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:	***2010.020aP***	(to be completed by ICTV officers)

Short title: 1 new species in the genus Potyvirus, family Potyviridae
(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:

N. Bejerman, F. Giolitti, S. de Breuil and S. Lenardon (slenard@infovia.com.ar)

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	***2010.020aP***

(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:**
Sunflower chlorotic mottle virus	GU181199

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

This proposal suggests that Sunflower chlorotic mottle virus (SuCMoV) should be considered a distinct species of the genus *Potyvirus*, family *Potyviridae.*

Throughout the family, species are distinguished by the following criteria:

- Genome sequence relatedness: different species have CP aa sequence identity less than ~about 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites.
- Host range and key host reactions; lack of cross protection.
- Different inclusion body morphology.
- Antigenic properties: serological relatedness may help in distinguishing species.

The complete genomes of the common (C) (Annex, Fig. 1a) and chlorotic ringspot (CRS) (Annex, Fig. 1b) strains were obtained, and have been deposited in the GenBank under GU181199 and GU181200 accession numbers, respectively. When the complete SuCMoV-C and –CRS genome sequences were compared to the sequences available for members of the PVY subgroup, the PVY-N-605 strain shared the highest nt identities (66.5 and 67 %, respectively). Whereas, when the nt and aa sequences of the SuCMoV-C and –CRS polyprotein were compared to the sequences available for members of the PVY subgroup, the PVY-N-605 and PVY-Lye84.2 strains showed the highest nt (66.5 and 66.9 %) and aa identities (69.8 and 69.7 %), respectively (Annex, Table 1). Furthermore, the P1 coding region was more than 100 aa longer than the P1 coding region of the other PVY subgroup members.

The last ICTV report includes SuCMoV as a PVY strain [2]. However, the relatively low nt identity of 67.0-66.9 % obtained for the complete genome and polyproteins, respectively, of the Argentine SuCMoV strains when compared to the corresponding sequences of the potyviruses belonging to the

PVY subgroup, fall under the minimum identity value that discriminates between potyvirus species and strains [1, 2]. Therefore, this result clearly supports the proposal that SuCMoV should be considered as a distinct species of the genus *Potyvirus.* This is supported by phylogenetic analysis (Annex, Figure 2).

Additional support for this proposal is included in the Annex and in [3].

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Adams MJ, Antoniw JF, Fauquet CM (2005). Molecular criteria for genus and species discrimination within the family Potyviridae. Arch. Virol. 150:459-479.
2. Berger PH, Adams MJ, Brunt AA, Hill JH, Hammond J, Jordan RL, Morales RJ, Ohki ST, Rybicki E, Uyeda I, Vetten HJ (2005). The Potyviridae. In: Virus Taxonomy-Classification and Nomenclature of Viruses, 8th Report of the ICTV. Fauquet C, Mayo M, Maniloff F, Desselberger U, Ball L (eds) Elsevier Academic Press, San Diego, CA, pp 819-841.
3. Bejerman, N., Giolitti, F., de Breuil, S. y Lenardon, S. Molecular characterization of Sunflower chlorotic mottle virus: a member of a distinct species in the genus Potyvirus. Archives of Virology. doi:10.1007/s00705-010-0703-3.

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.

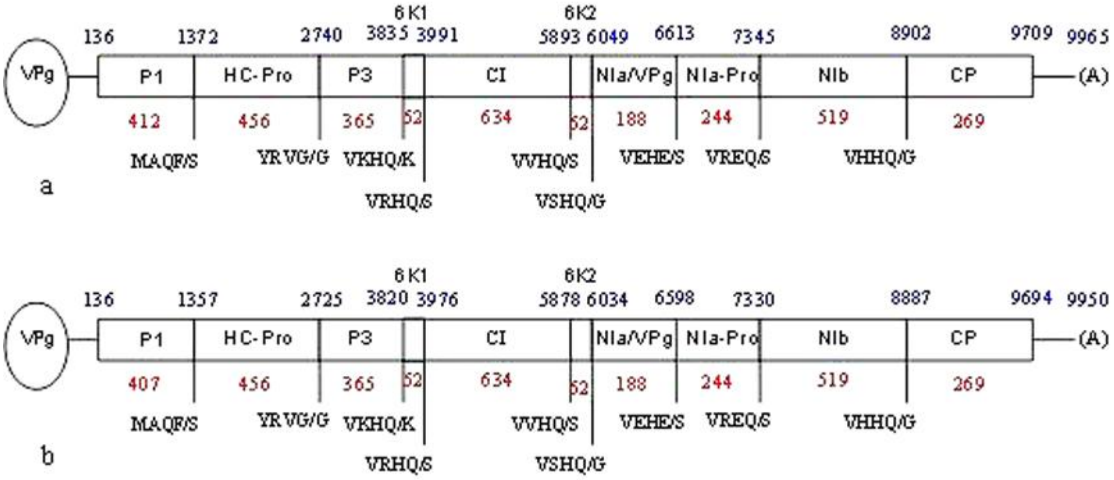

Figure 1. Schematic representation of the genome organization of both strains of Sunflower chlorotic mottle virus (SuCMoV): -C (a) and -CRS (b) depicting coding proteins in cistrons. The amino acid size of each SuCMoV strain protein is indicated below the genome, whereas the numbers above the genome indicate the start of each region. The putative proteinase cleavage sites in the polyproteins of -C and -CRS strains are indicated below the genome.

Figure 2. Section from phylogenetic tree based on the codon-aligned nucleotide sequences of the complete polyproteins of viruses in the genus *Potyvirus*. This section of the tree shows the PVY subgroup and supports the position of SuCMoV as a member of this group and a representative of a distinct species. One representative sequence was chosen for each species. The analysis was done in MEGA4 (maximum composite likelihood distances) and the numbers on the branches indicate percentage of bootstrap support out of 10,000 bootstrap replications (when >60%).

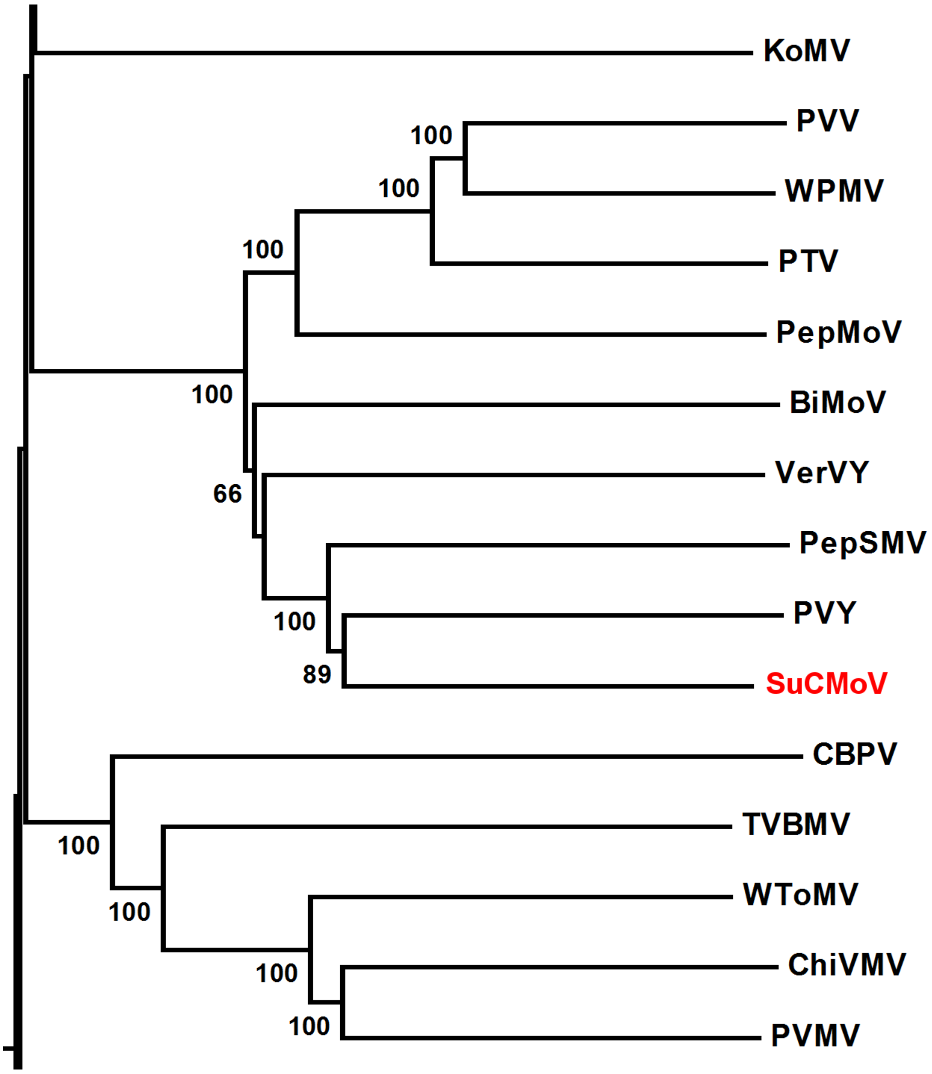

Table 1. Nucleotide (nt) and amino acid (aa) sequences identities (%) between Sunflower chlorotic mottle virus (SuCMoV) C and CRS strains, and average number of nt differences that result in one aa difference, for each gene and for both SuCMoV strains. Percentage range of nt and aa sequence identity between the SuCMoV strains and viruses belonging to the *Potato virus Y* (PVY) subgroup.

Genomic region	SuCMoV-C versus SuCMoV-CRS			SuCMoV-C and CRS versus PVY subgroup viruses		
	nt identity (%)	aa identity (%)	ratio of nt to aa changes		range of nt identity (%)	range of aa identity (%)
Whole genome	92.4	-	-	C	66.5 (N-605) - 60.5	-
				CRS	67.0 (N-605) - 60.6	-
5`-NCR	89.6	-	-	C	53.3 - 41.5	-
				CRS	54.0 - 38.2	-
Polyprotein	92.3	95.6	5.25	C	66.5 (N-605) - 60.4	69.8 (Lye84.2) - 57.2
				CRS	66.9 (N-605) - 60.7	69.7 (Lye84.2) - 56.8
P1	90.4	90.3	2.97	C	43.3 - 35.5	30.4 - 21.8
				CRS	44.7 - 37.2	31.2 - 22.3
HC-Pro	93.4	97.4	7.50	C	69.9 - 63.4	77.0 - 55.9
				CRS	70.0 - 62.0	76.5 - 56.1
P3	90.7	92.6	3.78	C	61.4 - 51.1	55.3 - 32.8
				CRS	62.9 - 51.2	57.0 - 33.4
6K1	89.7	94.2	5.33	C	69.2 - 59.0	81.0 - 55.8
				CRS	69.2 - 57.1	79.0 - 57.7
CI	94.2	97.3	6.47	C	71.9 - 65.5	80.6 - 70.3
				CRS	71.7 - 65.6	80.0 - 70.1
6K2	97.4	100	-	C	71.0 - 54.6	73.1 - 51.5
				CRS	71.6 - 51.9	73.1 - 51.5
NIa-VPg	95.7	96.3	3.42	C	73.6 - 66.7	82.3 - 67.6
				CRS	73.1 - 65.9	82.5 - 69.1
NIa-Pro	84.9	93.4	6.94	C	72.3 - 64.7	73.6 - 65.4
				CRS	70.5 - 63.5	72.4 - 63.9
NIb	96.1	99.0	12.2	C	74.3 - 66.1	82.9 - 71.9
				CRS	75.0 - 66.6	82.7 - 72.1
CP	87.1	94.8	7.43	C	76.5 - 66.1	80.7 - 71.1
				CRS	78.3 - 68.1	80.5 - 71.1
3´-NCR	97.3	-	-	C	62.6 - 36.1	-
				CRS	62.6 - 38.2	-