarMV, CbMV, HoRV, NLVCV, PFBV, SgCV), four (CCFV, HCRSV, JINRV, TCV), and four (CPMoV, MNSV, PSNV, SYMMV) carmoviruses was found with the third group most often branching earliest (Fig. 2 and data not shown), and this is the basis for the proposal to divide the carmoviruses into three new genera: *Alphacarmovirus, Betacarmovirus*, and *Gammacarmovirus*, respectively (Fig. 1). A larger monophyletic lineage of six unassigned tombusvirids and the alphacarmoviruses is formed in all 10 RdRp trees, but translation characteristics, the production of only one sgRNA, and protein similarities consistently separates the five viruses proposed to form a new genus *Pelarspovirus* (see Fig. 2 and separate proposal). Trailing lespedeza virus 1 (TLV1) shares predicted coding and translation characteristics with the pelarspoviruses [Scheets et al., 2011; Scheets and Melcher, 2014]. Its CP groups with pelarspoviruses in 6/10 trees (Fig. 4 and data not shown) and with alphacarmoviruses in 4/10 trees, while TLV1 grouping in RdRp trees is 5 and 5 for the same genera (Fig. 2 and data not shown), so it will remain unassigned in the family.

If whole genome nt sequence analysis with the PAirwise Sequence Comparison (PASC) tool at the NCBI Viral Genomes web site is applied to tombusvirid reference sequences under conditions suggested by Yiming Bao [Bao et al., 2014], current carmoviruses would be divided into eight genera (Fig. 3), and a new genus equivalent to the proposed pelarspovirus would also be formed. The only other change was the inclusion of MNeSV in genus *Tombusvirus* (Fig. 3) which would contradict the virion structural criteria. The MNeSV mis-assignment emphasizes why PASC should not be used as the genus demarcation criteria.

Genetic distances of viral proteins

Unlike the members of the related viruses in the proposed pelarspovirus genus, none of the CP, MP1, or MP2 trees produced monophyletic lineages for alphacarmovirus, betacarmovirus, or gammacarmovirus (Figs. 2-7 [Scheets et al., 2015] and data not shown) suggesting that several species arose through recombination. Thus, % identities for these proteins are not informative and only RdRp data is presented. All of the 15 sequenced carmoviruses showed $\leq$ 67% identity to any other family member, and the greatest identities to viruses outside each newly proposed genus (alphacarmovirus, betacarmovirus, gammacarmovirus, pelarspovirus) was to viruses in the three other proposed genera (Table 1 and data not shown). Unlike the pelarspoviruses and alphacarmovirses, which are most closely related to viruses within their genera, some betacarmoviruses and gammacarmoviruses have higher % identities to a virus in the other genera (Table 1 and data not shown). This was consistent with the RdRp phylogenetic tree analyses since betacarmoviruses and gammacarmovirses were further grouped in a larger monophyletic lineage in four trees, most often when **all** regions with gaps or missing data were eliminated ([Scheets et al., 2015] and data not shown). TLV1 RdRp showed highest % identities to alphacarmoviruses. For sequenced viruses in the other 11 genera of CP-encoding viruses, maximum % identities to viral

RdRps in the four newly proposed genera ranged from 36.5-40.9% while minimum % identities were 25.0-29.3% (data not shown).

Biological properties
All current members of the carmovirus genus are mechanically transmissible, and fungal transmission (MNSV, PSNV, CSBV), seed transmission (CPMoV), or beetle transmission (BMMV, TCV, CPMoV) have been reported for a few species [Rochon et al., 2011]. None of the known transmission characteristics are specific to any of the newly proposed genera. But so far the only transmission method that is universally found in all tombusvirid genera is mechanical transmission, while transmission via seed, fungus, or insects is found for a few species in various other tombusvirid genera. Thus, there will be no vector-specificity criteria associated with any of the proposed new genera.

The position of nonsequenced members of the current carmovirus genus
The biological data accumulated for AWV, CSBV, BMMV, and WWV suggest they are tombusvirids [Hari et al., 1989; Koenig et al., 1983; Li et al. 1992; Waterworth et al., 1977], but there is no sequence data for them, so they cannot be assigned to any of the three proposed new genera or other established tombusvirid genera. Also, the reported genome size estimates for AWV (4.7 kb, [Li et al. 1992]) and CSBV (1.5 x10^6 Da [Koenig et al. 1983]) are closer to those of tombusviruses than sequenced viruses in the 2014 carmovirus genus. AWV was predicted to be a carmovirus based on a weak signal of a northern blot probed with random-primed RNA complementary to WWV which had an estimated size of 4.1 kb [Li et al. 1992]. Thus, these four viruses will become unassigned tombusvirids.

Origin of the new genus name:

A Greek prefix is added to the existing designation to make *Alphacarmovirus*

Reasons to justify the choice of type species:

CarMV is currently the type member of genus *Carmovirus* and was the first virus in the proposed genus to be sequenced.

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.

1) Less than 75% aa sequence identity in the polymerase and
2) Less than 75% aa sequence identity in the coat protein
See “Reasons to justify the creation of a new genus” above

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.007dP***	(assigned by ICTV officers)

To create a new genus within:

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.007eP***	(assigned by ICTV officers)

To name the new genus: *Betacarmovirus*

Assigning the type species and other species to a new genus

Code	***2015.007fP***	(assigned by ICTV officers)

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

Turnip crinkle virus	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

4

Reasons to justify the creation of a new genus:

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

see reasons for creation of genus *Alphacarmovirus* (above)

Origin of the new genus name:

A Greek prefix is added to the existing designation to make *Betacarmovirus*

Reasons to justify the choice of type species:

TCV was the first betacarmovirus to be completely sequenced and is the best-studied.

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.

1) Less than 75% aa sequence identity in the polymerase and
2) Less than 75% aa sequence identity in the coat protein
See "Reasons to justify the creation of a new genus" above

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.007gP***	(assigned by ICTV officers)

To create a new genus within:

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.007hP***	(assigned by ICTV officers)

To name the new genus: *Gammacarmovirus*

Assigning the type species and other species to a new genus

Code	***2015.007iP***	(assigned by ICTV officers)

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

Melon necrotic spot virus	Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

4

Reasons to justify the creation of a new genus:

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

see reasons for creation of genus *Alphacarmovirus* (above)

Origin of the new genus name:

A Greek prefix is added to the existing designation to make *Gammacarmovirus*

Reasons to justify the choice of type species:

MNSV was the first gammacarmovirus to be completely sequenced and is the most well-studied.

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.

1) Less than 75% aa sequence identity in the polymerase and
2) Less than 75% aa sequence identity in the coat protein
See "Reasons to justify the creation of a new genus" above

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

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

Code	***2015.007jP***	(assigned by ICTV officers)

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

Angelonia flower break virus, Calibrachoa mottle virus, Carnation mottle virus, Honeysuckle ringspot virus, Nootka lupine vein clearing virus, Pelargonium flower break virus, Saguaro cactus virus

The present taxonomic position of these taxon/taxa:

Genus:	***Carmovirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.

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:
Explain why the taxon (or taxa) should be removed

Genus *Carmovirus* will no longer exist after the reorganization of the family as outlined above, so these 7 species need to be removed and reassigned (below).

Part (b) re-assign to a higher taxon

Code	***2015.007kP***	(assigned by ICTV officers)

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

Genus:	***Alphacarmovirus*** **(new)**
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See first module 3 (above) and appendix for supporting figures and tables. Table 2 of appendix contains accession numbers.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

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

Code	***2015.007lP***	(assigned by ICTV officers)

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

Cardamine chlorotic fleck virus, Hibiscus chlorotic ringspot virus, Japanese iris necrotic ring virus, Turnip crinkle virus

The present taxonomic position of these taxon/taxa:

Genus:	***Carmovirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.

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:
Explain why the taxon (or taxa) should be removed

Genus *Carmovirus* will no longer exist after the reorganization of the family as outlined above, so these 4 species need to be removed and reassigned (below).

Part (b) re-assign to a higher taxon

Code	***2015.007mP***	(assigned by ICTV officers)

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

Genus:	***Betacarmovirus*** **(new)**
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See first module 3 (above) and appendix for supporting figures and tables. Table 2 of appendix contains accession numbers.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

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

Code	***2015.007nP***	(assigned by ICTV officers)

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

Cowpea mottle virus, Melon necrotic spot virus, Soybean yellow mottle mosaic virus, Pea stem necrosis virus

The present taxonomic position of these taxon/taxa:

Genus:	***Carmovirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.

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:
Explain why the taxon (or taxa) should be removed

Genus *Carmovirus* will no longer exist after the reorganization of the family as outlined above, so these 4 species need to be removed and reassigned (below).

Part (b) re-assign to a higher taxon

Code	***2015.007oP***	(assigned by ICTV officers)

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

Genus:	***Gammacarmovirus*** **(new)**
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See first module 3 (above) and appendix for supporting figures and tables. Table 2 of appendix contains accession numbers.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:
- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

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

Code	***2015.007pP***	(assigned by ICTV officers)

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

Ahlum waterborne virus, Bean mild mosaic virus, Cucumber soil-borne virus, Weddel waterborne virus

The present taxonomic position of these taxon/taxa:

Genus:	***Carmovirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.

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:
Explain why the taxon (or taxa) should be removed

These species are currently assigned to genus *Carmovirus*, and they must be removed/reassigned because that genus will no longer exit after reorganization.

Part (b) re-assign to a higher taxon

Code	***2015.007qP***	(assigned by ICTV officers)

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

Genus:	**unassigned**
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:
- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See module 3 (above)

MODULE 7: **REMOVE and MOVE**

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

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

Code	***2015.007rP***	(assigned by ICTV officers)

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

genus *Carmovirus*

The present taxonomic position of these taxon/taxa:

Genus:	***Carmovirus***
Subfamily:	
Family:	***Tombusviridae***
Order:	

Fill in all that apply.

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

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

This genus will disappear in the proposed reorganization.

MODULE 10: **APPENDIX**: supporting material.

References:

Bao, Y., Chetvernin, V., Tatusova, T., 2014. Improvements to pairwise sequence comparison (PASC): a genome-based web tool for virus classification. Arch. Virol. 159, 3293-3304.

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Huang, M., Koh, D.C.-Y., Weng, L.-J., Chang, M.-L., Yap, Y.-K., Zhang, L., Wong, S.-M., 2000. Complete nucleotide sequence and genome organization of hibiscus chlorotic ringspot virus, a new member of the genus *Carmovirus*: evidence for the presence and expression of two novel open reading frames. J. Virol. 74, 3149-3155.

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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.

Table 1. Percent amino acid sequence identity[a] ranges between RdRps of carmovirus-like genera members.

	Alpha-carmovirus	Beta-carmovirus	Gamma-carmovirus	Pelarspo-virus	TLV1
Alpha-carmovirus	**47.9-64.6**				37.8-41.6
Beta-carmovirus	39.5-41.8	**47.1-67.0**			36.8-38.9
Gamma-carmovirus	37.9-42	39.9-45.0	**42.9-64.7**		34.8-37.1
Pelarspo-virus	38.1-46.5	38.0-44.0	37.2-41.1	**55.0-69.4**	37.7-40.3

[a] based on MUSCLE

Table 2. Virus abbreviations and accession numbers for proposal

	Alphanecrovirus	
OLV1	Olive latent virus 1	X85989
OMMV	Olive mild mosaic virus	AY616760
TNVA	Tobacco necrosis virus A	M33002
	Aureusvirus	
CLSV	Cucumber leaf spot virus	EU127904
JCSMV	Johnsongrass chlorotic stripe mosaic virus	AJ557804
MWLMV	Maize white line mosaic virus	EF589670
PoLV	Pothos latent virus	X87115
YSV	Yam spherical virus (proposed)	KF482072
	Avenavirus	
OCSV	Oat chlorotic stunt virus	X83964
	Betanecrovirus	
BBSV	Beet black scorch virus	AF452884
LWSV	Leek white stripe virus	X94560
TNVD	Tobacco necrosis virus D	U62546
	Carmovirus (2014)	
	Alphacarmovirus (proposed)	
AnFBV	Angelonia flower break virus	DQ219415
CbMV	Calibrachoa mottle virus	GQ244431
CarMV	Carnation mottle virus	X02986
HoRSV	Honeysuckle ringspot virus	HQ677625
NLVCV	Nootka lupine vein clearing virus	EF207438
PFBV	Pelargonium flower break virus	AJ514833
SgCV	Saguaro cactus virus	U72332
	Betacarmovirus (proposed)	
CCFV	Cardamine chlorotic fleck virus	L16015
HCRSV	Hibiscus chlorotic ringspot virus	X86448
JINRV	Japanese iris necrotic ring virus	D86123
TCV	Turnip crinkle virus	M22445
	Gammacarmovirus (proposed)	
CPMV	Cowpea mottle virus	U20976
MNSV	Melon necrotic spot virus	M29671
PSNV	Pea stem necrosis virus	AB086951
SYMMV	Soybean yellow mottle mosaic virus	FJ457015
	move to unassigned (proposed)	
AWV	Ahlum waterborne virus	na
BMMV	Bean mild mottle virus	na
CSBV	Cucumber soil-borne virus	na
WWV	Weddel waterborne virus	na
	Dianthovirus	
CRSV	Carnation ringspot virus	L18870, M88589
RCNMV	Red clover necrotic mosaic virus	J04357, X08021
SCNMV	Sweet clover necrotic mosaic virus	L07884, S46028
	Gallantivirus	
GaMV	Galinsoga mosaic virus	Y13463
	Macanavirus	
FNSV	Furcraea necrotic streak virus	FJ768020

	Machlomovirus	
MCMV	Maize chlorotic mottle virus	X14736
	Panicovirus	
CMMV	Cocksfoot mild mosaic virus	EU081018
PMV	Panicum mosaic virus	U55002
TPAV	Thin paspalum asymptomatic virus	JX848617
	Tombusvirus	
AMCV	Artichoke mottled crinkle virus	X62493
CIRV	Carnation Italian ringspot virus	X85215
CBV	Cucumber Bulgarian virus	AY163842
CNV	Cucumber necrosis virus	M25270
CyRSV	Cymbidium ringspot virus	X15511
EMCV	Eggplant mottled crinkle virus	JQ864181
GALV	Grapevine Algerian latent virus	AY830918
MPV	Moroccan pepper virus	JX197071
PNSV	Pelargonium necrotic spot virus	AJ607402
TBSV	Tomato bushy stunt virus	M21958
	Zeavirus	
MNeSV	Maize necrotic streak virus	AF266518
	unassigned Tombusviridae	
TLV1	Trailing lespedeza virus 1	HM640935
	Pelarspovirus (proposed)	
ELV	Elderberry latent virus	AY038066
PCRPV	Pelargonium chlorotic ring pattern virus	AY038069
PLPV	Pelargonium line pattern virus	AY613852
PelRSV	Pelargonium ringspot virus	AY038068
RrLDV	*Rosa rugosa* leaf distortion virus	KC166238
	other viral sequences	
HCV	Hepatitis C virus RdRp	ADC54804
HEV	Hepatitis E virus CP	AAA45727

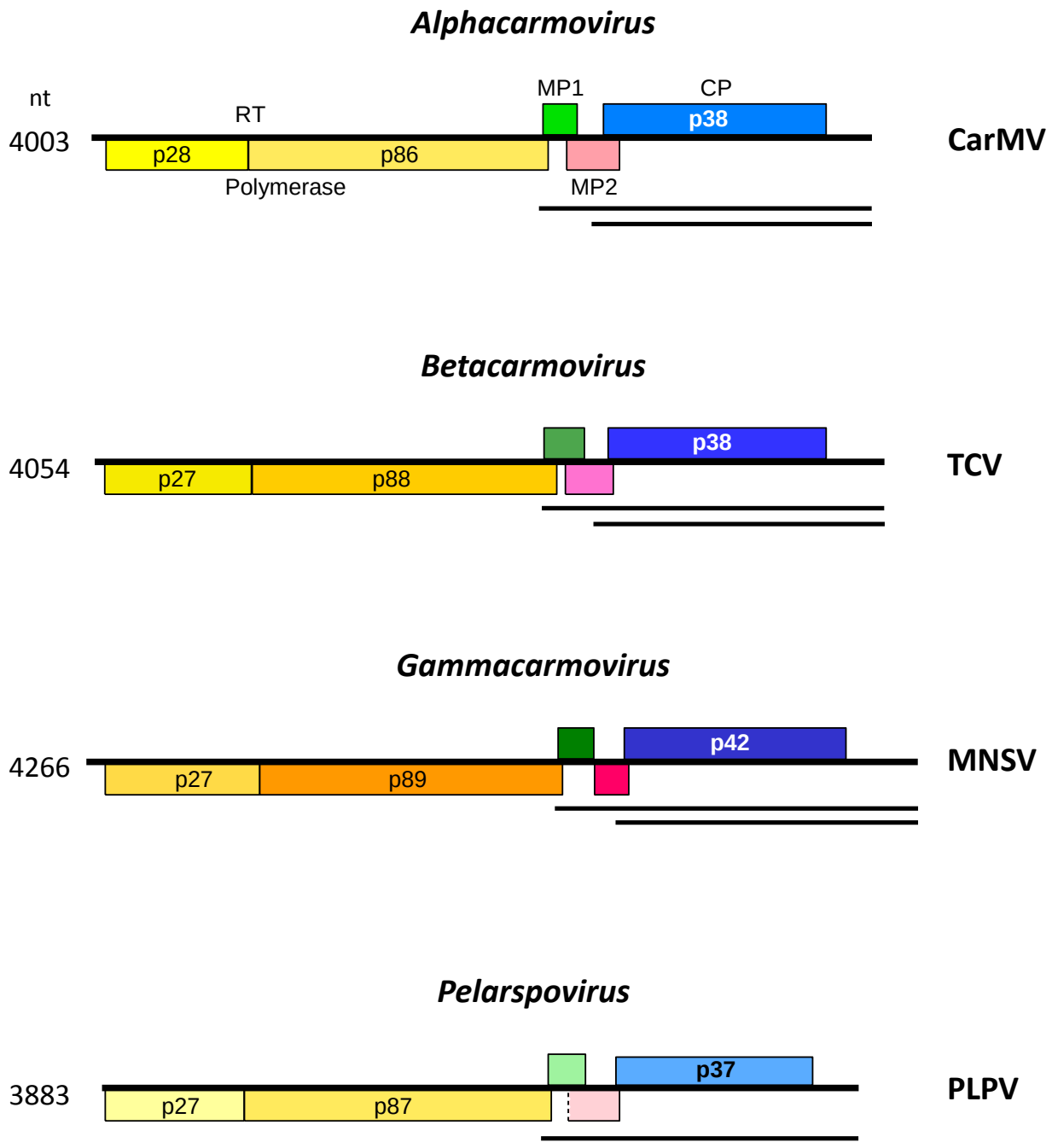

Figure 1. Lengths, proposed genus names, and genome organizations of type viruses for proposed carmovirus-like genera. RT marks the read through stop codon. Thin lines under genomes indicate sgRNAs. ORFs with similar functions are shaded in similar color-families. Dashed line of PLPV MP2 marks a noncanonical start codon. Thin lines under genomes indicate sgRNAs. See Table 2 for virus acronyms.

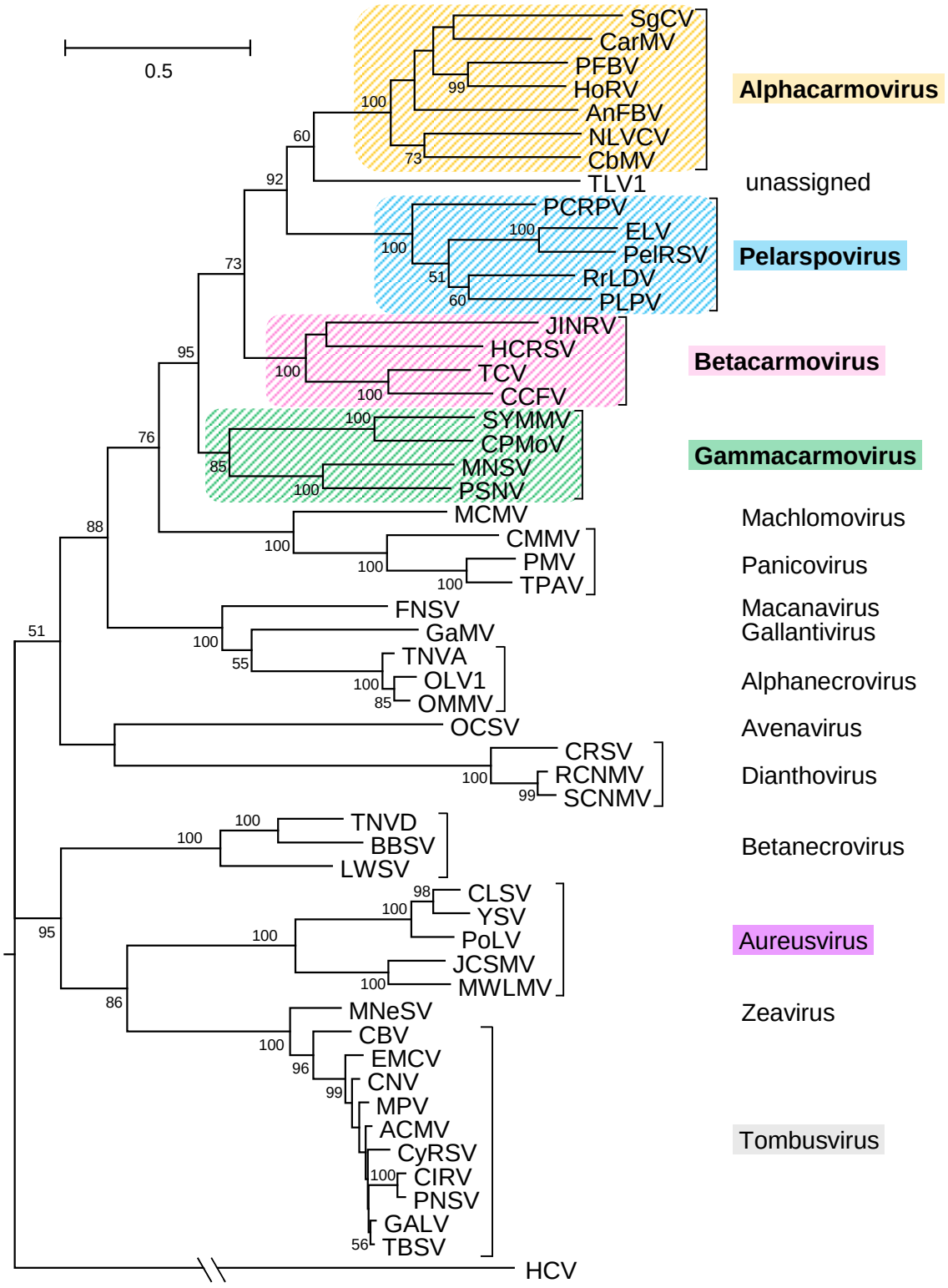

Figure 2. Phylogenetic (distance) analysis of the RdRps of CP-encoding tombusvirids. Alignments were made using MUSCLE while trees were generated with the Maximum Likelihood (ML) algorithm using 1000 bootstrap replicates (showing values >50%). Positions with < 50% site coverage were eliminated, leaving 765 positions in the final dataset. Hepatitis C virus (HCV) RdRp was used as the outgroup. Brackets mark monophyletic lineages.

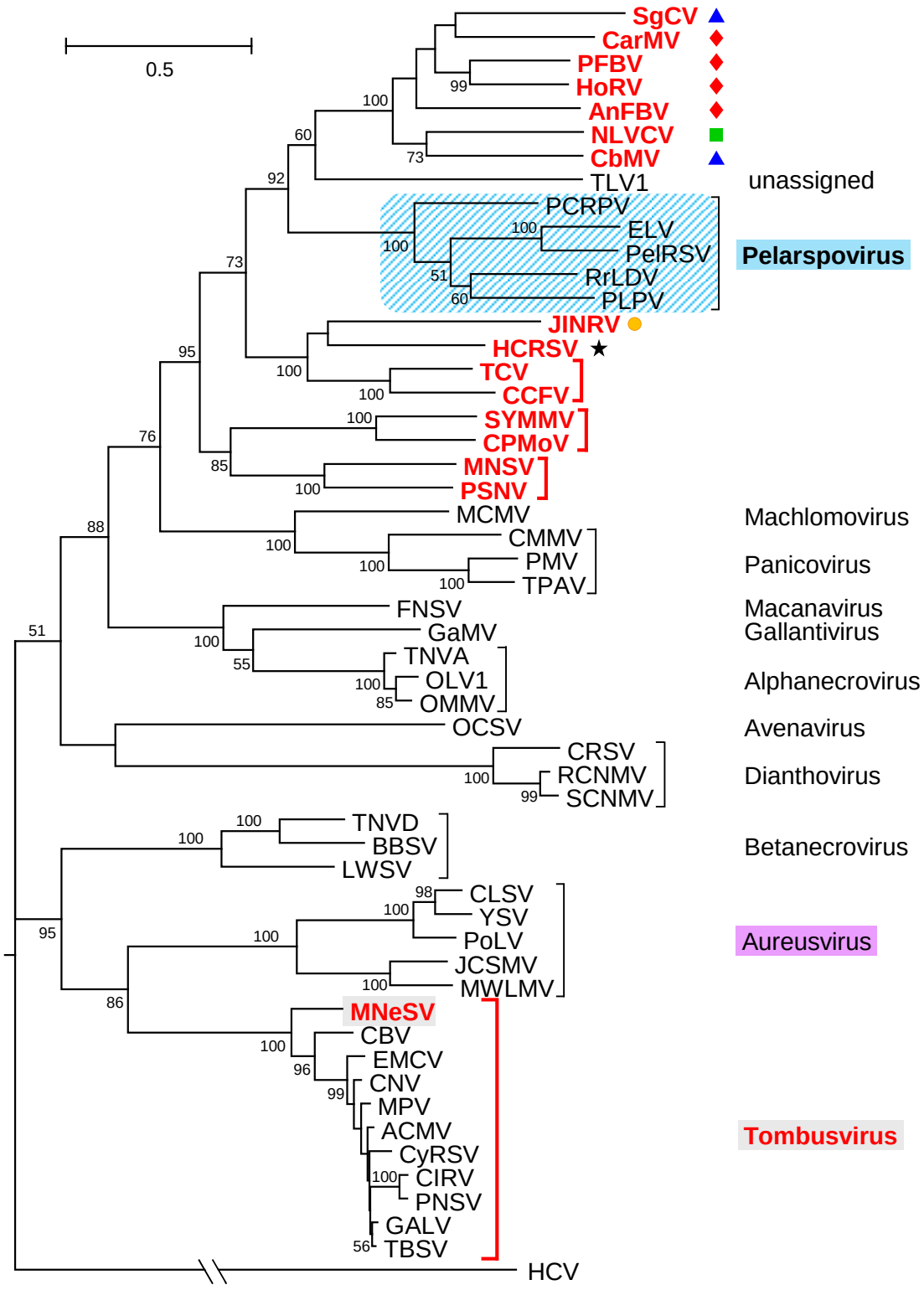

Figure 3. Phylogenetic tree from Fig. 2 with genera identified by using PASC analysis with the following nt % identity cutoffs: merge species above 82%; separate species below 80%; merge genera above 45%; separate genera below 44%. Species in alternative genera have bold red font. Brackets mark monophyletic lineages. Species that would represent alternative genera that are monotypic or not monophyletic are marked with color- and shape-specific symbols.

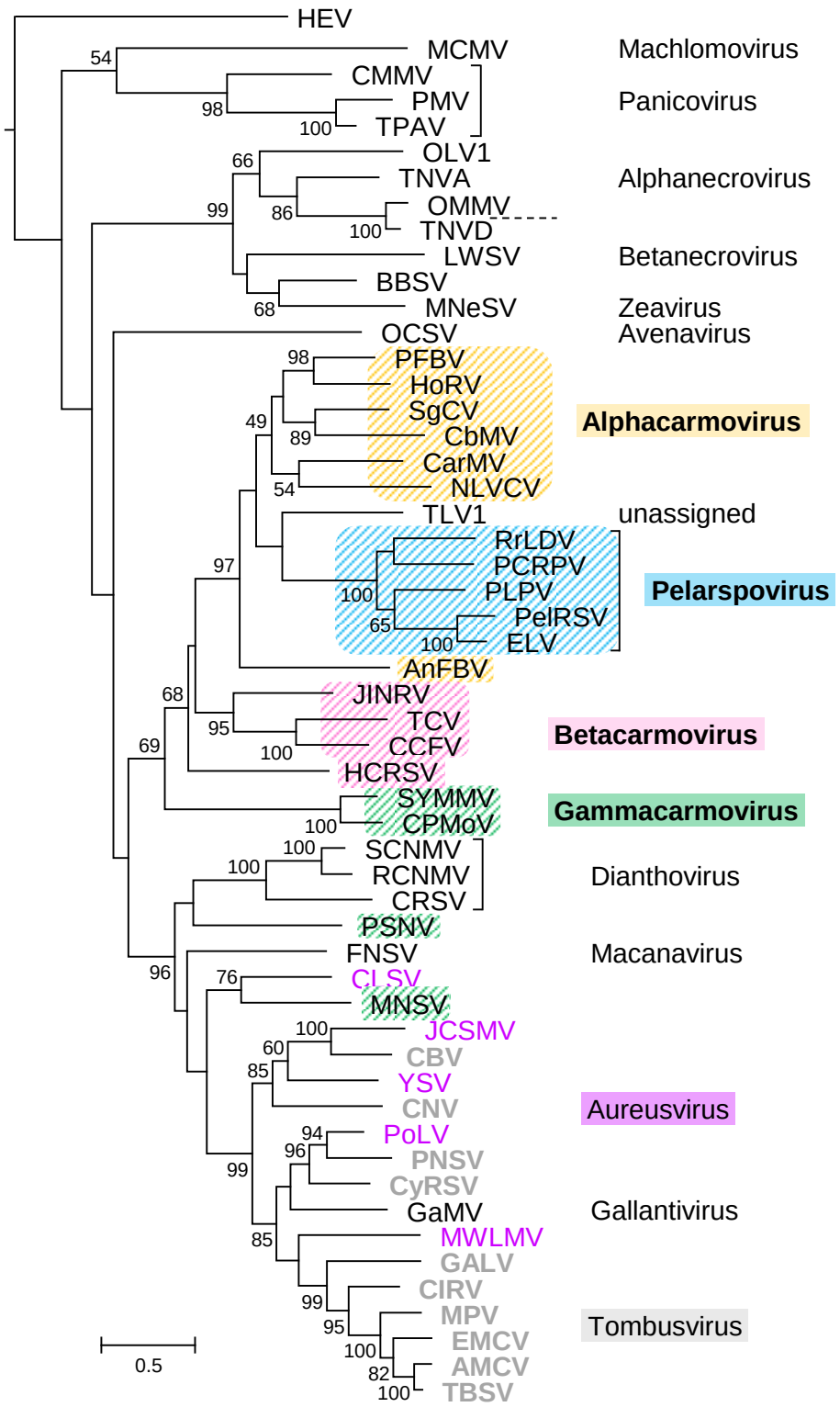

Figure 4. Phylogenetic (distance) analysis of the CPs of CP-encoding tombusvirids. Trees were generated using the same conditions as Fig. 2. There were 356 positions in the final dataset. Hepatitis E virus (HEV) CP was used as the outgroup. Brackets mark monophyletic lineages.

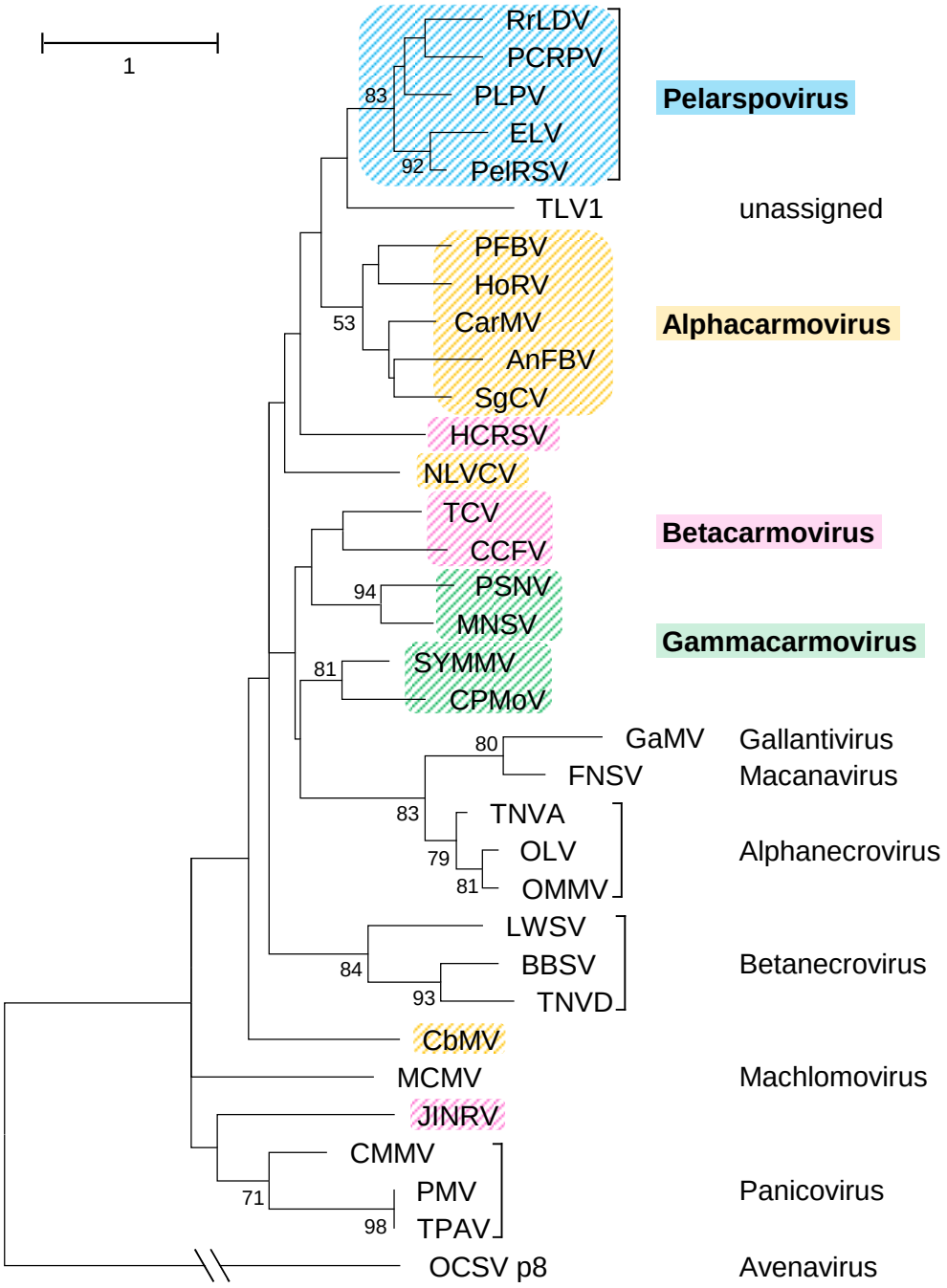

Figure 5. Phylogenetic (distance) analysis of the MP1s of CP-encoding tombusvirids. Trees were generated using the same conditions as Fig. 2. Positions with < 50% site coverage were eliminated, leaving 70 positions in the final dataset. Oat chlorotic stunt virus (OCSV) p8 was used as the outgroup. Brackets mark monophyletic lineages.

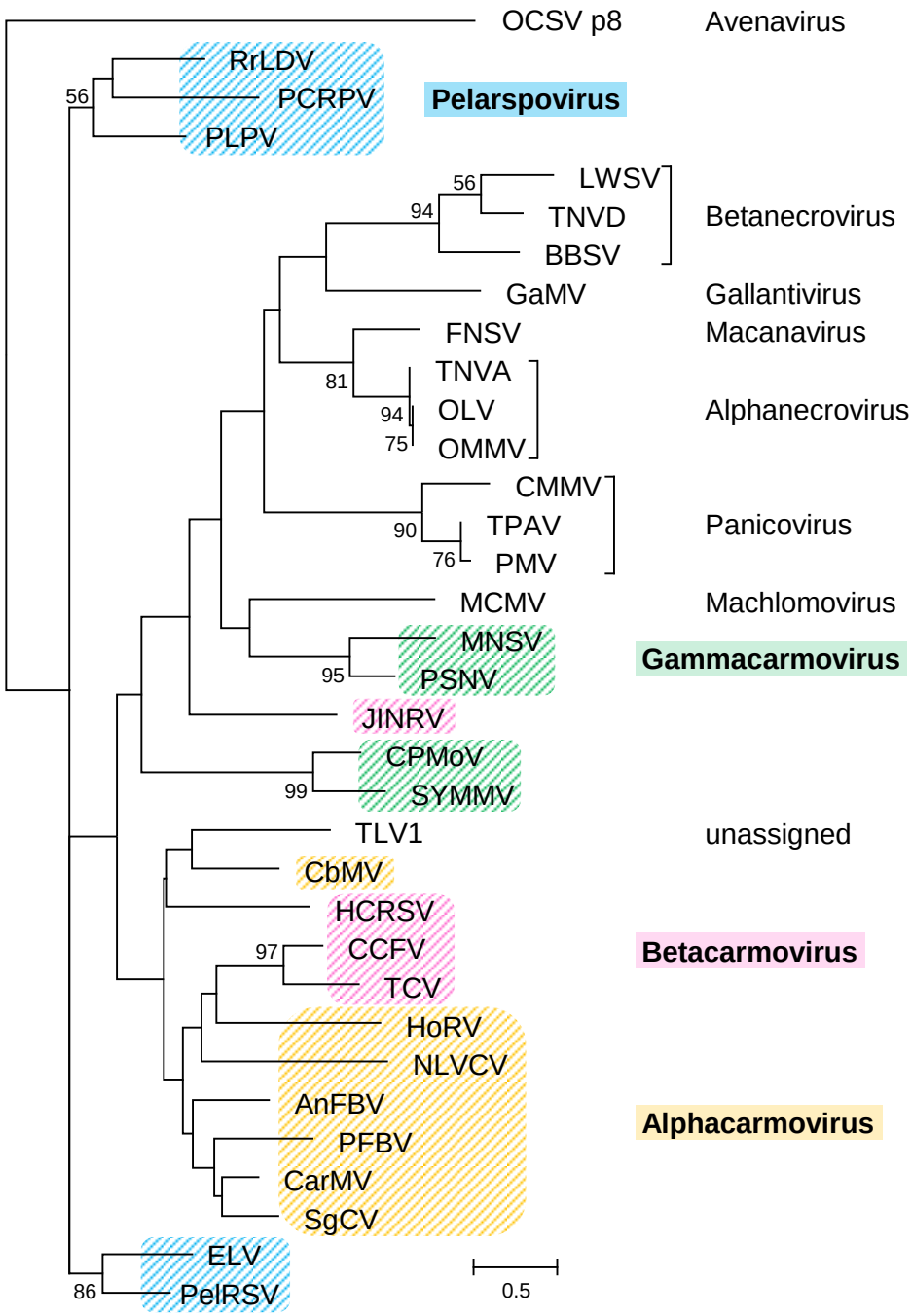

Figure 6. Phylogenetic (distance) analysis of the MP2s of CP-encoding tombusvirids. Trees were generated using the same conditions as Fig. 2. Positions with < 50% site coverage were eliminated, leaving 81 positions in the final dataset. OCSV p8 was used as the outgroup. Brackets mark monophyletic lineages.

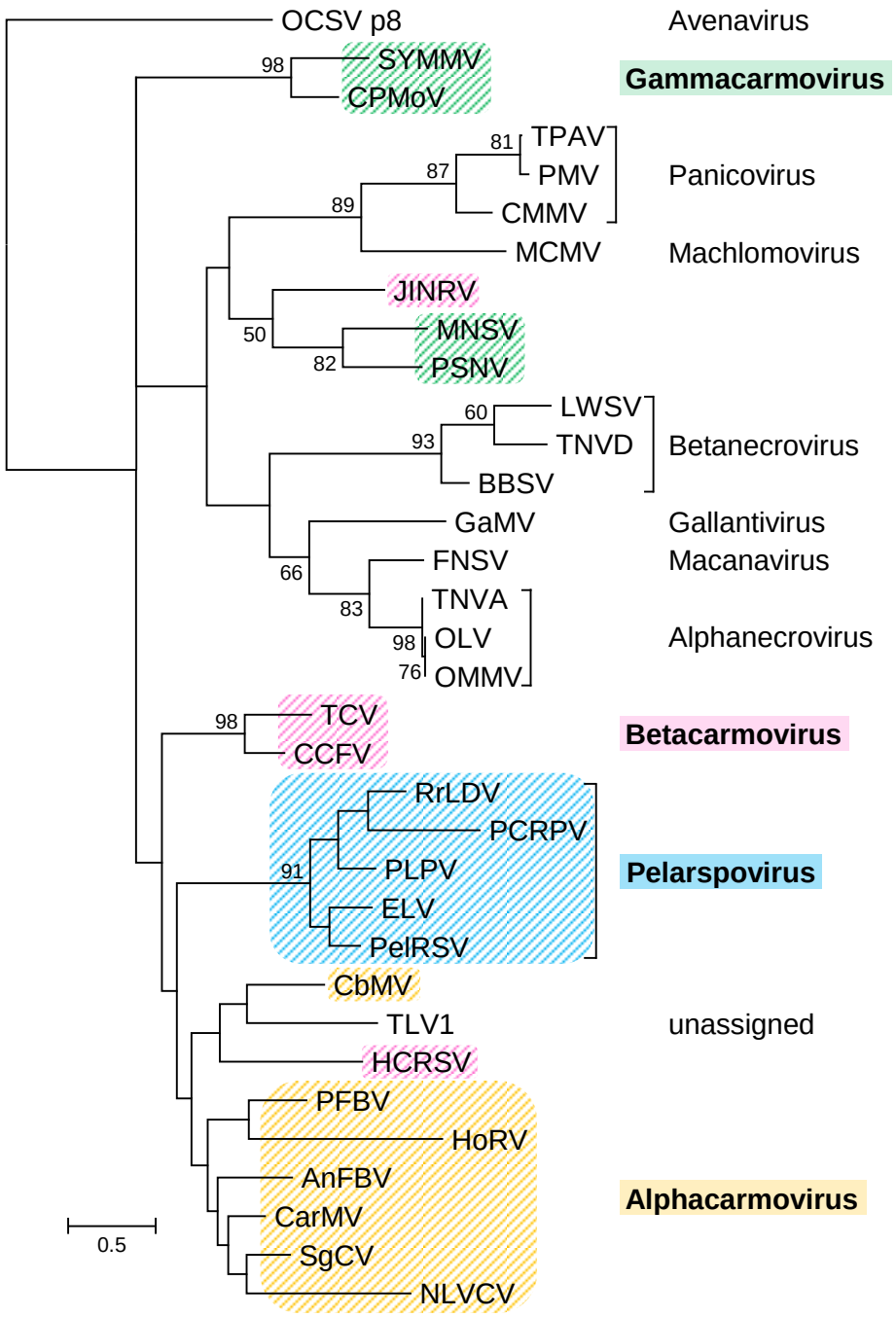

Figure 7. Phylogenetic (distance) analysis of the MP2s of CP-encoding tombusvirids. Trees were generated using the same conditions as Fig. 2 except initial alignment was performed with ClustalOmega. Positions with < 50% site coverage were eliminated, leaving 83 positions in the final dataset. OCSV p8 was used as the outgroup. Brackets mark monophyletic lineages.