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:	***2016.001aP***	(to be completed by ICTV officers)

Short title: Create two new species in the genus *Tobamovirus*, family *Virgaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Adams MJ, Kumar A, Mandal B, Salem N, Turina M, Adkins S, Bragard C, Gilmer D, Li D, MacFarlane SA, Man WS, Melcher U, Ratti C, Ryu KH

Corresponding author with e-mail address:

Mike Adams (mike.adams.ictv@gmail.com)

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)	Virgaviridae and Benyviridae

ICTV Study Group comments (if any) and response of the proposer:

Approved unanimously

Date first submitted to ICTV: June 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2016.001aP***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Tobamovirus***
Subfamily:	
Family:	***Virgaviridae***
Order:	

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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Plumeria mosaic virus	Plu-Ind-1	KJ395757
Tomato brown rugose fruit virus	Tom1-Jo	KT383474

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 11

The genus *Tobamovirus* contains viruses with a monopartite ssRNA+ genome encapsidated in rigid rod-shaped particles. They have no known natural vectors but are readily transmitted by mechanical inoculation. Viruses belonging to other genera in the family *Virgaviridae* have divided genomes with 2 or 3 components and have different modes of transmission (seed, nematodes, fungoid protists) but there are clear phylogenetic relationships between some of the major gene products. Genome organization is conserved within each of the genera. In members of the genus *Tobamovirus* the first major ORF is a replication protein of 126-130 kDa with a 'leaky' stop codon that, when suppressed, extends the protein into an RdRp domain and results in a product of about 185 kDa. A cell-to-cell movement protein of about 30 kDa and a single coat protein of about 18 kDa are encoded in ORFs located downstream or the replicase and are translated from separate subgenomic mRNAs.

Species discrimination criteria within the genus as listed in the 9th report are:

- Sequence similarity: less than 10% overall nt sequence difference is considered to characterize strains of the same species, although most of the sequenced species have considerably less than 90% sequence identity
- Host range: many of these viruses have wider and more overlapping host ranges in experimental rather than natural situations
- Antigenic relationships between the CPs

Sequence comparisons and phylogenetic analysis (Annex Fig. 1) justify the creation of two new species as summarized below:

Plumeria mosaic virus (Kumar *et al.*, 2013)

Virus isolates were obtained from frangipani (*Plumeria rubra* f. *acutifolia*) plants in India showing greenish mosaic, vein banding, necrotic spots and ring symptoms on their leaves. Purified virus was transmitted to *Nicotiana benthamiana* and seven other plant species and the variety of symptoms produced following transfer from *Gomphrena globosa* to *N. benthamiana* suggested that more than one virus might be present. RNA isolated from virus purified from frangipani was used for sequencing using degenerate primers designed to amplify tobamoviruses and two distinct sequences were obtained. One was clearly an isolate of the existing species, *Frangipani mosaic virus* (FrMV) having 98.3% sequence identity to an American isolate. A second isolate named Plumeria mosaic virus (PluMV) had only 71.7-71.9% sequence identity to FrMV isolates and <50% to other tobamoviruses.

Tomato brown rugose fruit virus (Salem *et al.*, 2016)

A virus was isolated from greenhouse-grown tomatoes in Jordan that had mild foliar symptoms at the end of the season but strong brown rugose symptoms on fruits that greatly affected the market value of the crop. Back-inoculation from a single local lesion on *Nicotiana tabacum* cv. White Burley reproduced mosaic symptoms on tomato plants. The virus was sequenced from overlapping RT-PCR clones and the genome ends determined by RACE. In phylogenetic analyses the sequence obtained forms a distinct branch within the tobamoviruses infecting solanaceous plants but does not group convincingly with any of the existing species. It had the highest nucleotide sequence identity (82.4 %) with the strain Ohio V of tobacco mosaic virus and thus fulfils the criteria for creation of a new species. The name tomato brown rugose fruit virus (ToBRFV) was suggested. The viruses infecting tobacco, tomato and other solanaceous plants form a tight cluster within the genus *Tobamovirus* and species demarcation criteria may need re-examination in the future, but this proposal is consistent with recent policy on species creation.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

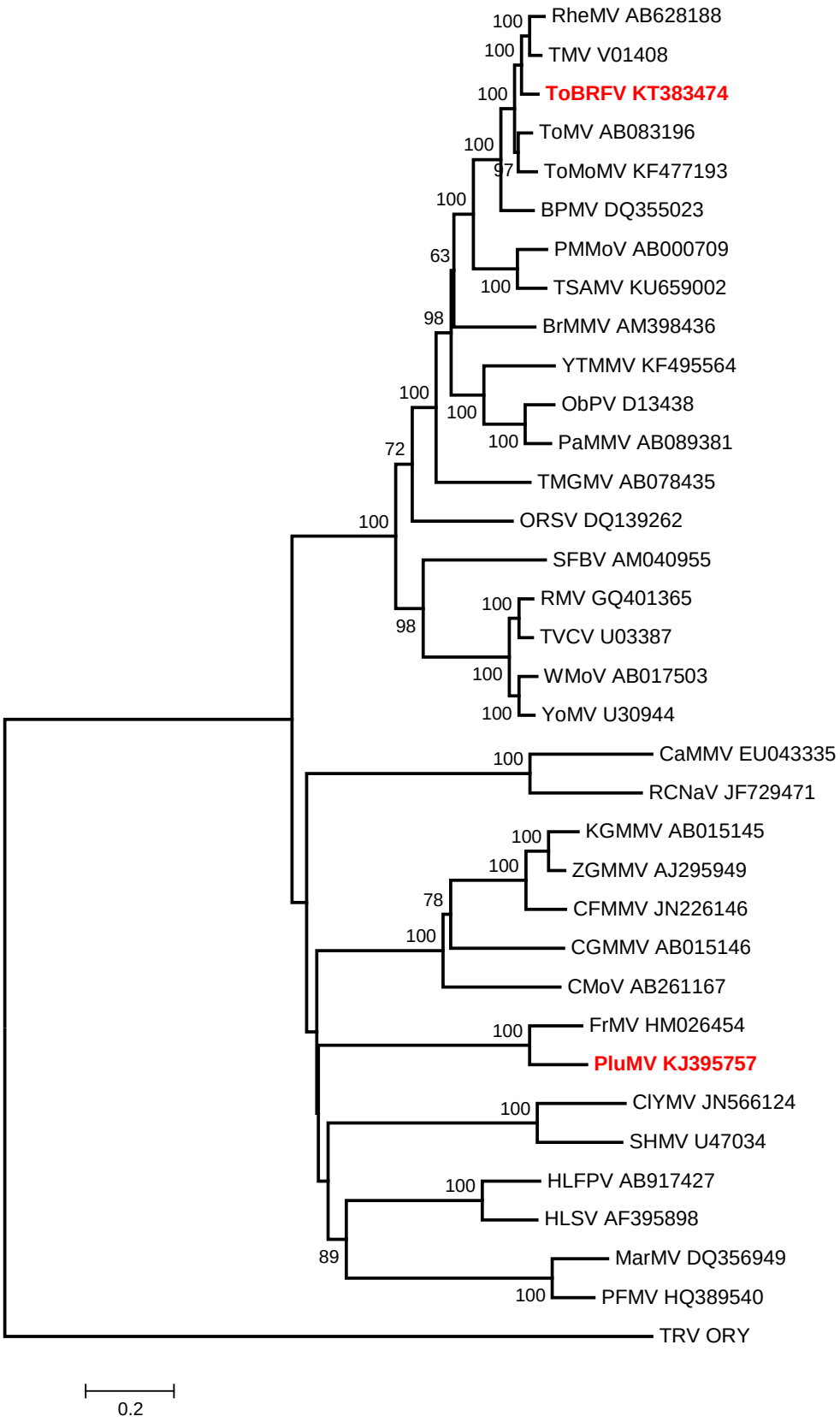
Kumar A., Solanki V., Madal, B. (2013). Frangipani mosaic virus and Plumeria mosaic virus: Identification and Comparison of two tobamovirus infecting Frangipani in India. Proceedings of the Asia-Pacific Congress of Virology, 2013, at Amity University Noida.

Salem N., Mansour A., Ciuffo M., Falk B.W., Turina M. (2016). A new tobamovirus infecting tomato crops in Jordan. Arch. Virol. 161(2):503-506.

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. Phylogenetic (Neighbor joining) tree of the concatenated protein sequences (entire proteome) of tobamoviruses with Tobacco rattle virus (TRV, genus *Tobravirus*) as outgroup. A single sequence has been chosen to represent each of the existing species for which a complete genome sequence is available. Tree prepared in MEGA7 with JTT amino acid substitutions. Bootstrap percentages from 1000 replicates are shown at the branches (where >60%). Viruses being used to propose new species are shown in red. BPMV, bell pepper mottle virus; BrMMV, Brugmansia mild mottle virus; CaMMV, cactus mild mottle virus; ClYMV, Clitoria yellow mottle virus; CFMMV, cucumber fruit mottle mosaic virus; CGMMV, cucumber green mottle mosaic virus; CMoV, cucumber mottle virus; FrMV, Frangipani mosaic virus; HLFPV, Hibiscus latent Fort Pierce virus; HLSV, Hibiscus latent Singapore virus; KGMMV, Kyuri green mottle mosaic virus; MarMV, Maracuja mosaic virus; ObPV, Obuda pepper virus; ORSV, Odontoglossum ringspot virus; PaMMV, paprika mild mottle virus; PFMV, passion fruit mosaic virus; PMMoV, pepper mild mottle virus; PluMV, Plumeria mosaic virus; RCNaV, rattail cactus necrosis-associated virus; RheMV, Rehmannia mosaic virus; RMV, ribgrass mosaic virus; SFBV, Streptocarpus flower break virus; SHMV, sunn-hemp mosaic virus; TMGMV, tobacco mild green mosaic virus; TMV, tobacco mosaic virus; ToBRFV, tomato brown rugose fruit virus; ToMV, tomato mosaic virus; ToMoMV, tomato mottle mosaic virus; TSAMV, tropical soda apple mosaic virus; TVCV, turnip vein-clearing virus; WMoV, Wasabi mottle virus; YTMMV, yellow tailflower mild mottle virus; YoMV, Youcai mosaic virus; ZGMMV, zucchini green mottle mosaic virus.


RheMV AB628188
TMV V01408
ToBRFV KT383474
ToMV AB083196
ToMoMV KF477193
BPMV DQ355023
PMMoV AB000709
TSAMV KU659002
BrMMV AM398436
YTMMV KF495564
ObPV D13438
PaMMV AB089381
TMGMV AB078435
ORSV DQ139262
SFBV AM040955
RMV GQ401365
TVCV U03387
WMoV AB017503
YoMV U30944
CaMMV EU043335
RCNaV JF729471
KGMMV AB015145
ZGMMV AJ295949
CFMMV JN226146
CGMMV AB015146
CMoV AB261167
FrMV HM026454
PluMV KJ395757
ClYMV JN566124
SHMV U47034
HLFPV AB917427
HLSV AF395898
MarMV DQ356949
PFMV HQ389540
TRV ORY
0.2