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:	***2010.012aP***	(to be completed by ICTV officers)

Short title: To create a new species unassigned in the family Tymoviridae
(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:

Dreher, Theo W. theo.dreher@oregonstate.edu (on behalf of Tymoviridae 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)	Tymoviridae

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

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

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2010.012aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Unassigned***
Subfamily:	
Family:	***Tymoviridae***
Order:	***Tymovirales***

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 genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Poinsettia mosaic virus	AJ271595

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

- 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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Key genus demarcation criteria of the family *Tymoviridae* are (see 8th ICTV Report, Dreher et al., 2005):
• 30 nm non-enveloped icosahedral particles showing the presence of both full and empty (stain-penetrating) particles when observed by negative staining EM;
• 6-7.5 kb positive strand RNA viral genome.

Members of the genus *Tymovirus*:
• have 6.0-6.7 kb genome and a single c. 0.6 kb subgenomic RNA (sgRNA);
• have genomes encoding 3 proteins: (1) RP, a c. 200 kDa replication polyprotein with methyltransferase (MTR), papain-like protease (PRO), helicase (HEL) and RNA-dependent RNA polymerase (RdRp, POL) domains; (2) OP, a 50-80 kDa proline-rich protein encoded by an almost entirely overlapping ORF that serves as movement protein and RNAi suppressor; (3) a c. 20 kDa coat protein encoded near the 3' end that is expressed from the sgRNA;
• have a 16 nt Tymobox sequence (GAGUCUGAAUUGCUUC) involved in subgenomic RNA synthesis;
• have a nonpolyadenylated genome, typically wth a tRNA-like structure at the 3' end;
• mechanically transmissible
• spread to all main tissues of the host
• associated with the formation of double-membrane vesicles at the peripheries of chloroplasts in infected leaves.

Members of the genus *Marafivirus*:
• have 6.3-6.8 genome and typically a 0.6-1.0 kb sgRNA;
• have genomes with a large polyprotein ORF that covers most of the genome and includes MTR, PRO, HEL, PRO and CP domains; a second ORF may be present;
• have a 16 nt Marafibox sequence [CA(G/A)GGUGAAUUGCUUC] related to but distinct from the Tymobox;
• have a polyadenylated genome (except MRFV);
• have particles comprised of major and minor CP forms (21 kDa and 23-25 kDa, respectively);
• are phloem-restricted and not mechanically transmissible;

• in some cases (OBDV, MRFV, BELV) are vectored by insects in a persistent-propagative manner with replication occurring in the insect.

Within the genera of the *Tymoviridae*, species demarcation criteria include:
• overall nucleotide sequence identity less than 80%

- Overall sequence identity less than 80%
- Coat protein sequences less than 90% identical
- Differential host range

Poinsettia mosaic virus (PnMV) properties

PnMV was listed in the 8th ICTV Report (Dreher et al., 2005) as an unassigned species, following earlier submission to ICTV recommending this status (before creation of the family *Tymoviridae*). Apparently the records relating to this recommendation and subsequent ICTV decision cannot now be found. This submission is thus not new, but intended to complete formal taxonomic placement for PnMV.

PnMV infection is restricted to Poinsettia, *Euphorbia pulcherrima*, in which commercially traded plants it has world-wide distribution. Symptoms range from inapparent to light mottling. The virus is mechanically transmissible and not phloem-limited. The genome of an isolate from Germany (Poinsettia cv Angelika) has been completely sequenced (Bradel et al., 2000, Virology, 271:289-297). The genome sequence revealed close similarities to the marafiviruses (Fig. 1), while infection properties are more like those of the tymoviruses. Sequence relationships support classification that is distinct from either genus (Fig. 2).

Properties like those of genus *Marafivirus:*
• the genome encodes a long polyprotein ORF that spans most of the genome, with MTR, PRO, HEL, POL and CP domains;
• the genome is polyadenylated;
• a Marafibox sequence is present in the genome;

Properties like those of genus *Tymovirus:*
• mechanical transmissibility
• replication in leaf tissues to high titre, not phloem-restricted
• apparently comprised of a single CP

PnMV thus has characteristics of both tymoviruses and marafiviruses, and thereby fits into neither genus. PnMV RNA has only 60% identity to the OBDV marafivirus genome and 35% identity in CP sequences. Further, phylogenetic trees of both the POL and CP sequences indicate that PnMV is distinct from the marafivirus and tymovirus lineages (Fig. 2) and may be more closely related to the maculaviruses. Maculavirus genomes do not possess a tymobox or marafibox sequence and have a CP ORF that is separate from the replication polyprotein ORF. Maculaviruses are phloem-limited and not mechanically transmissible.

PnMV thus has properties distinct from all three genera of the *Tymoviridae*, supporting classification as an Unassigned Species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Dreher T.W., Edwards M.C., Gibbs A.J., Haenni A-L., Hammond R.W., Jupin I., Koenig R., Sabanadzovic S., Abou Ghanem-Sabanadzovic N., Martelli G.P. (2005). Family Tymoviridae. In Fauquet C.M., Mayo M., Maniloff J., Desselberger U., Ball L.A. (Eds.): Virus Taxonomy (Eight Report of the ICTV). Elsevier/Academic Press, London pp 1061-1074.

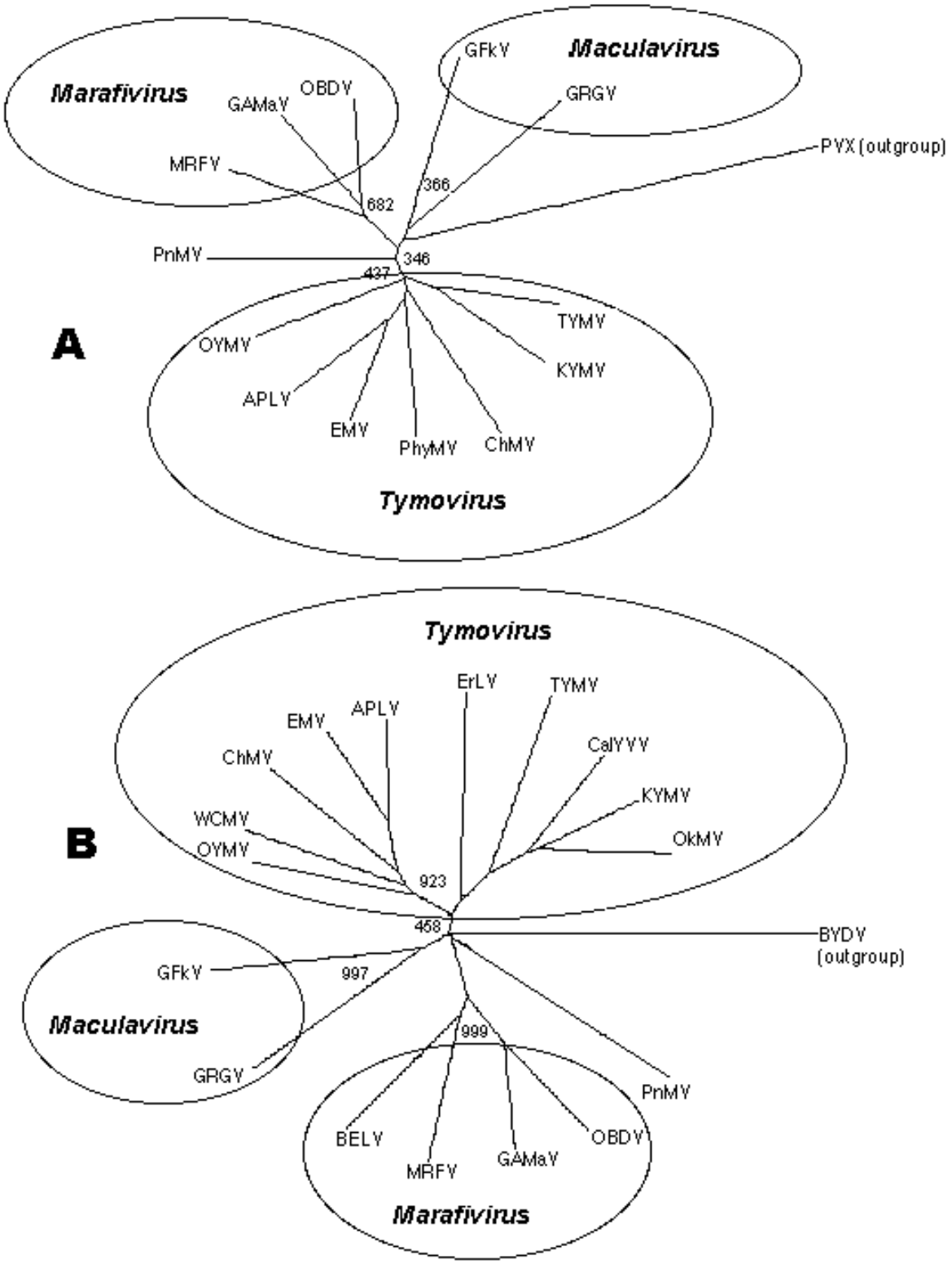
Bradel, B.G.,, Preil, W. and Jeske, H. (2000) Sequence analysis and genome organization of Poinsettia mosaic virus (PnMV) reveal closer relationship to marafiviruses than to tymoviruses. Virology 271, 289-297.

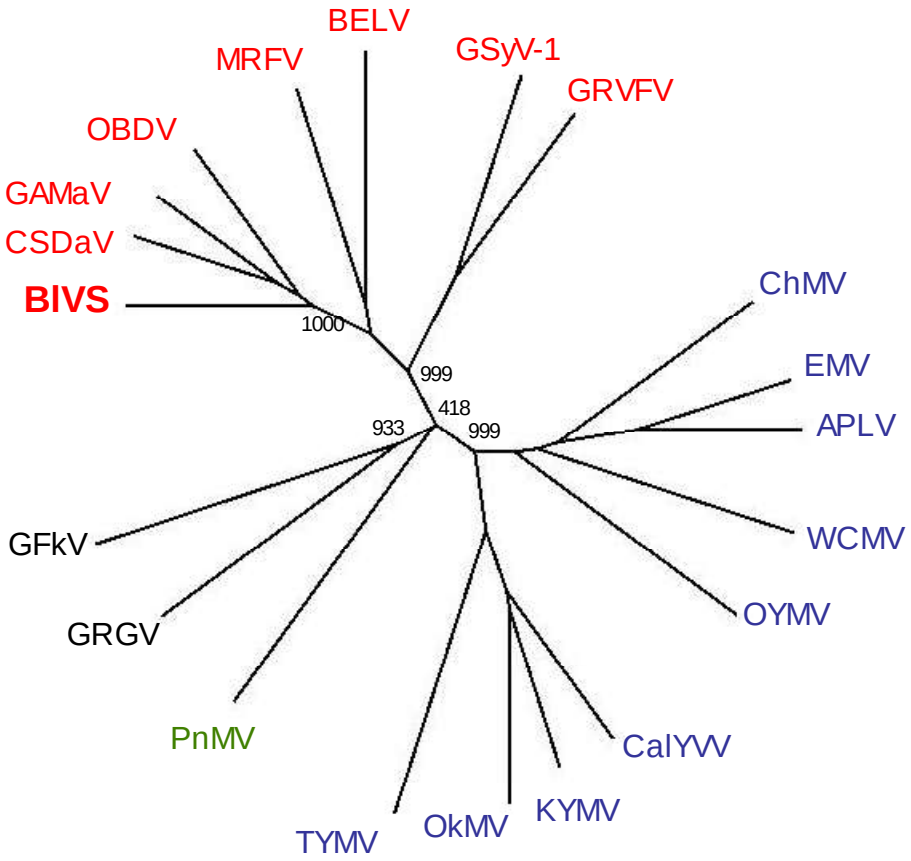
Annex:

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.

Figure 1. Diagrammatic representation of the PnMV genome indicating the domains within the single long open reading frame (from 8th ICTV Report, Dreher et al., 2005).

Figure 2. Phylogenetic tree showing the relationship of PnMV to other species and genera of the family *Tymoviridae.* (A) Unrooted tree constructed with RdRp (Pol) sequences and (B) tree constructed with CP sequences.





Additional CP phylogeny, showing absence of clustering with either the marafiviruses (red) or tymoviruses (blue). Maculaviruses are shownin black.