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:	***2014.013aP***	(to be completed by ICTV officers)

Short title: Create *Pigeonpea sterility mosaic virus* (PPSMV) as a new species in the genus *Emaravirus*
(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:

Toufic Elbeaino, email:elbeaino@iamb.it

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)	Emaravirus Study Group

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

SG comment: PPSMV has been long discussed as a putative member of the genus Emaravirus and the work of Toufic Elbeaino and his coworkers could confirm this idea by deep sequencing of the viral RNA genome. The Emaravirus Study Group strongly supports the proposal, to include PPSMV into the genus Emaravirus.

EC comment: this proposal was conditionally approved. Fig. 1 should be modified to properly depict the F motif upstream of the A motif.

SG response: Done

Date first submitted to ICTV:	July 2014
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	***2014.013aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Emaravirus***
Subfamily:	
Family:	
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:**	**GenBank sequence accession number(s)**
Pigeonpea sterility mosaic virus	Isolate “P” (Germplasm line ICP 8863)	HF568801, HF568802, HF568803, HF568804, HF945448.

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

Species dermarcation criteria for the genus Emaravirus

1. Amino acid sequence of relevant gene products (polymerase, nucleocapsid protein) differing by more than 25%
2. Differences in the natural host range
3. Differences in vector species

The molecular information on Pigeonpea sterility mosaic virus (PPSMV), the agent of sterility mosaic disease (SMD) of pigeonpea (*Cajanus cajan*, *Fabaceae)* (Kumar et al., 2004), remained elusive for decades despite the intensive efforts to determine the sequences and the number of RNA segments composing its genome. This lack of information has always hindered its final classification into a definite genus. The results of Deep sequencing conducted on dsRNA templates extracted from a PPSMV-infected plant (isolate “P”; Kumar et al., 2002) indicate that its genome consists of five RNA segments (Elbeaino et al., 2014). Each of the five RNAs encodes a single protein on the negative-sense strand with an open reading frame (ORF) of 6885, 1947, 927, 1086, and 1422 nts, respectively. In order, from RNA1 to RNA5, these ORFs encode the RNA-dependent RNA polymerase (p1, 267.9 kDa), a putative glycoprotein precursor (p2, 74.3 kDa), a putative nucleocapsid protein (p3, 34.6 kDa), a putative movement protein (p4, 40.8 kDa), while p5 (55 kDa) has an unknown function. All RNA segments of PPSMV showed the highest identity with *Fig mosaic virus* (FMV) and *Rose rosette virus* (RRV). In phylogenetic trees constructed with the amino acid sequences of p1, p2 and p3, PPSMV clustered consistently with other emaraviruses, close to clades comprising members of other genera of the family

Bunyaviridae. Based on the morphological (Double-membraned bodies, DMBs), epidemiological (transmission by eriophyid mites, *Aceria cajani*) and molecular characteristics (multipartite genome), all features similar to emaraviruses, PPSMV seems to be the fifth species to join the list of emaraviruses known to date and accordingly, its classification in the genus *Emaravirus* seems now legitimate.

PPSMV properties

1-Virus particles: DMBs with a diameter of 80-200 nm (Kumar et al., 2002, 2003).
2- Transmission in a semi-persistent manner by the eriophyid mite *Aceria cajani* (Kulkarni et al., 2002).
3- Mechanically transmissible from pigeonpea to *Nicotiana benthamiana*, and erratically from *N. bethamaniana to N. benthamiana* (Kumar et al., 2002).
4- dsRNAs profile: 5 segments (reported as 5-7 segments by Kumar et al., 2003).
5- Multipartite genome structure (see annex) resembling that of other emaraviruses (Kumar et al., 2003, Elbeaino et al., 2014).
6- RNA segments consistof single stranded-negative sense encoding the RNA-dependent RNA polymerase (RNA1: 7,022 nt; p1:267.9 kDa), a putative glycoprotein precursor (RNA2: 2,223 nt; p2: 74.3 kDa), a putative nucleocapsid protein (RNA3: 1,442 nt; p3: 34.6 kDa), a putative movement protein (RNA4: 1,563 nt; p4: 40.8 kDa), RNA5: 1,801 nt; p5: 55 kDa, unknown function) (Elbeaino et al., 2014).
6- In phylogenetic trees constructed with p1, p2 and p3 sequences, PPSMV clustered consistently with other emaraviruses (see annex).

The above mentioned data support the classification of PPSMV as a new species in the newly established genus *Emaravirus* (Mielke-Ehret, N. & Mühlbach, H.P., 2012).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Elbeaino T., Digiaro M., Uppala M., Sudini H., 2014. Deep sequencing of Pigeonpea sterility mosaic virus discloses five RNA segments related to emaraviruses. *Virus Research*, 188, 27-31.

Kulkarni, N.K., Kumar, P.L., Muniyappa, V., Jones, A.T., Reddy, D.V.R., 2002. Transmission of Pigeonpea sterility mosaic virus by the eriophyid mite, *Aceria cajani* (Acari: Arthropoda). *Plant Dis*. 86, 1297–1302.

Kumar, P.L., Jones, A.T., Waliyar, F., 2004. Biology, etiology and management of pigeonpea sterility mosaic disease. *Annu. Rev. Plant Pathol*. 3, 1-24.

Kumar, P.L., Jones A.T., Reddy, D.V.R., 2003. A novel mite-transmitted virus with a divided RNA genome closely associated with pigeonpea sterility mosaic disease. *Phytopathology* 93, 71-81

Kumar, P.L., Duncan, G.C., Roberts, I.M., Jones, A.T., Reddy, D.V.R., 2002. Cytopathology of *Pigeonpea sterility mosaic virus* in pigeonpea and *Nicotiana benthamiana*: similarities with those of eriophyid mite-borne agents of undefined aetiology. *Ann. Appl. Biol*. 140, 87-96.

Mielke-Ehret, N. & Mühlbach, H.P., 2012. *Emaravirus*: a novel genus of multipartite, negative strand RNA plant viruses. *Viruses* 4, 1515-1536.

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.

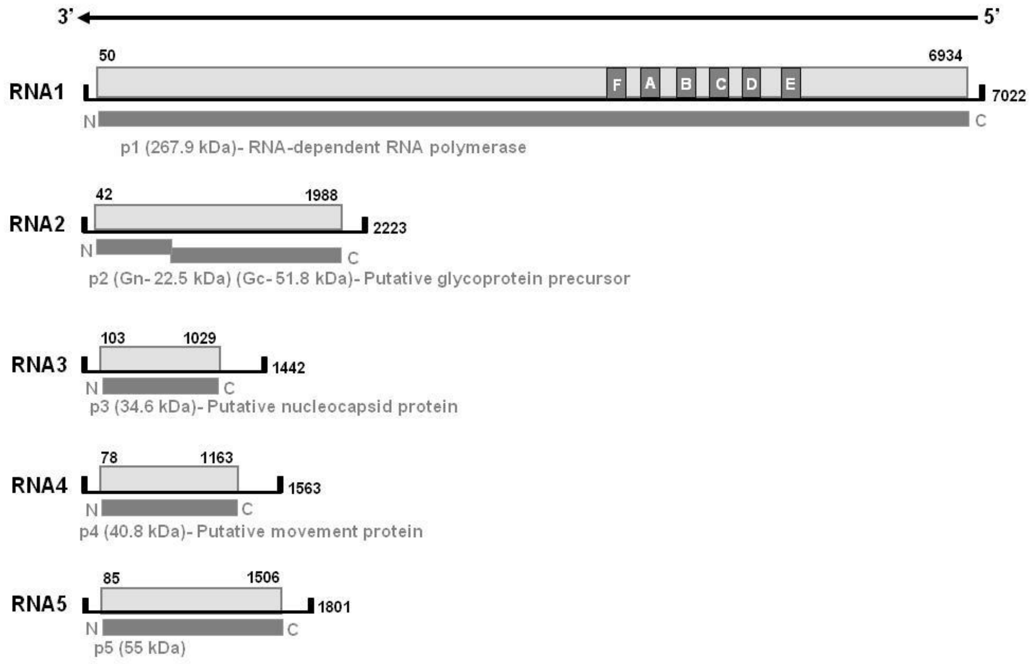

Fig.1: Schematic representation of the organization of the PPSMV genomic RNA segments. The terminal 13 nucleotides conserved at the 5′ and 3′ termini are indicated as black boxes on each segment. Letters (A-F) represents the conserved motifs on the RdRp (RNA1) gene. Expression products of each RNA (p1 to p5) are represented as dark grey boxes. Protein function and estimated mol. wt of each segment are reported below each RNA. Figure not drawn to scale.

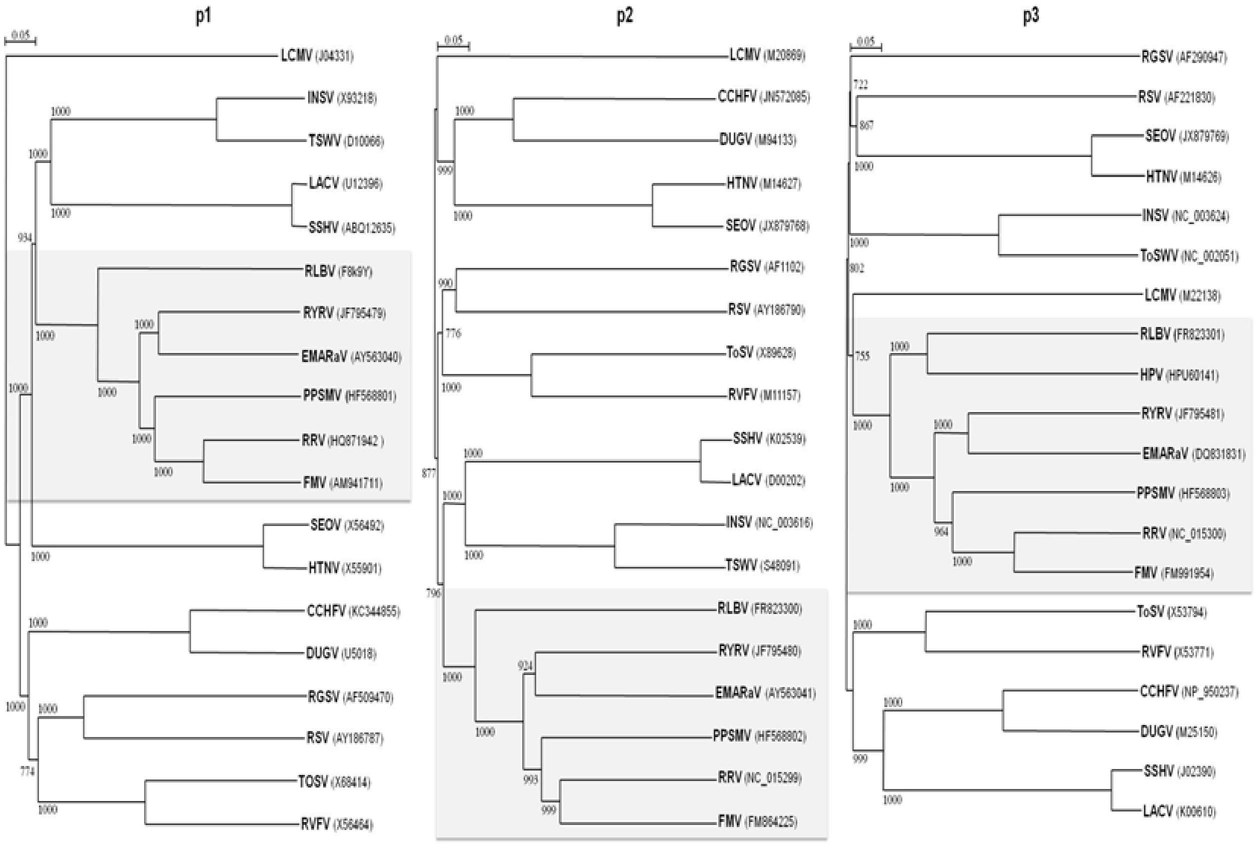

Fig. 2: Phylograms constructed with predicted aa sequences of RNA1 (RNA-dependent RNA polymerase, p1), RNA2 (glycoprotein precursor, p2) and RNA3 (nucleocapsid,p3) of PPSMV together with orthologues (denoted as L, M and S) of members of the family *Bunyaviridae*. The following genera and virus species were used to construct the phylogenetic trees: *Phlebovirus* (TOSV, *Toscana virus*; RVFV, *Rift valley fever virus*), *Tenuivirus* (RGSV, *Rice grassy stunt virus*; RSV, *Rice stripe virus*), *Nairovirus* (CCHFV, *Crimean-Congo hemorrhagic fever virus*; DUGV, *Dugbe virus*), *Hantavirus* (HTNV, *Hantaan virus*; SEOV, *Seoul virus*), *Orthobunyavirus* (LACV, *California encephalitis virus* [isolate La Crosse virus]; SSHV, *Snowshoe hare virus*), *Tospovirus* (INSV, *Impatiens necrotic spot virus*; TSWV, *Tomato spotted wilt virus*), *Emaravirus* (EMARaV, *European mountain ash ringspot-associated virus*; FMV, *Fig mosaic virus*; RRV, *Rose rosette virus*; RYRV, redbud yellow ringspot virus; RLBV, *Raspberry leaf blotch virus*). *Lymphocytic choriomeningitis virus* (LCMV) was used as an outgroup species. Accession numbers of viruses are reported between brackets.