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

Code assigned:	*2011.008aP*	(to be completed by ICTV officers)

Short title: Create one new species, *Cocksfoot mild mosaic virus*, in the genus *Panicovirus*, family *Tombusviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	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 Tombusviridae Study Group

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 SG

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

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

Code	*2011.008aP*	(assigned by ICTV officers)

To create 1 new species within:

Genus:	*Panicovirus*
Subfamily:	
Family:	*Tombusviridae*
Order:	

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Cocksfoot mild mosaic virus	EU081018 = NC_011108

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

Cocksfoot mild mosaic virus (CMMV) is a virus of grasses known for many years (Huth & Paul, 1972). More recent data, including a complete genome sequence (Ziegler et al., 2009) has shown that it is most closely related to Panicum mosaic virus (PMV; the type – and currently the only- member of the genus *Panicovirus*, family *Tombusviridae*). This is demonstrated by its genome structure (Fig. 1), phylogenetic analyses (Figs. 2-4), and sequence identity in the polymerase and coat proteins (Table 1). The two viruses are serologically distinct and share only 54% amino acid sequence identity in the polymerase and 35% identity in the coat protein (Table 1).

As a monotypic genus, there are no formal species demarcation criteria but in line with other genera in the family we suggest that less than 70% amino acid sequence identity in the polymerase and less than 40% in the coat protein would justify a new species.

MODULE 9: **APPENDIX**: supporting material

References:

Huth & Paul (1972). Cocksfoot mild mosaic virus. *AAB Descriptions of Plant Viruses*, no 107.

Ziegler et al., (2009) Comparative sequence analysis and serological and infectivity studies indicate that cocksfoot mild mosaic virus is a member of the genus *Panicovirus. Arch. Virol* 154:1545-1549
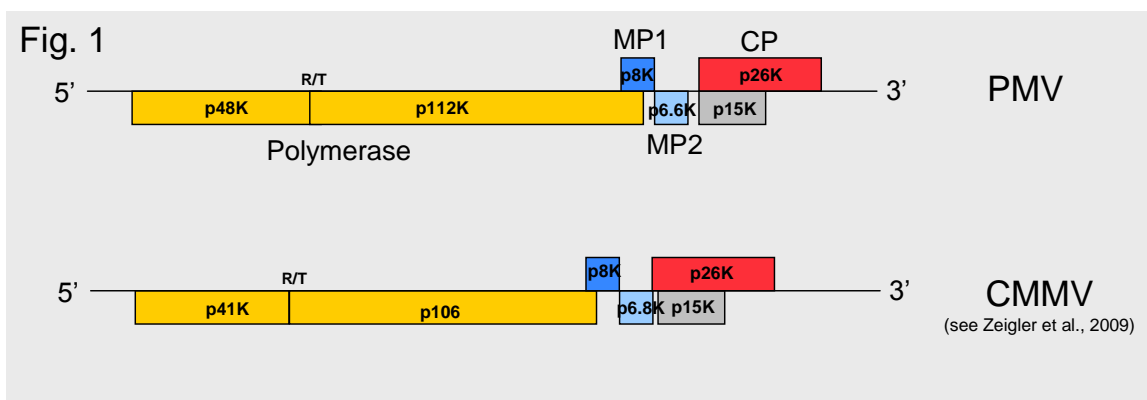

Figure 1. Comparison of the genome structure of CMMV with that of panicum mosaic virus (PMV)
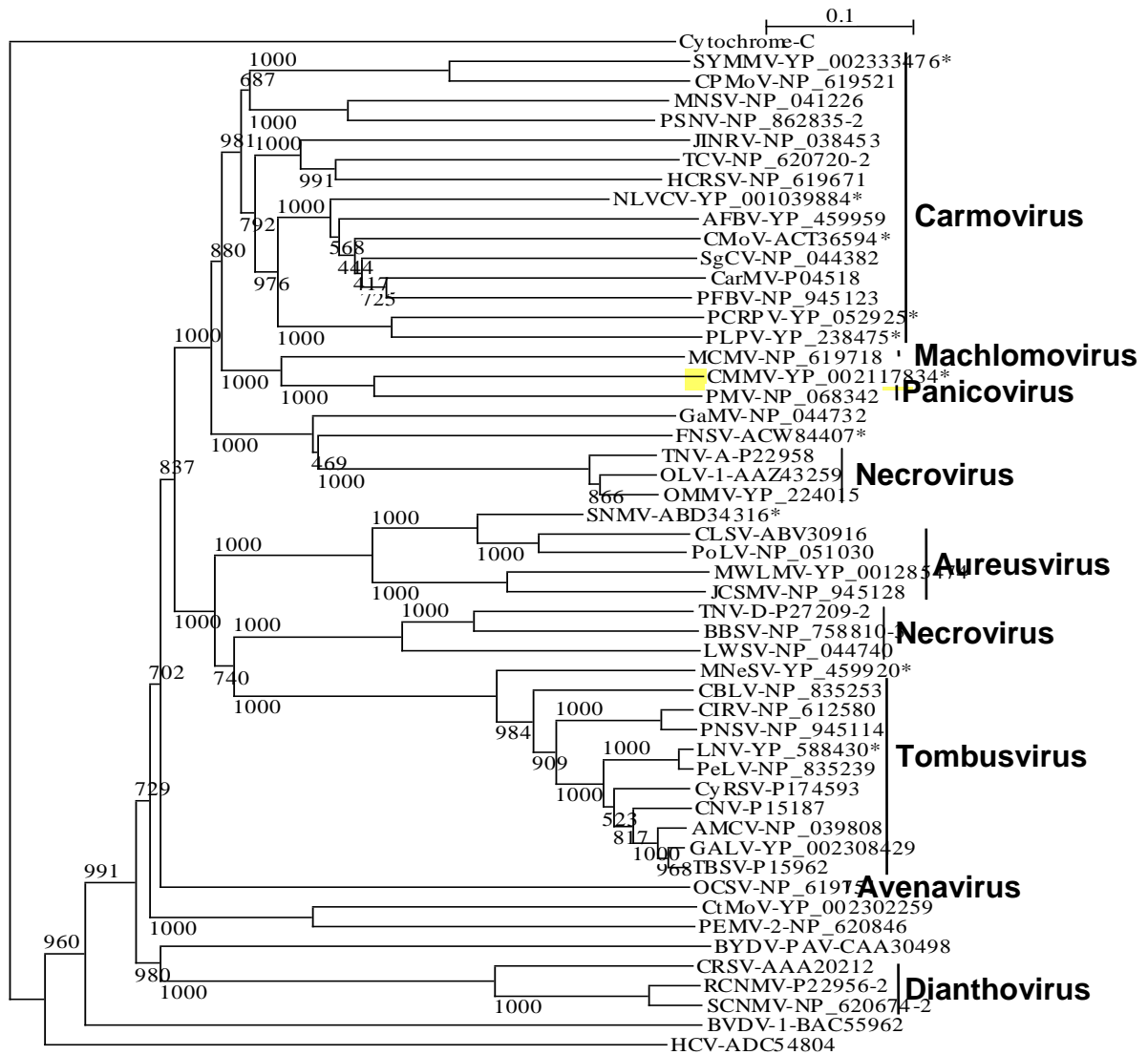
Figure 2. Phylogenetic (distance) analysis of the polymerase of *Tombusviridae* members showing the position of CMMV (highlighted in yellow) in the same lineage as PMV. Sequences were aligned using ClustalX 2.1 and trees were generated with the Neighbor Joining algorithm using 1000 bootstrap replicates.
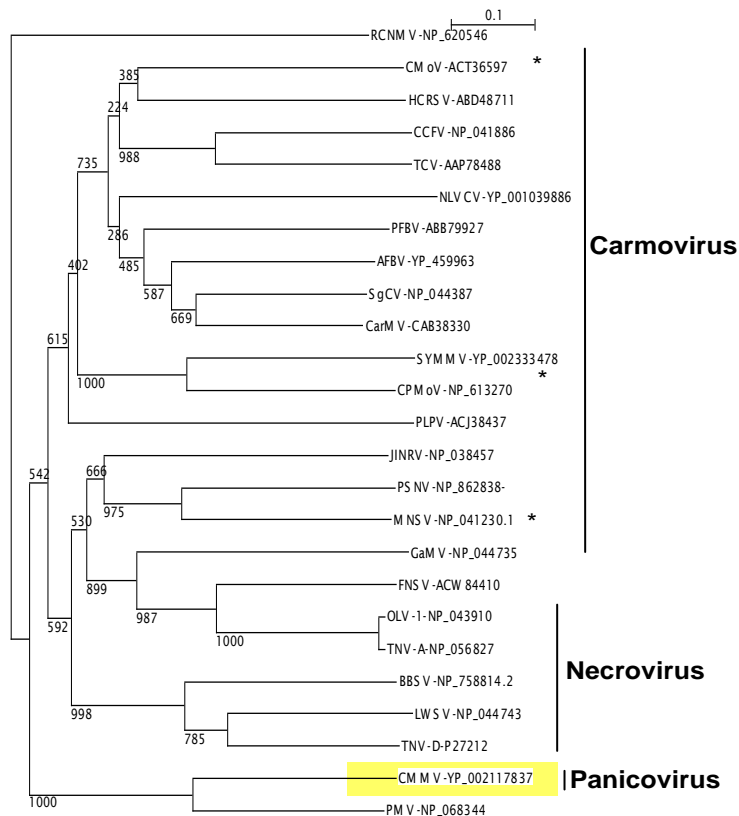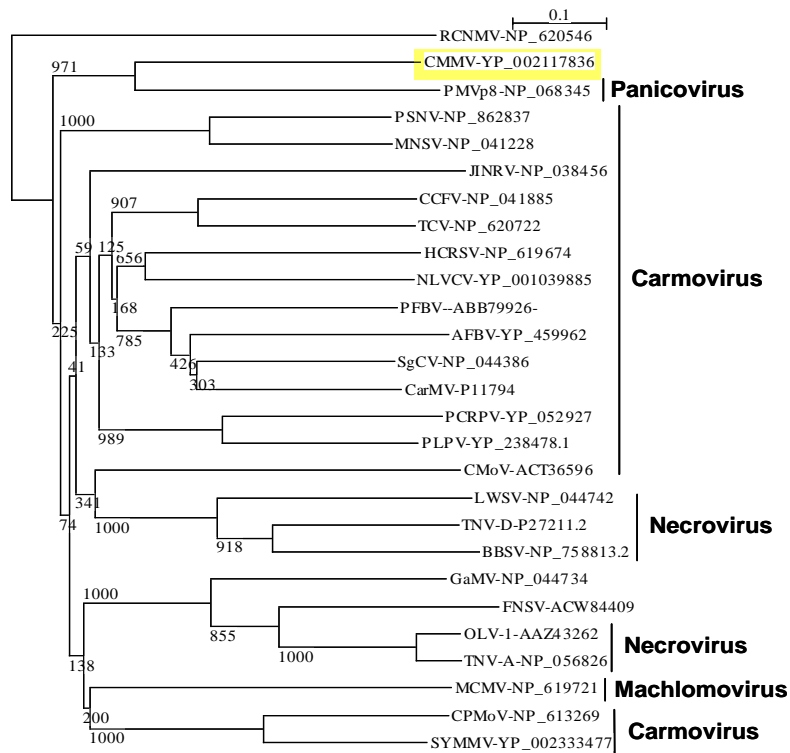
Figure 3. Phylogenetic (distance) analysis of MP1 (top) and MP2 (bottom) of *Tombusviridae* members showing the position of CMMV (highlighted in yellow) in the same lineage as PMV. Sequences were aligned using ClustalX 2.1 and trees were generated with the Neighbor Joining algorithm using 1000 bootstrap replicates.
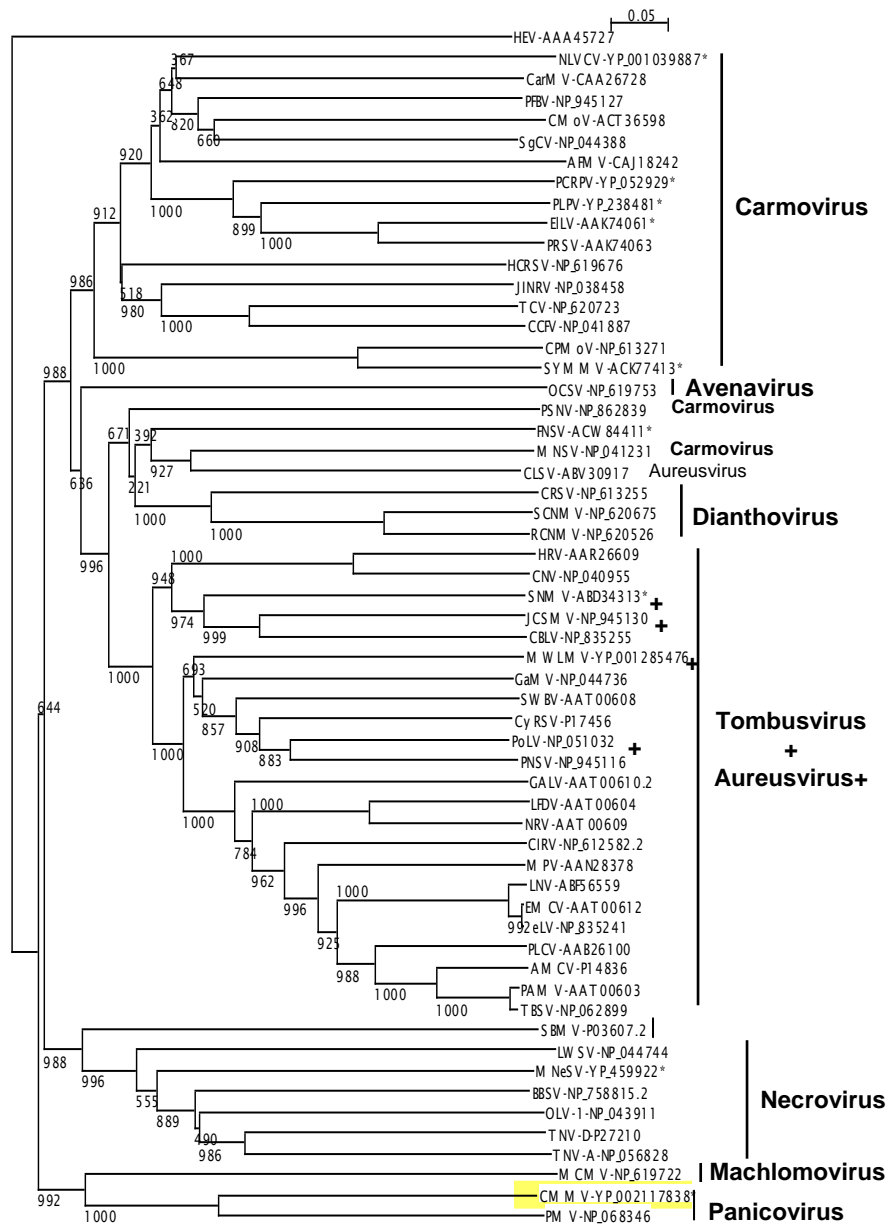
Figure 4. Phylogenetic (distance) analysis of the coat protein of *Tombusviridae* members showing the position of CMMV (highlighted in yellow) in the same lineage as PMV. Sequences were aligned using ClustalX 2.1 and trees were generated with the Neighbor Joining algorithm using 1000 bootstrap replicates.

Table 1. Percent amino acid sequence identity between proteins encoded by CMMV and those encoded by PMV and other *Tombusviridae* members.

	% Amino acid sequence identity* between CMMV and:	
	PMV	Other *Tombusviridae* members
Pre-readthrough of polymerase	34	5-27
Full polymerase	54	22-43
Coat protein	35	5-23
p8	30	8-24
p6.8K	52	5-21
p15	30	Not applicable

*Percent identity was determined using Clustal W2.