MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2013.013aP*	(to be completed by ICTV officers)

Short title: One new species in the genus *Tymovirus*
(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:

Jan Kreuze (j.kreuze@cgiar.org)

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)	Tymoviridae study group

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):	

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	*2013.013aP*		(assigned by ICTV officers)

To create one new species within:

		Fill in all that apply.
Genus:	*Tymovirus*	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Subfamily:	*-*	
Family:	*Tymoviridae*	• If no genus is specified, enter "**unassigned**" in the genus box.
Order:	*Tymovirales*	

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Andean potato mild mosaic virus	JX508290

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 genomes of tymoviruses contain two extensively overlapping ORFs that begin 7 nt apart, and a third ORF (for capsid protein) that is expressed from a 3'-coterminal subgenomic RNA (sgRNA). The longest ORF encodes a replication polyprotein of about 220 kDa that contains recognized domains for a methyltransferase (Mtr), a papain-like cysteine protease (P-Pro), an RNA helicase (Hel) and an RNA-dependent RNA polymerase (RdRp). The criteria demarcating species in the genus Tymovirus are: i) Overall genome sequence identity of less than 80%; ii) Capsid protein sequences less than 90% identical; iii) Differential host range; iv) Differences in the 3'-terminal structure and v) Serological specificity.

Andean potato mild mosaic virus (APMMV; Kreuze et al., 2013)

The complete genomic RNA sequences of the tymovirus isolates Hu and Col from potato, which originally had been considered to be strains of the same virus species, i.e. *Andean potato latent virus* (APLV), were determined by siRNA sequencing and assembly, and found to share only c. 65% nt sequence identity over their entire genomes, and <60% for their CP encoding genes. Serological tests also showed that specific antibodies raised against either virus only recognized their cognate virus in DAS-ELISA tests. These results, together with phylogenetic analysis of entire genomes of other tymoviruses (Fig 1) and coat protein gene sequences of additional tymovirus isolates from potato (Fig 2), suggest that the species *Andean potato latent virus* should be subdivided into two species, i.e. APLV and *Andean potato mild mosaic virus* (APMMV). Whereas the 3' terminal structures were similar between the two species, and extensive host range analysis was not performed, the remaining three criteria for species demarcation were clearly met, supporting the division into two species.

MODULE 9: **<u>APPENDIX</u>**: supporting material

Fig 1 Phylogenetic tree generated after aligning the complete nt sequences of selected tymoviruses using the neighbor-joining and Kimura 2 parameter models. When using maximum likelihood or minimum evolution algorithms (Tamura et al., 2011), trees with similar topology were generated. Bootstrap values obtained following 1000 bootstrap replications are given at each node when they exceeded 50%. APLV: Andean potato latent virus, APMMV: the new suggested species Andean potato mild mosaic virus.
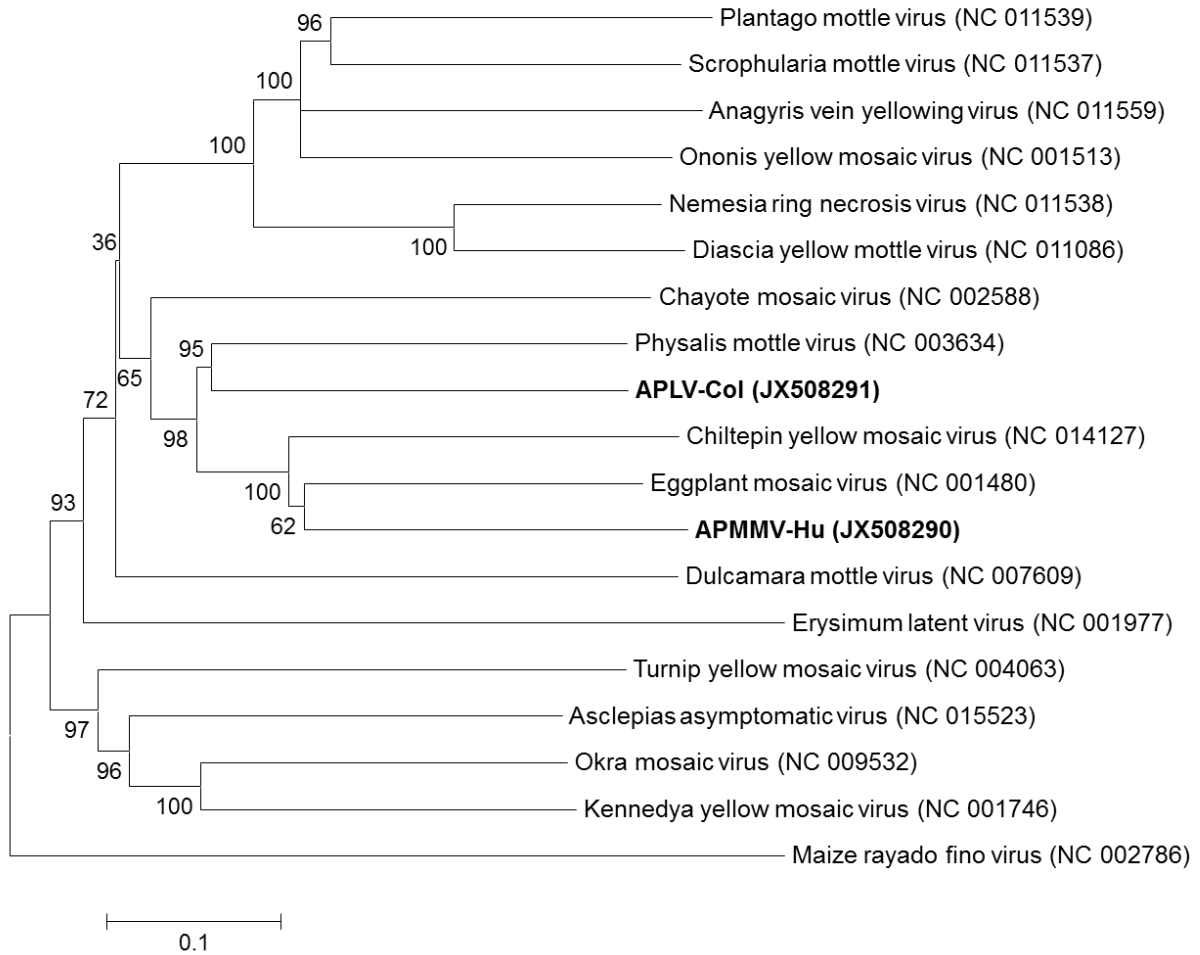
Fig 2 Average percentages of nt and aa sequence identities for the CP genes and the CPs, respectively of eleven potato-infecting tymoviruses, an incompletely sequenced isolate submitted as APLV (GenBank accession No. AF035402) and EMV. The trees were generated by the DNAMAN software using the UPGMA method. Phylogenetic trees almost identical in topology were obtained by the neighbor-joining method. APLV: Andean potato latent virus; APMMV: the new suggested species Andean potato mild mosaic virus; EMV: eggplant mosaic virus.

additional material in support of this proposal
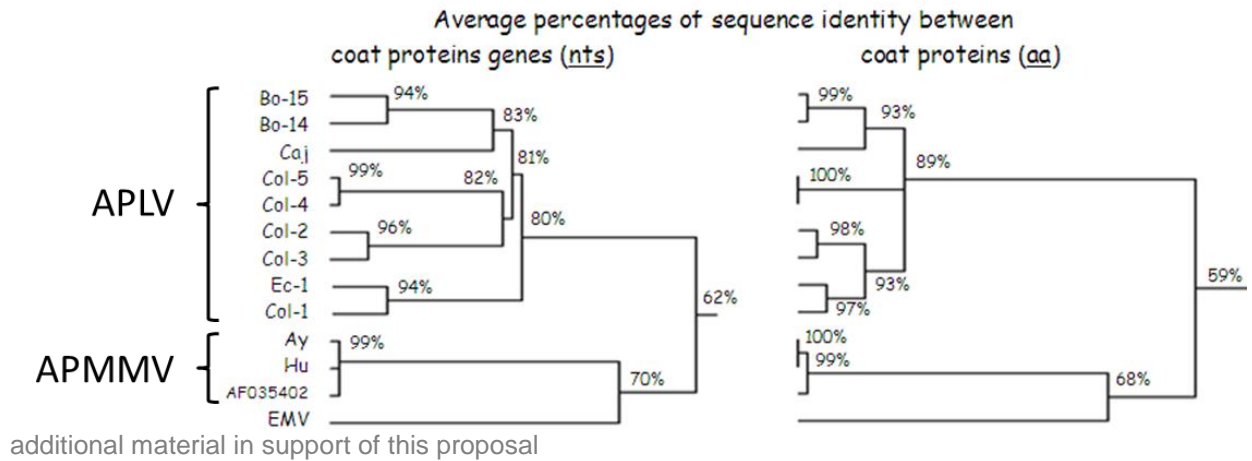
References:

Kreuze, J., Koenig, R., De Souza, J., Vetten, H.J., Muller, G., Flores, B., Ziebell, H., Cuellar, W., 2013. The complete genome sequences of a Peruvian and a Colombian isolate of Andean potato latent virus and partial sequences of further isolates suggest the existence of two distinct potato-infecting tymovirus species. Virus Research 173, 431-435.

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.