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:	***2012.006aP***	(to be completed by ICTV officers)

Short title: One new species in the genus *Fabavirus*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

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and in consultation with Cheng-Gui Han (hanchenggui@cau.edu.cn)

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)	Secoviridae

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	***2012.006aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Fabavirus***
Subfamily:	***Comovirinae***
Family:	***Secoviridae***
Order:	***Picornavirales***

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:**
Cucurbit mild mosaic virus	EU881936 (RNA1) EU881937 (RNA2)

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

A new virus sequence has been isolated from squash (*Cucurbita moschata*) in China consisting of two RNAs of 5870nts (RNA1) and 3294nts (RNA2). Presence of the virus in squash was associated with inconspicuous mosaic symptoms (Dong et al., 2012). Virion morphology, host range, cytopathology and mode of transmission are not yet determined.

RNA1 contains a single ORF encoding a 1,825aa protein with highest similarity (55%) to the fabavirus *Broad bean wilt virus 2 (BBWV-2*). Motifs consistent with the presence of a putative protease cofactor, protease, helicase, RNA-dependent RNA polymerase were also identified. RNA2 contains a single ORF encoding a 1,017aa protein with highest similarity (54%) to the fabavirus *Broad bean wilt virus 1 (BBWV-1*) with motifs consistent with the presence of movement (MP) and large (L) and small (S) coat (CP) proteins. The predicted LCP and SCP had highest identities with the fabaviruses BBWV-1 (58.5%) and GeMV (58.9%).

Phylogenetic analysis using the deduced amino acid sequence of the Pol, LCP and SCP showed the virus to group with other fabaviruses but as a distinct sub-branch (Dong et al., 2012). To provide further evidence for the grouping of the virus with other fabaviruses, we have produced a new sequence alignment using the deduced amino acid sequence of the Pro-Pol region (region between the conserved CG motif of the proteinase and the conserved GDD motif of the polymerase) (see Fig. 1). The Pro-Pol sequence was previously shown to be a useful indicator of taxonomy within the order *Picornavirales* (Le Gall et al., 2008) and within the family *Secoviridae* (Sanfacon et al., 2009). In this analysis, we included all available sequences from the type isolates of members of the family *Secoviridae*. We also included the corresponding sequences from representatives of other families in the order *Picornavirales* and from *Potato virus Y*, a member of the family *Potyviridae*, which was used as an outgroup. The analysis confirmed the grouping of the virus with other members of the genus *Fabavirus* (Fig. 1)

Current species demarcation criteria within the family *Secoviridae* (as defined in the Ninth Report) are: CP amino acid (aa) sequence with less than 75% identity and Pro-Pol region aa sequence with less than 80% identity. CuMMV has the highest percent identity with BBMV-2 of 67% in the Pro-Pol region. Other useful criteria include antigenic reactions, host range and vector specificity. Serological assays using antiserum produced in *Escherichia coli* against the SCP demonstrated no cross-reaction with *BBWV-1* and *BBWV-2*. Nor did BBWV-2 monoclonal antibody react with CuMMV. The latter two criteria have yet to be established. By RT-PCR and Western blot, CuMMV was also detected in three other cucurbit crops besides squash, including bitter melon (*Momordica charantia*), fat melon (*Benincasa hispida*) and cucumber (*Cucumis sativus*) (Cheng-Gui Han - personal communication).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Dong, S.W., Xiang, H.Y., Shang, Q.X., Li, D.W., Yu, J.L., Han, C.G., 2012. Complete genomic sequence analysis reveals a novel fabavirus infecting cucurbits in China. Arch Virol 157(3), 597-600.

Le Gall, O., Christian, P., Fauquet, C.M., King, A.M., Knowles, N.J., Nakashima, N., Stanway, G., Gorbalenya, A.E., 2008. Picornavirales, a proposed order of positive-sense single-stranded RNA viruses with a pseudo-T = 3 virion architecture. Arch Virol 153(4), 715-727.

Maddison, W.P., Maddison, D.R., 2010. Mesquite: a modular system for evolutionary analysis. Version 2.73.

Sanfacon, H., Wellink, J., Le Gall, O., Karasev, A., van der Vlugt, R., Wetzel, T., 2009. Secoviridae: a proposed family of plant viruses within the order Picornavirales that combines the families Sequiviridae and Comoviridae, the unassigned genera Cheravirus and Sadwavirus, and the proposed genus Torradovirus. Arch Virol 154(5), 899-907.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S., 2011. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol 28(10), 2731-2739.

Figure 1. Neighbor-joining tree of the Pro-Pol amino acid sequences of members of the Picornavirales

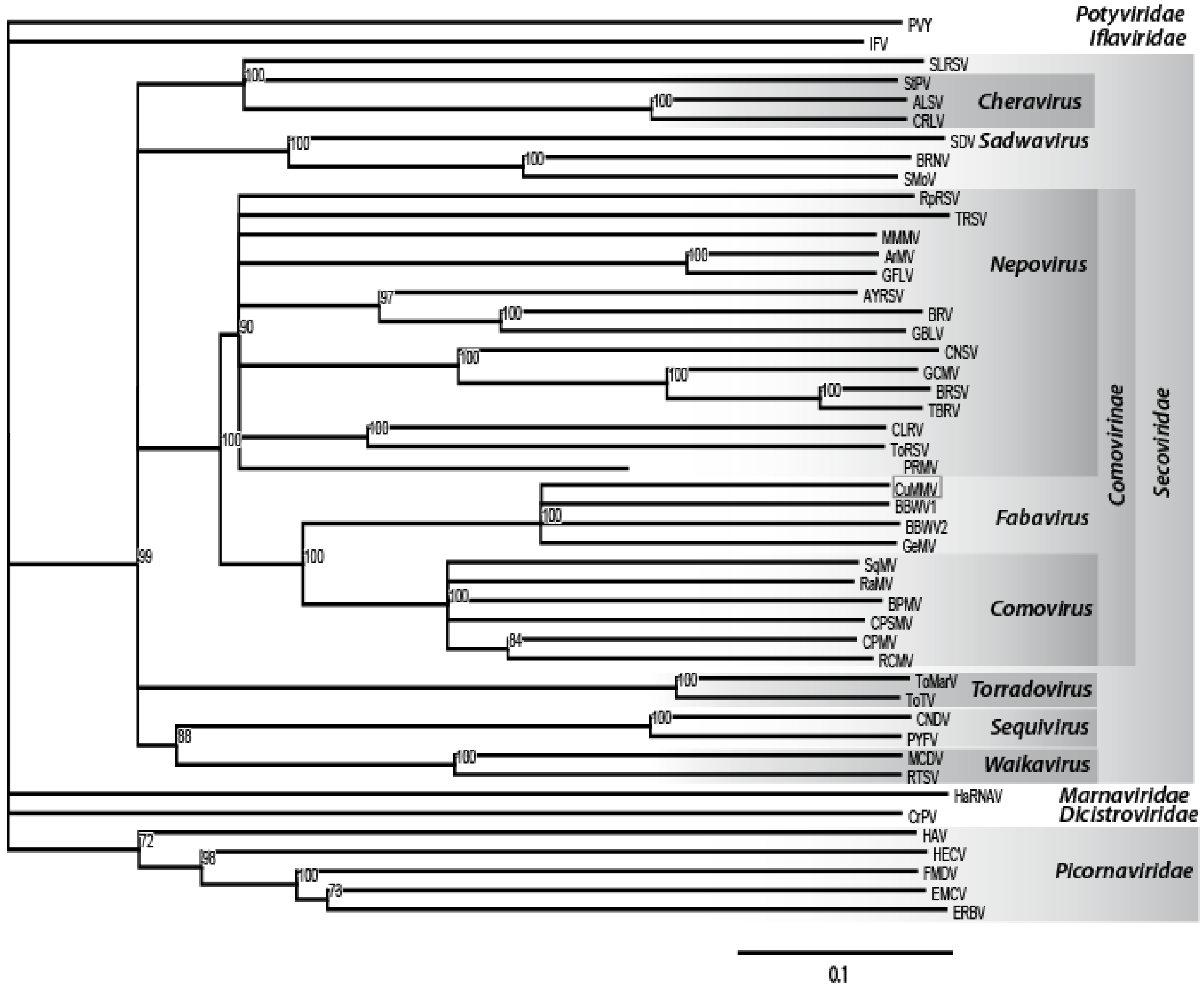

Fig1. Neighbor-joining tree of members of the order *Picornavirales* based on the amino acid sequences of the conserved domains between the “CG” motif of the 3C-like proteinase and the “GDD” motif of the polymerase (Pro-Pol region). The alignment and the tree were generated using MEGA5 (Tamura et al., 2011) and Mesquite (Maddison and Maddison, 2010). Potato virus Y (PVY) a member of the family *Potyviridae* was used as an outgroup. Representative sequences were included for the family *Secoviridae* while only representative members of other families within the order *Picornavirales* were included. The families and genera are delineated on the right. Numbers on nodes show bootstrap values (1000 replicates) above 70%. The bar represents a P distance of 0.1. The GenBank accession numbers used for each virus are as follows: potato virus Y (PVY, NC_001616 = X12456), infectious flacherie virus (IFV, NC_003781 = AB000906), hepatitis A virus (HAV, NC_001489 = M14707), human enterovirus C (HECV, NC_002058.3 = V01149), foot-and-mouth disease virus-type C (FMDV, NC_002554 = AF274010), encephalomyocarditis virus (EMCV, NC_001479 = M81861), equine rhinitis B virus 1 (ERBV, NC_003983 = X96871), cricket paralysis virus (CrPV, NC_003924 = AF218039), *Heterosigma akashiwo* RNA virus (HaRNV, NC_005281 = AY337486), parsnip yellow fleck virus (PYFV, NC_003628 = D14066), carrot necrotic dieback virus (CNDV, EU980442), maize chlorotic dwarf virus (MCDV, NC_003626 = U67839), rice tungro spherical virus (RTSV, NC_001632 = M95497),

tomato torrado virus (ToTV, NC_009013 = DQ388879), tomato marchitez virus (ToMarV, NC_010987 = EF681764), strawberry latent ringspot virus (SLRSV, NC_006964 = AY860978), stocky prune virus (StPV, DQ143874), apple latent spherical virus (ALSV, NC_003787 = AB030940), cherry rasp leaf virus (CRLV, NC_006271 = AJ621357), satsuma dwarf virus (SDV, NC_003785 = AB009958), strawberry mottle virus (SMoV, NC_003445 = AJ311875), black raspberry necrosis virus (BRNV, NC_008182 = DQ344639), raspberry ringspot virus (RRSV, NC_005266 = AY303787), peach rosette mosaic virus (PRMV, AF016626), tobacco ringspot virus (TRSV, NC_005097 = U50869), melon mild mottle virus (MMMoV, AB518485), arabis mosaic virus (ArMV, NC_006057 = AY303786), grapevine fanleaf virus (GFLV, NC_003615 = D00915), artichoke yellow ringspot virus (AYRSV, AM087671), blackcurrant reversion virus (BRV, NC_003509 = AF368272), grapevine Bulgarian latent virus (GBLV, NC_015492 = FN691934), cycas necrosis stunt virus (CNSV, NC_003791 = AB073147), grapevine chrome mosaic virus (GCMV, NC 003622 = X15346), beet ringspot virus (BRSV, NC_003693 = D00322), tomato black ring virus (TBRV, NC_004439 = AY157993), tomato ringspot virus (ToRSV, NC_003840 = L19655), cherry leaf roll virus (CLRV, NC_015414 = FR851461), squash mosaic virus (SqMV, NC_003799 = AB054688), radish mosaic virus (RaMV, NC_010709 = AB295643), cowpea mosaic virus (CPMV, NC_003549 = X00206), red clover mottle virus (RCMV, NC_003741 = X64886), bean pod mottle virus (BPMV, NC_003496 = U70866), cowpea severe mosaic virus (CPSMV, NC_003545 = M83830), broad bean wilt virus 1 (BBWV1, NC_005289 = AB084450), BBWV2 (NC_003003 = AF225953), gentian mosaic virus (GeMV, BAD99001).