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:	***2014.011aP***	(to be completed by ICTV officers)

Short title: create species *Soybean Putnam virus* in genus *Caulimovirus*, family *Caulimoviridae*
(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:

A.D.W. Geering, a.geering@uq.edu.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* study group

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

EC comments: This proposal was conditionally approved. The SG should clarify the wording in the figure legend of the phylogenetic tree to state that the tree was built using the maximum likelihood method (current phrasing is confusing). The SG should also confirm which virus was used as an outgroup and ensure that the tree is properly rooted.

AG comments: Wording in figure legend has been changed to address comments. The *Metaviridae* is a sister taxon to the *Caulimoviridae* and therefore is an appropriate outgroup for the phylogenetic analyses.

EC comments: Finally, the SG should provide details on the methods used to determine the genome sequence (deep sequencing? Other?) and provide further evidence for the existence of the virus (virions identified etc?).

AG comments: The taxonomic justification has been revised to include details of the method of discovery. Although virions were not observed, RNA-Seq data combined with PCR-amplification of viral DNA from the source plant provide strong evidence of the existence of the virus. The genome of the virus is typical of a member of the genus *Caulimovirus*, suggesting that the virus genome has been assembled correctly. Comparison of the virus sequence with the *Glycine max* genome sequence suggests that it is not an endogenous virus.

Date first submitted to ICTV:	June 2014
Date of this revision (if different to above):	September 2014

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	***2014.011aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Caulimovirus***
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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Soybean Putnam virus	Ohio	JQ926983

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

Soybean Putnam virus (SPuV) should be considered a new species in the genus *Caulimovirus* for the following reasons:

1. SPuV was discovered as part of a high throughput RNA-Seq survey of soybean viruses from 24 Ohio counties. This virus was discovered in a single source plant from Putnam County. The RNA-Seq data allowed assembly of two large contigs of 3.7-4 kbp and these two contigs were later assembled into a complete virus genome by sequencing of PCR-amplified fragments from the source plant that bridged the contigs. No virions were observed and no symptoms of infection were described by the authors of the original virus description (Han *et al*., 2012).
2. SPuV is clearly an exogenous virus as the soybean (*Glycine max*) plant genome has now been sequenced and no significant matches are obtained in a BLASTN search using the virus genome sequence as the query. Furthermore, the virus was only found in a single soybean plant.
3. SPuV has six open reading frames (ORF) and an identical genome organization to that of *Cauliflower mosaic virus*, the type species of this virus genus. As is characteristic of the genus, ORFI encodes a movement protein; ORFII, an aphid transmission factor; ORFIII, a virion-associated protein; ORFIV, a capsid protein; ORFV, a polyprotein containing aspartic protease, reverse transcriptase (RT) and RNase H1 (RH) domains; ORFVI, a transcriptional transactivator.
4. In a phylogenetic analysis using conserved RT-RH gene sequences, SPuV groups within the genus *Caulimovirus* (Figure 1, Annex).
5. SPuV has ≤71% nucleotide identity with other caulimovirus species within the RT-RH

domains, thus easily falling below the 80% nt threshold for demarcation of species.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Han JH, Domier LL, Dorrance A, Qu F (2012) Complete genome sequence of a novel pararetrovirus isolated from soybean. Journal of Virology 86: 9555.

Annex:

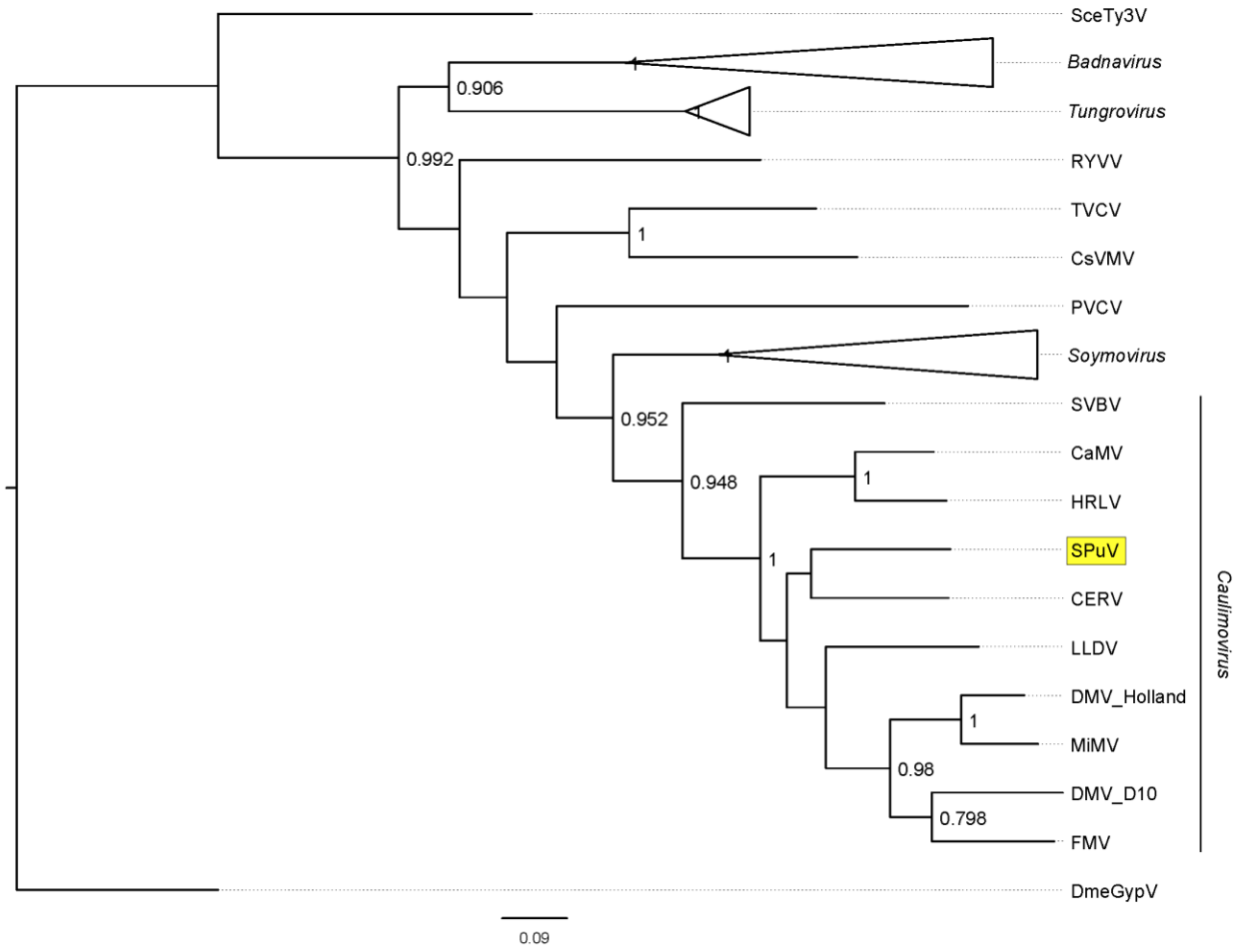

Figure 1. Phylogram of the *Caulimoviridae* built using the maximum likelihood method provided in the MEGA 6.06 suite of software. Reverse transcriptase-RNase H1 gene sequences, equivalent to nucleotides 4449-5648 of the cauliflower mosaic virus genome (NCBI accession NC_001497.1), were used for phylogenetic inference. Abbreviations of species in the genus *Caulimovirus* are: SVBV, *Strawberry vein banding virus*; CaMV, *Cauliflower mosaic virus*;

HRLV, *Horseradish latent virus*; SPuV, Soybean Putnam virus; CERV, *Carnation etched ring virus*; DMV, *Dahlia mosaic virus*; MiMV, *Mirabilis mosaic virus*; FMV, *Figwort mosaic virus*. Other abbreviations are: PVCV, *Petunia vein clearing virus* (type species, genus *Petuvirus*); TVCV, *Tobacco vein clearing virus* (type species, genus *Solendovirus*); CsVMV, *Cassava vein mosaic virus* (type species, genus *Cavemovirus*); RYVV (rose yellow vein virus; unassigned). The phylogram has been rooted using *Saccharomyces cerevisiae Ty3 virus* (SceTy3V, type species of genus *Metavirus*) and *Drosophila melanogaster Gypsy virus* (DMeGypV, type species of genus *Errantivirus*). Clades containing soymovirus, tungrovirus and badnavirus species have been collapsed. Bootstrap values for 500 replicates are shown in the nodes of the branches.