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:	***2013.012a,bP***	(to be completed by ICTV officers)

Short title: Re-assign the species *Tomato mild mottle virus* to the genus *Ipomovirus*
(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** ☒	

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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)	*Potyviridae*

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

Date first submitted to ICTV: June 2013
Date of this revision (if different to 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	***2013.012aP***	(assigned by ICTV officers)

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

Tomato mild mottle virus

The present taxonomic position of these taxon/taxa:

Genus:	***Unassigned***	Fill in all that apply.
Subfamily:		
Family:	***Potyviridae***	
Order:		

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

Part (b) re-assign to a higher taxon

Code	***2013.012bP***	(assigned by ICTV officers)

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

Genus:	***Ipomovirus***	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.
Subfamily:		
Family:	***Potyviridae***	
Order:		

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

Tomato mild mottle virus (ToMMoV) is currently an unassigned species in the family *Potyviridae*. There is now a complete sequence of this virus (HE600072) and also of the related eggplant mild leaf mottle virus (HQ840786; Dombrovsky et al., 2012). The two sequences are about 80% identical and Abraham et al., (2011) therefore suggest that EMLMV should be regarded as a strain of ToMMoV. Both viruses have been transmitted experimentally by whiteflies while Abraham et al., (2011) were unable to confirm earlier reports that ToMMoV could be transmitted by aphids. Phylogenetic analysis using the complete polyprotein suggests that these viruses are distant members of the genus *Ipomovirus* (Annex, Figure 1). Whitefly transmission is a distinctive feature of viruses in this genus. We therefore propose that the species *Tomato mild mottle virus* should be re-assigned to the genus *Ipomovirus* and that Eggplant mild leaf mottle virus should be regarded as a strain. It is clearly distinct from existing species in the genus: the polyprotein of ToMMoV has about 51% nt and 38% aa identity to that of *Sweet potato mild mottle*, the type (and genetically closest) member of the genus. In a recent report by Dombrovsky et al. (2013) it was suggested that the formerly named EMLMV is unequivocally a whitefly-transmitted virus and should be considered a distant strain of ToMMoV.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Abraham A, Menzel W, Vetten HJ, Winter S (2011). Analysis of the tomato mild mottle virus genome indicates that it is the most divergent member of the genus *Ipomovirus* (family *Potyviridae*). Archives of Virology 157(2), 353-357, DOI: 10.1007/s00705-011-1167-9

Adams MJ, Zerbini FM, French R, Rabenstein F, Stenger DC, Valkonen JPT. (2011). Family *Potyviridae*. In: Virus Taxonomy, Ninth Report of the International Committee on Taxonomy of Viruses (A.M.Q. King, M.J. Adams, E.B. Carstens & E.J. Lefkowitz, eds), pp. 1069-1089. Elsevier Academic Press, London.

Dombrovsky A, Sapkota R, Lachman O, Antignus Y (2012). Eggplant mild leaf mottle virus (EMLMV), a new putative member of the genus *Ipomovirus* that harbors an HC-Pro gene. Virus Genes 44(2):329-337, DOI: 10.1007/s11262-011-0686-5

Dombrovsky A, Sapkota R, Lachman O, Pearlsman M, Antignus Y (2012). A new aubergine disease caused by a whitefly-borne strain of *Tomato mild mottle virus* (TomMMoV). Plant Pathology. DOI: 10.1111/ppa.12004

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: Maximum likelihood phylogenetic tree using the codon-aligned complete polyprotein coding sequences of fully sequenced members of the family *Potyviridae*. Only selected viruses in the genus *Potyvirus* are shown. Tree produced in MEGA5.10 with 1,000 bootstrap replicates. Tomato mild mottle virus (ToMMV) is highlighted in red. Virus abbreviations were as listed in the *Potyviridae* chapter of the Ninth Report of the ICTV (Adams et al., 2011). Accession numbers used in this alignment were also as listed in the Ninth Report for the type isolate of each species with the caladenia virus A (CalV-A, accession number JX156425) and rose yellow mosaic virus (RoYMV, accession number JF280796).