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:	***2010.018aP***	(to be completed by ICTV officers)

Short title: A new species in the genus Soymovirus
(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:

Andrew Geering (andrew.geering@deedi.qld.gov.au)

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)	Caulimoviridae

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	***2010.018aP***	(assigned by ICTV officers)

To create a new species within:

Genus:	***Soymovirus***
Subfamily:	
Family:	***Caulimoviridae***
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:**
Cestrum yellow leaf curling virus	AF364175

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 criteria demarcating species in the genus (as given in the 8th report) are:

- Differences in host ranges,
- Differences in polymerase (RT + RNAse H) nt sequences of more than 20%.
- Differences in gene product sequences.

Cestrum yellow leaf curling virus can be considered a new species in the genus *Soymovirus* for the following reasons:

1. It has a circular, double-stranded DNA genome that is 8,253 bp long.
2. It has virions that are isometric in shape and *c.* 50 nm in diameter.
3. It contains all the characteristic protein domains of members of the family *Caulimoviridae*.
4. It produces cytoplasmic inclusion bodies like that of the genus *Caulimovirus* and *Soymovirus*.
5. Like all members of the genus *Soymovirus*, CmYMV has three ORFs between the movement protein and coat protein-coding ORFs. Members of the genus *Caulimovirus* have only two ORFs in this part of the genome. Furthermore, like the soymovirus *Blueberry red ringspot virus*, the minus-strand primer-binding site is located in a small intergenic region immediately downstream of ORF1b. The position of the minus-strand primer-binding site is a feature the differentiates caulimoviruses from soymoviruses.
6. Using whole genome sequences, CmYLV has highest sequence identity to *Soybean chlorotic mottle virus* (47.8%) and *Peanut chlorotic streak virus* (45.5%). In pairwise comparisons of conserved *pol* gene sequences, it has a maximum of 58.9% nt identity to other soymoviruses, which is well below the 80% nt identity threshold for demarcation

of strains and species of soymovirus.

7. In phylogenetic analyses using conserved polymerase gene sequences, it is a sister taxon of SbCMV and forms a strongly supported clade with other members of the genus *Soymovirus*.
8. It is serologically unrelated to members of the genus *Caulimovirus* including *Cauliflower mosaic virus*, *Dahlia mosaic virus* and *Carnation etched ring virus*.
9. Its experimental host range consists of *Cestrum parqui*, *Cestrum elegans* and *Nicotiana clevelandii* (all in the family *Solanaceae*), which is different from that of any other soymovirus. The host ranges of soymoviruses are very narrow and differences are strongly indicative of new species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

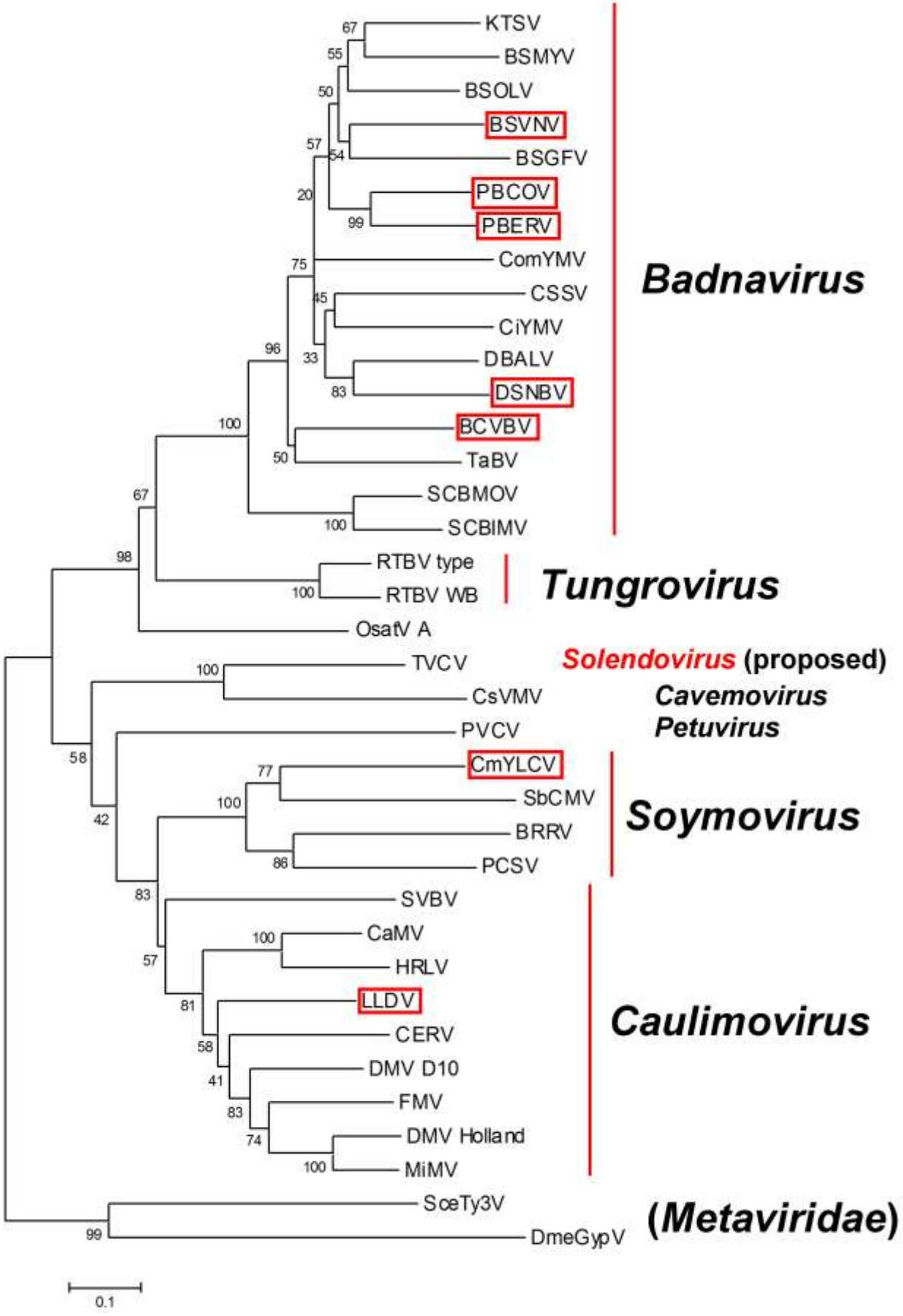
Bousalem, M., Douzery, E., and Seal, S. (2008). Taxonomy, molecular phylogeny and evolution of plant reverse transcribing viruses (family Caulimoviridae) inferred from full-length genome and reverse transcriptase sequences. Archives of Virology 153, 1085-1102.

Stavolone, L., Ragozzino, A., and Hohn, T. (2003). Characterization of Cestrum yellow leaf curling virus: a new member of the family Caulimoviridae. Journal of General Virology 84, 3459-3464.

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. Evolutionary relationships of viruses in the family *Caulimoviridae* based on *pol* gene nucleotide sequences. The tree was generated using the maximum likelihood method implemented using the online version of PhyML version 3. Acronyms are: *Drosophila melangaster Gypsy virus* (DmeGypV), *Saccharomyces cerevisae Ty3 virus* (SceTy3V), *Petunia vein clearing virus* (PVCV), *Cassava vein mosaic virus* (CsVMV), *Tobacco vein clearing virus* (TVCV), *Soybean chlorotic mottle virus* (SbCMV), *Cestrum yellow leaf curling virus* (CmYLCV), *Blueberry red ringspot virus* (BRRV), *Peanut chlorotic stunt virus* (PCSV), *Strawberry vein banding virus* (SVBV), *Carnation etched ring virus* (CERV), Lamium leaf distortion virus (LLDV), *Figwort mosaic virus* (FMV), *Dahlia mosaic virus* strain D10 (DMV-D10), *Mirabilis mosaic virus* (MiMV), *Dahlia mosaic virus* strain Holland (DMV-Holland), *Horseradish latent virus* (HRLV), *Cauliflower mosaic virus* (CaMV), *Commelina yellow mottle virus* (ComYMV), *Banana streak MY virus* (BSMysV), *Banana streak GF virus* (BSGFV), Banana streak VN virus (BSVNV), *Kalanchoe top-spotting virus* (KTSV), *Banana streak OL virus* (BSOLV), Pineapple bacilliform ER virus (PBERV), Pineapple bacilliform CO virus (PBCOV), Dioscorea bacilliform SN virus (DBSNV), Dioscorea bacilliform AL virus (DBALV), Citrus yellow mosaic virus (CiYMV), *Cassava swollen shoot virus* (CSSV), Bougainvillea chlorotic vein banding virus (BCVBV), Taro bacilliform virus (TaBV), *Sugarcane bacilliform IM virus* (SCBIMV), *Sugarcane bacilliform Mor virus* (SCBMorV), Oryza sativa virus sequence cluster A (OsatV-A), *Rice tungro bacilliform virus* strains type and West Bengal (RTBV-type and -WB).


KTSV
BSMYV
BSOLV
BSVNV
BSGFV
PBCOV
PBERV
ComYMV
CSSV
CiYMV
DBALV
DSNBV
BCVBV
TaBV
SCBMOV
SCBIMV
RTBV type
RTBV WB
OsatV A
TVCV
CsVMV
PVCV
CmYLCV
SbCMV
BRRV
PCSV
SVBV
CaMV
HRLV
LLDV
CERV
DMV D10
FMV
DMV Holland
MiMV
SceTy3V
DmeGypV
0.1
Badnavirus
Tungrovirus
Solendovirus (proposed)
Cavemovirus
Petuvirus
Soymovirus
Caulimovirus
(Metaviridae)