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:	***2011.005a-eP***	(to be completed by ICTV officers)

Short title: Create genus named *Zeavirus* 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 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:	Aug 3, 2011
Date of this revision (if different to above):	

MODULE 3: **NEW GENUS**

creating a new genus

Code	***2011.005aP***	(assigned by ICTV officers)

To create a new genus within:

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

naming a new genus

Code	***2011.005bP***	(assigned by ICTV officers)

To name the new genus: *Zeavirus*

Assigning the type species and other species to a new genus

Code	***2011.005cP***	(assigned by ICTV officers)

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

Maize 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:

Genome structure: Maize necrotic streak virus (MNeSV) is currently classified as an unassigned species of the family *Tombusviridae*. MNeSV is similar to members of the genus *Tombusvirus* in genome structure with the exception that the coat protein ORF is shorter (Fig.1). The genome contains in order beginning from the 5' terminus: an ORF for a replicase with the polymerase being present in a readthrough domain; an ORF for the coat protein and 2 ORFs in nested open reading frames encoding the movement protein (MP) and the silencing suppressor protein.

Phylogenetic analyses: Analysis of each encoded protein, except the coat protein (see below), shows that MNeSV is most closely related to the tombusviruses but is present in a separate lineage (Figs. 2,3,4).

The coat protein: The presence or absence of a coat protein protruding domain is a genus demarcation criterion in the family *Tombusviridae*. Unlike tombusviruses, the MNeSV coat protein lacks the protruding domain (Fig. 5). Phylogenetic analyses shows that the coat protein is most similar to the necrovirus coat protein which lacks a protruding domain (Fig. 6).

Genetic distance: Comparisons of the aa sequences of the proteins encoded by MNeSV and tombuviruses shows that MNeSV is genetically distinct from the tombusviruses, most strikingly in the coat protein sequence (Tables 1-4). The MNeSV polymerase is 69-74% identical to the tombusvirus polymerase, whereas tombusvirus polymerases are 75-92% identical to each other. The MP and silencing suppressor of MNeSV share 69-76% and 54-59% identity with that of tombusviruses whereas the corresponding proteins of tombusviruses share 80-97% and 60-90% identity. The coat protein shares only 9-18% identity with the tombusvirus CP versus 26-86% identity among the coat proteins of existing tombusviruses (Table 1).

Other distinguishing features: 1) Multivesicular bodies characteristic of tombusvirus infected cells are not observed in MNeSV infections; 2) MNeSV is not infectious by rub-inoculation; 3) MNeSV infects monocots whereas only one tombusvirus is known to infect monocots; 4) MNeSV is not efficiently transmitted in the soil unlike tombusviruses.

Other: MNeSV appears to have arisen from recombination between a tombusvirus and a necrovirus and it is proposed that a new genus be formed to accommodate this recombinant.

Origin of the new genus name:

From the genus name of the host, *Zea mays*

Reasons to justify the choice of type species:

Monotypic

Species demarcation criteria in the new genus:

Not applicable

MODULE 7: **REMOVE and MOVE**

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

Code	***2011.005dP***	(assigned by ICTV officers)

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

Maize necrotic streak virus

The present taxonomic position of these taxon/taxa:

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

Part (b) re-assign to a higher taxon

Code	***2011.005eP***	(assigned by ICTV officers)

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

Genus:	***Zeavirus*** (new genus: this proposal)	.
Subfamily:		
Family:	***Tombusviridae***	
Order:		

Reasons to justify the re-assignment:

See the reasons to justify the new genus (above) and the summary in Module 9

MODULE 9: **APPENDIX**: supporting material

Maize necrotic streak virus (MNeSV) Summary

Biological and physical properties:

- First identified in field corn plants in Arizona in 1998
- Symptoms include long chlorotic bands that coalesce and that may become translucent or necrotic on the edges. Stalks have chlorotic streaks that become necrotic.
- No known vector
- Particles are 32 nm in diameter
- Not transmissible by rub-inoculation

Genome properties:

- Accession number is: AF266518 = NC_007729
- The genome structure of MNeSV resembles those of tombusviruses except the CP is smaller due to the fact that it lacks a P-domain.
- The polymerase, movement protein and silencing suppressors are most similar in aa sequence to those of tombusviruses
- The coat protein is most similar to those of necroviruses
- Regulatory elements involved in transcription and replication are tombusvirus-like.

Current taxonomic status:

Unassigned member of the family *Tombusviridae*

Evolutionary considerations:

MNeSV appears to be a recombinant virus with a necrovirus CP and a tombusvirus "backbone"

Features that distinguish MNeSV from tombusviruses:

- Unlike tombusviruses MNeSV lacks the protruding domain characteristic of tombusvirus coat proteins
- Unlike most tombusviruses, MNeSV infects monocots
- Not transmissible by rub-inoculation
- Inefficient soil transmission
- Absence of distinctive multivesicular bodies characteristic of tombusvirus infected cells

References:

Louie, R. et al. (2000) Plant Dis. 84: 1133-1139.
Scheets, K. and Redinbaugh, M.G. (2006) Virology 350: 171-183.
De Stradis A., Redinbaugh M.G., Abt J.J., Martelli G.P. (2005) J Plant Path 87: 213-221

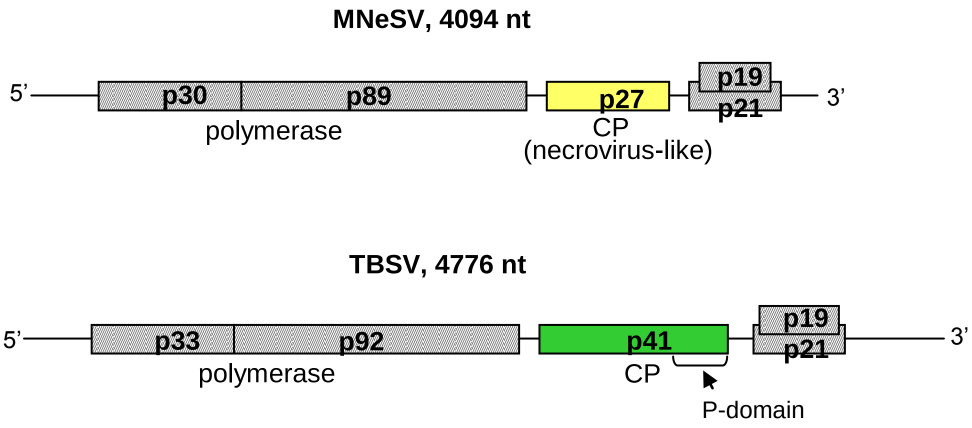

Figure 1. Genome organization of MNeSV and the tombusvirus, tomato bushy stunt virus. Shading indicates regions of aa sequence similarity (see Tables 1-4).

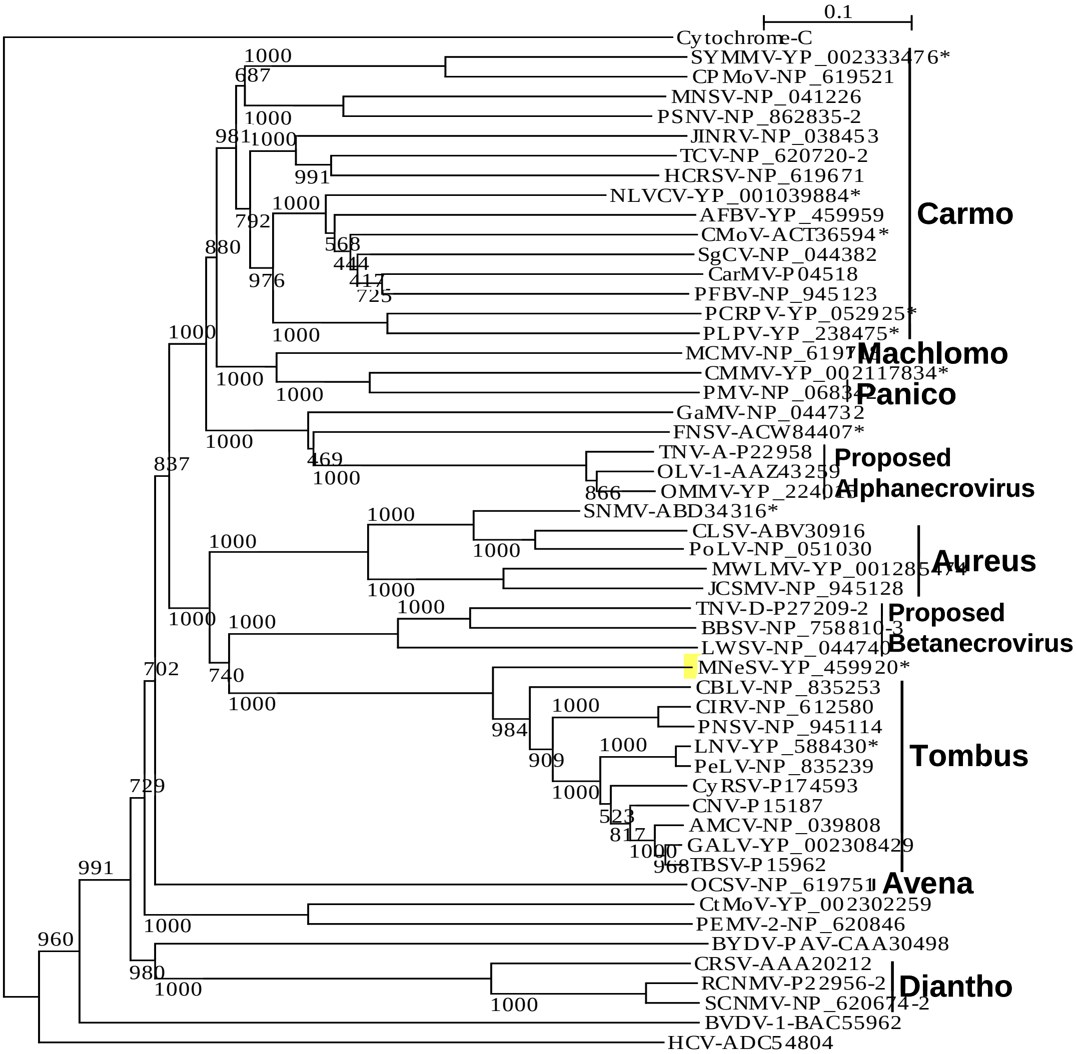

Figure 2. Phylogenetic (distance) trees of the aa sequences of the polymerase proteins of members of the *Family Tombusviridae*. The position of the MNeSV polymerase is highlighted in yellow. Sequences were aligned using ClustalX 2.1 and trees were generated by the Neighbor Joining algorithm using 1000 boostrap replicates.

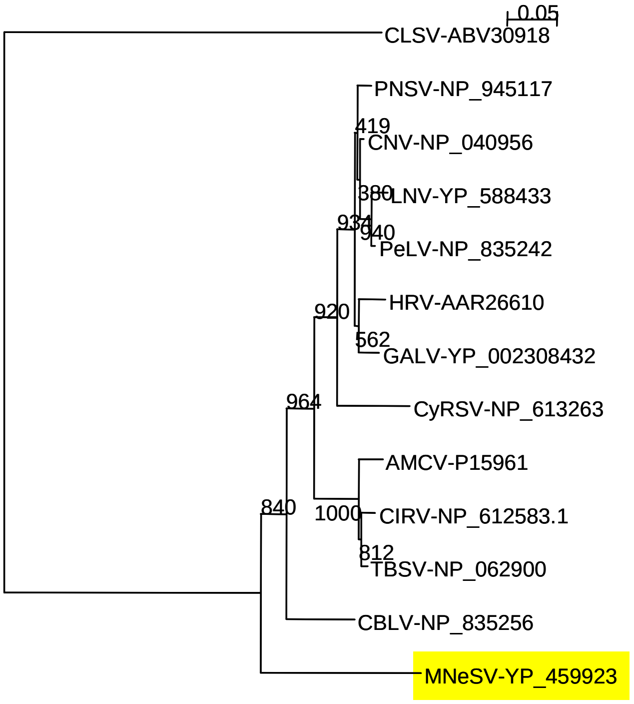

Figure 3. Phylogenetic distance trees of the movement proteins of MNeSV (highlighted in yellow) and tombusviruses. See Fig. 2 for details on tree construction.

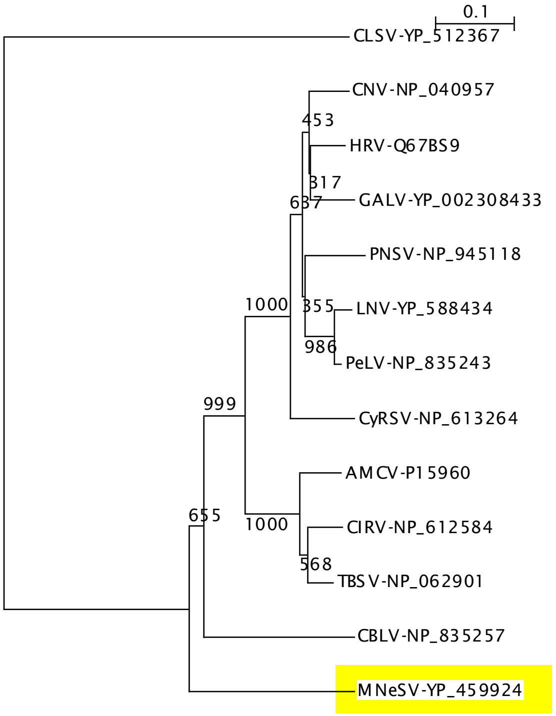

Figure 4. Phylogenetic distance trees of the silencing suppressor proteins of MNeSV (highlighted in yellow) and tombusviruses. See Fig. 2 for details on tree construction.

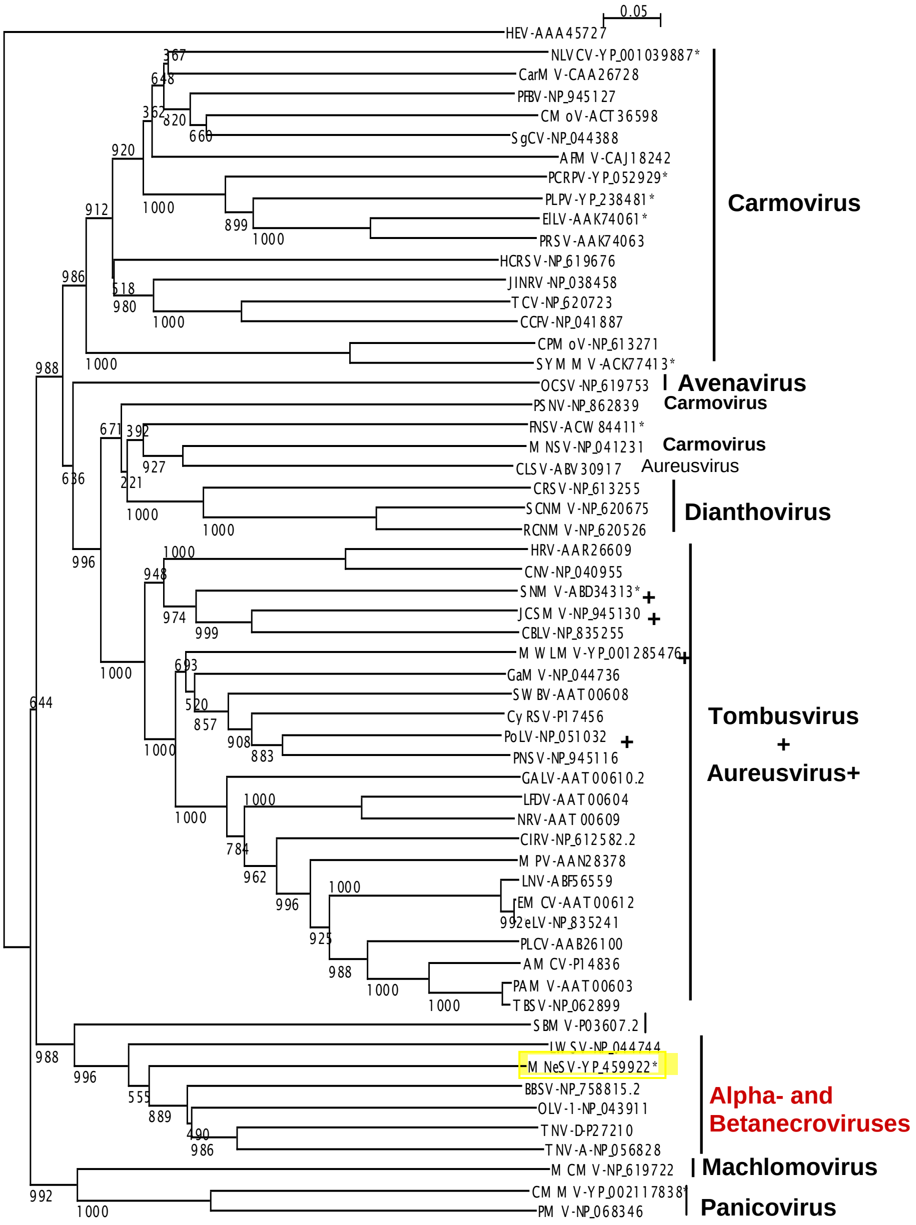

Figure 5. Phylogenetic distance tree of the coat proteins of members of the *Family Tombusviridae*. The position of the MNeSV CP is highlighted in yellow. See Fig. 2 for details on tree construction.

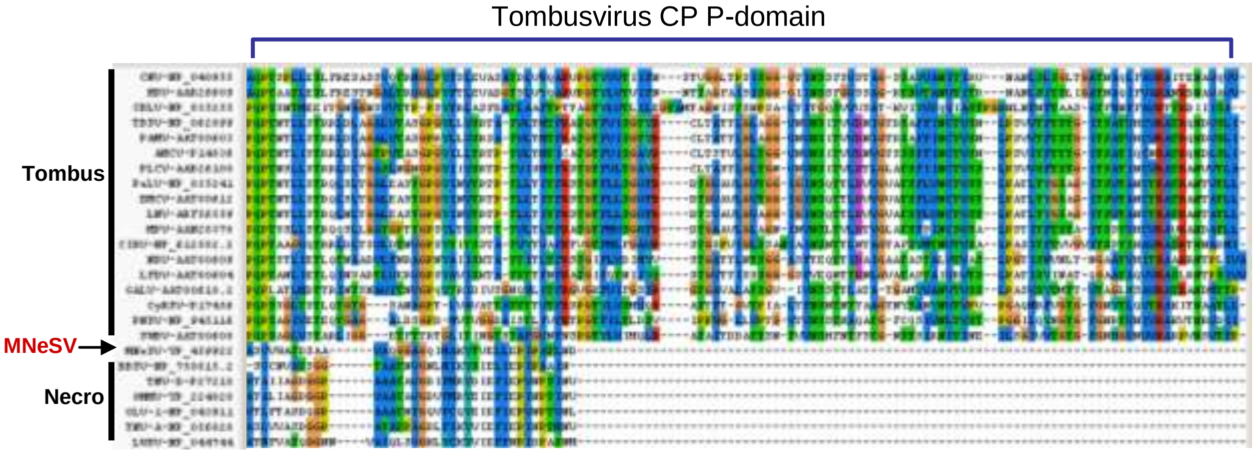

Figure 6. Alignment of the C-terminal region of the coat proteins of tombuviruses, necroviruses and MNeSV noting the absence of the P-domain in MNeSV (as in necroviruses).

Table 1

	% aa sequence identity in polymerase		
	MNeSV	Tombus	Necro
MNeSV	-	69-74	32-37
Tombus	-	75-92	31-38
Necro	-	-	32-92

Table 2

	% aa sequence identity in the movement protein	
	MNeSV	Tombus
MNeSV	-	69-76
Tombus	-	80-97

Table 3

	% aa sequence identity in the silencing suppressor	
	MNeSV	Tombus
MNeSV	-	54-59
Tombus	-	60-90

Table 4

	% aa sequence identity in coat protein		
	MNeSV	Tombus	Necro
MNeSV	-	9-18	26-38
Tombus	-	24-85	8-22
Necro	-	-	26-86

Tables 1-4. Percent aa sequence identities among the 4 indicated proteins encoded by MNeSV, tombusviruses and necroviruses. % identities were determined using Clustal W2. Note that in each case the % identity observed between MNeSV and tombusviruses is less than that observed between tombusviruses and that the % identity in the coat protein is significantly lower.