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:	***2011.004aP***	(to be completed by ICTV officers)

Short title: Create species named *Yambean mosaic virus* in the genus *Potyvirus*
(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:

Kreuze, J.F. (j.kreuze@cgiar.org); Fuentes, S.

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 Study Group

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	***2011.004aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Potyvirus***
Subfamily:	
Family:	***Potyviridae***
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Yambean mosaic virus	JN190431

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

The proposed new virus species was found infecting yambean (*Pachyrhizus* spp.) plants in San Ramon, Peru, showing severe mosaic and leaf deformation (Fig 1). The complete genome sequence (9648 nt excluding poly A tail) of a potyvirus related to *Bean common mosaic virus* (BCMV) was determined by siRNA deep sequencing and assembly from one of the samples and deposited in the NCBI Genbank database under accession number JN190431. Pair wise sequence comparison and phylogenetic analysis using complete genomes of related potyviruses (Fig 2) showed that YBMV was most closely related to BCMV with 71.3% nt identity. This is below the potyvirus species demarcation limit of 76%. YBMV was detected by potyvirus specific antibodies (CAB 27200). Comparison to partial sequences available from Genbank, identified a fragment corresponding to the 3' 2.7 kb of potyvirus (accession number AB289438) found infecting yambean in Indonesia [1] with 96.6% nucleotide identity, suggesting it is the same virus. YBMV isolate from Indonesia was shown to be transmitted by *Aphis gossypii* and *A. craccivora* with 100% efficiency, and *A. glycines* with 70% efficiency and reacts with antisera to potyvirus (AS-573/1) and WMV2 (watermelon mosaic virus) antisera [1]. There is also evidence for seed transmission through PCR of bulked seed samples [1]. In studies of its host range [1] it caused symptomless infection on *Gomphrena globosa* (*Amarathaceae*), chlorosis on the inoculated leaves of tomatoes (*Solanaceae*) and infected several members of the *Leguminosae*, causing symptoms on the upper leaves of *Phaseolus vulgaris* (mosaic), *Pisum sativum* (mild mosaic) and *Vigna sinensis* (chlorosis).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Damayanti, T. A., Susilo, D., Nurlaelah, S., Sartiami, D., Okuno, T., and Mise, K. 2008. First report of Bean common mosaic virus in yam bean [Pachyrhizus erosus (L.) Urban] in Indonesia. J Gen Plant Pathol. 74:438-442

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. Leaves from yambean plants infected by a potyvirus and showing vein clearing or mosaic with/without leaf deformation. Enlarge image (72) was selected for extracting small interfering RNA (siRNA) for detecting/identify the virus infecting the plant.

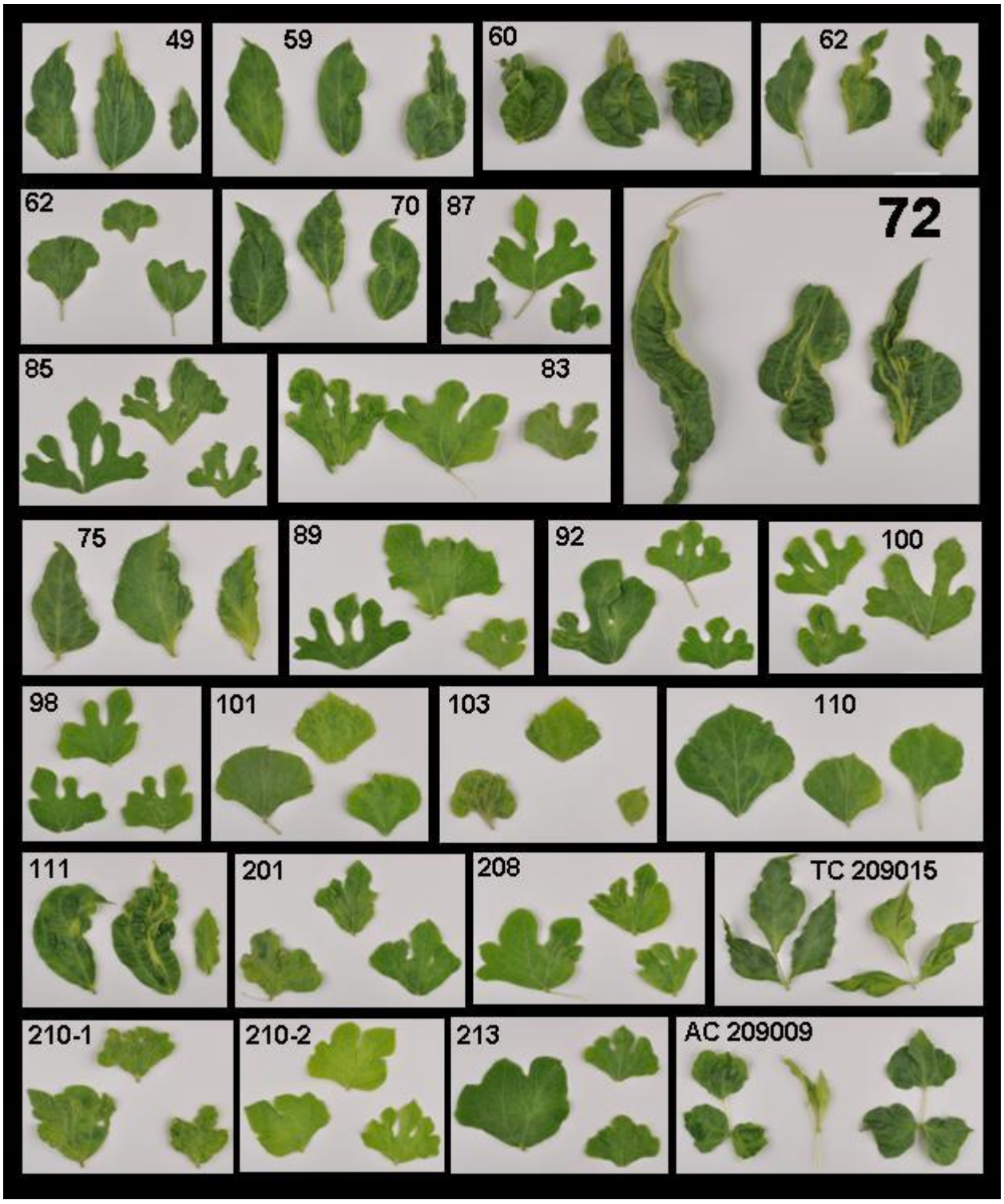

Figure 2. Phylogenetic tree of complete genome sequences (A) and NIa-CP region (2553 nt) (B) of YBMV and related viruses. YBMV shows only 71.3% nt sequence identity to *Bean common mosaic virus* over the complete genome indicating a new species (species demarcation: 76%). On the other hand partial sequence comparison in (B) indicates it is the same virus as identified in yam-bean in Indonesia. Analysis was performed using the MEGA5 program. Complete potyvirus genomes were downloaded from the NCBI database and aligned using the Clustal W algorithm. A tree was then generated using neighbour-joining with the maximum composite likelihood method and 500 bootstrap replicates, and branches corresponding to recognized viruses were collapsed into triangles.