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:	***2011.007aP***	(to be completed by ICTV officers)
Short title: create 4 new species in the genus *Carmovirus*		
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 study group.

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

	Tombusviridae

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

Date first submitted to ICTV: August 4, 2011
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Code	***2011.007aP***

To create 4 new species within:

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

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Calibrachoa mottle virus *Honeysuckle ringspot virus* *Nootka lupine vein clearing virus* *Soybean yellow mottle mosaic virus*	GQ244431 HQ677625 = NC_014967 EF207438 = NC_009017 FJ457015 = NC_016643

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

Biological properties of the four viruses are summarized as follows:

- Calibrachoa mottle virus (CMoV) [Gulati-Sakhuja & Liu, 2010]
  - Infected plants show interveinal chlorosis and mottling or blotching under stressed conditions
  - Mechanically transmissible
  - Not transmitted by certain tested aphids and whiteflies
  - Virions are spherical and 29-31 nm in diameter
- Honeysuckle ringspot virus (HnRSV) [Gulati-Sakhuja et al., 2011]
  - Identified in honeysuckle obtained from San Luis Obispo, California
  - Induces yellow to purple rings on honeysuckle
  - Spherical particles with 29-31 nm diameter
  - Mechanically transmissible to *Chenopodium murale*
- Nootka lupine vein clearing virus (NLVCV) [Robertson et al., 2007]
  - Originally isolated from wild lupine, *Lupinus nootkatensis* Donn in the Talkeetna Mountains of Alaska
  - Older infected plants show prominent leaf vein clearing and seedlings show mosaic symptoms
  - Virions are spherical with ~ 30 nm diameter
- Soybean yellow mottle mosaic virus (SYMMV) [Nam et al., 2009]
  - Isolated from soybean plants displaying bright yellow mosaic symptoms and reduced growth
  - Spherical particles ~30 nm diameter

Complete sequences of each have been determined (see accession numbers listed above) and these, together with the biological data, are consistent with them all being members of the genus *Carmovirus* but distinct from any of the existing species:

1. Genome organization: Figure 1 summarizes the organization of the 4 viruses. Each contains a replication protein (with the RdRp in a readthrough domain), two small cell-to-cell movement proteins (MP1 and MP2) and a coat protein of 37-38 kDa. This is similar to the type member of the genus, carnation mottle virus (CarMV). Additional possible ORFs have been identified in some viruses.
2. Phylogenetic analyses: Analyses of each gene support the inclusion of the 4 viruses with the genus *Carmovirus*. The trees for the polymerase and coat protein are shown in Figure 2. Trees for the movement proteins MP1 and MP2 are less-well supported but usually place the 4 viruses with other members of the genus *Carmovirus* (data not shown).
3. Genetic distance: Each of the proposed species show between 35 and 66% aa sequence identity (and usually less than <56%) to other members of the genus in the polymerase and between 13 and 66% (and usually less than 56%) in the coat protein (Table 1). The species demarcation criteria for the polymerase and coat protein are given as 57% and 52%, respectively, in the 9th Report but these values are lower than those for most of the other genera in the family and were derived from the actual differences between a more limited set of sequences. It is suggested that the demarcation criteria should be redefined to accommodate the new data.

MODULE 9: **APPENDIX**: supporting material

References:

Castano, A. and C. Hernandez (2005). "Complete nucleotide sequence and genome organization of Pelargonium line pattern virus and its relationship with the family Tombusviridae." Archives of virology **150**(5): 949-965.

Gulati-Sakhuja, A. and H. Y. Liu (2010). "Complete nucleotide sequence and genome organization of Calibrachoa mottle virus (CbMV)--a new species in the genus Carmovirus of the family Tombusviridae." Virus research **147**(2): 216-223

Gulati-Sakhuja, A., L. Rains, et al. (2011). "The complete nucleotide sequence and genome organization of a novel carmovirus - honeysuckle ringspot virus isolated from honeysuckle." Archives of virology. Published online May 12 2011

Kinard, G.R. and Jordan, R. (2002) Genome organization of Pelargonium chlorotic ring pattern virus: further implications for Tombusviridae taxonomy. Proc. 10th IS Virus Diseases Ornamentals, Acta Hort. 568: 17-27

Nam, M., S. M. Kim, et al. (2009). "Nucleotide sequence and genomic organization of a newly identified member of the genus Carmovirus, soybean yellow mottle mosaic virus, from soybean." Archives of virology **154**(10): 1679-1684.

Robertson, N. L., F. Cote, et al. (2007). "Complete nucleotide sequence of Nootka lupine vein-clearing virus." Virus genes **35**(3): 807-814.

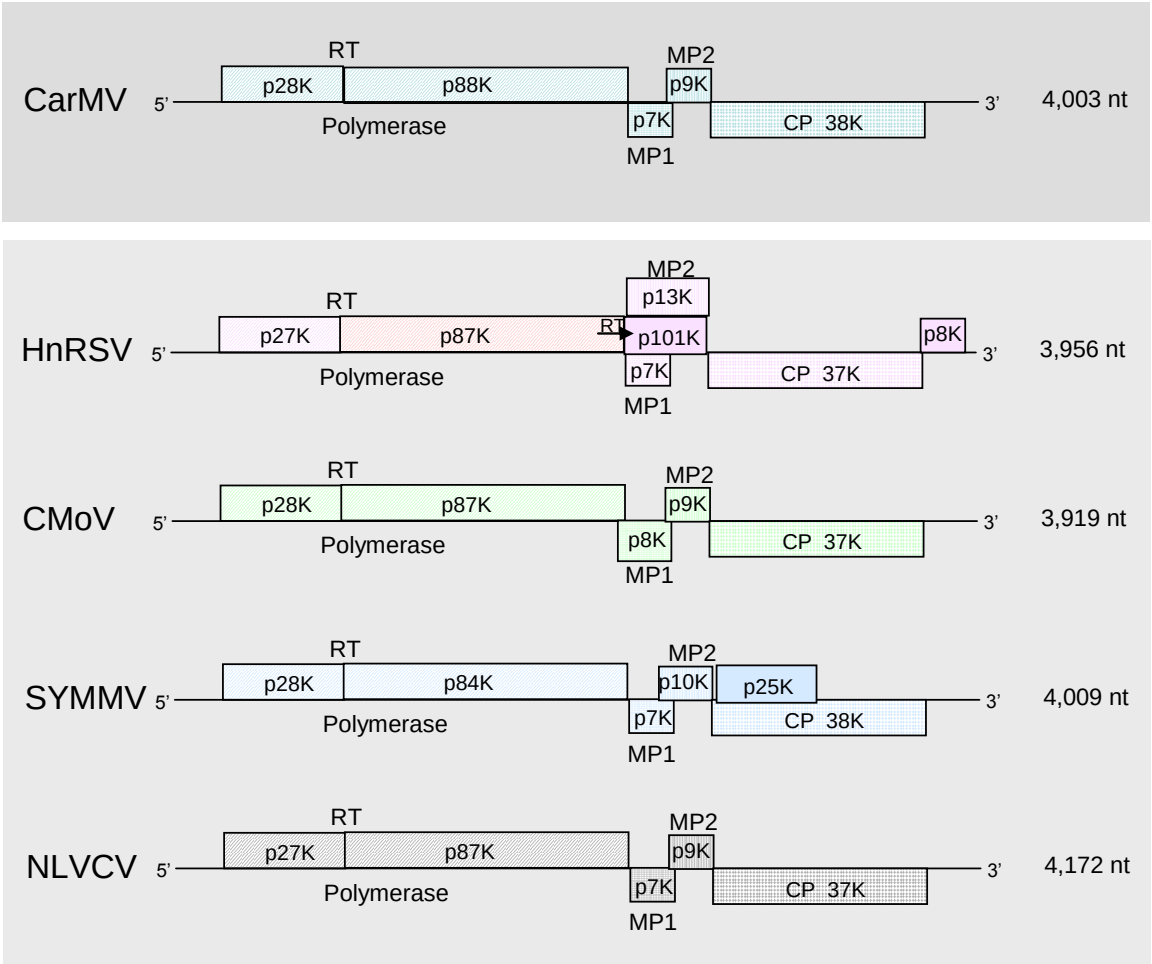

Figure 1: Genome organisation of carnation mottle virus (CarMV) and the six proposed new members of the genus *Carmovirus*. Similar line patterns indicate significant amino acid sequence identity.

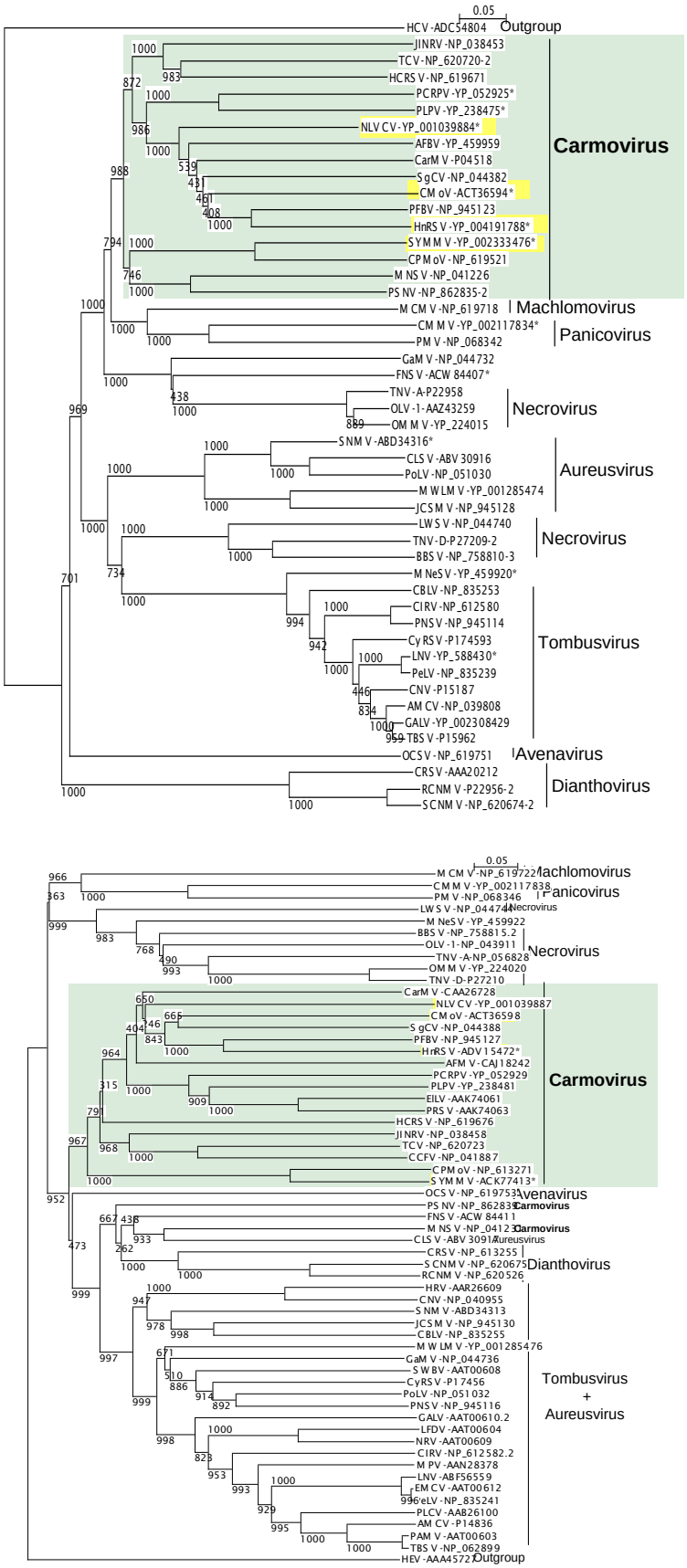

Figure 2: Phylogenetic (distance) trees of the amino acid sequences of the polymerase (top) and coat protein (bottom) genes of members of the family *Tombusviridae* showing the placing of the 4 proposed new carmoviruses (highlighted in yellow). Sequences were aligned using ClustalX 2.1 and trees generated with the Neighbor Joining algorithm using 10000 boostrap replicates.

Table 1. Comparisons between the proposed new members of the genus and existing members of the genus *Carmovirus* and other members of the family *Tombusviridae* in the four proteins encoded.

	% amino acid sequence identity to:	
	Carmoviruses*	**Other Tombusviridae Members**
CMoV		
Pol	37 - 55	23 - 37
MP1	14 - 32	5 - 23
MP2	13 - 49	10 - 21
CP	16 - 43	7 - 21
NLVCV		
Pol	35 - 50	23 - 35
MP1	19 - 32	6 - 23
MP2	9 - 36	3 - 14
CP	13 - 38	7 - 20
SYMMV		
Pol	35 - 42	22 - 37
MP1	18 - 55	8 - 25
MP2	10- 47	8 - 17
CP	16 - 66	12 - 23
HnRSV		
Pol	36 - 66	25 - 36
MP1	23 - 42	7 - 26
MP2	16 - 36	11 - 22
CP	18 - 55	7 - 21

Note that each of the new proposed carmoviruses show the greatest % identity in their encoded proteins to established members of the genus *Carmovirus*.