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:	***2010.017a-eP***	(to be completed by ICTV officers)

Short title: New genus Solendovirus in the 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:

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:

EC commented that a phylogenetic tree would be helpful. This has now been added (as a copy from a related proposal)

Date first submitted to ICTV:	04/06/2010
Date of this revision (if different to above):	03/07/2010

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2010.017aP***	(assigned by ICTV officers)

To create a new genus within:

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2010.017bP***	(assigned by ICTV officers)

To name the new genus: *Solendovirus*

Assigning the type species and other species to a new genus

Code	***2010.017cP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Tobacco vein clearing virus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Tobacco vein clearing virus is currently a species in the genus *Cavemovirus* (family *Caulimoviridae*). However, it has a significantly different genome organization to *Cassava vein mosaic virus*, the type species of the genus *Cavemovirus* (see Fig. 1 in the Appendix). These differences are:

1. ORF1 of CsVMV encodes a protein containing the coat protein and movement protein precursors. These proteins are encoded by two ORFs in TVCV: ORF1 (coat protein) and ORF2 (movement protein).
2. The ORF1 protein of CsVMV has a 124 amino acid N-terminal extension of unknown function when compared to the ORF1 protein of TVCV.
3. CsVMV has an additional small ORF located between ORF2 (movement protein) and ORF3 (coat protein) in TVCV.

Other than differences in genome organization, the genetic distance (% amino acid identity) between CsVMV and TVCV in the polymerase protein is equivalent to that of different virus genera in the family *Caulimoviridae* (see Table 1 and Fig. 2 in the Appendix).

GenBank Accession for TVCV: AF190123 (= NC_003378).

Origin of the new genus name:

From *Sol*anaceae *endo*genous *virus*

Reasons to justify the choice of type species:

This is a monotypic genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2010.017dP***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Tobacco vein clearing virus

The present taxonomic position of these taxon/taxa:

Genus:	***Cavemovirus***
Subfamily:	
Family:	***Caulimoviridae***
Order:	

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

See module 3 for creation of the genus *Solendovirus*.

Part (b) re-assign to a higher taxon

Code	***2010.017eP***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***Solendovirus*** **(new)**
Subfamily:	
Family:	***Caulimoviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

See module 3 for creation of the genus *Solendovirus*.

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.

de Kochko, A., Verdaguer, B., Taylor, N., Carcamo, R., Beachy, R.N., and Fauquet, C. (1998). Cassava vein mosaic virus (CsVMV), type species for a new genus of plant double stranded DNA viruses? Archives of Virology 143, 945-962.

Geering, A.D.W., Scharaschkin, T., and Teycheney, P.-Y. (2010). The classification and nomenclature of endogenous viruses of the family Caulimoviridae. Archives of Virology 155, 123-131.

Lockhart, B.E., Menke, J., Dahal, G., and Olszewski, N.E. (2000). Characterization and genomic analysis of tobacco vein clearing virus, a plant pararetrovirus that is transmitted vertically and related to sequences integrated in the host genome. Journal of General Virology 81, 1579-1585.

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.

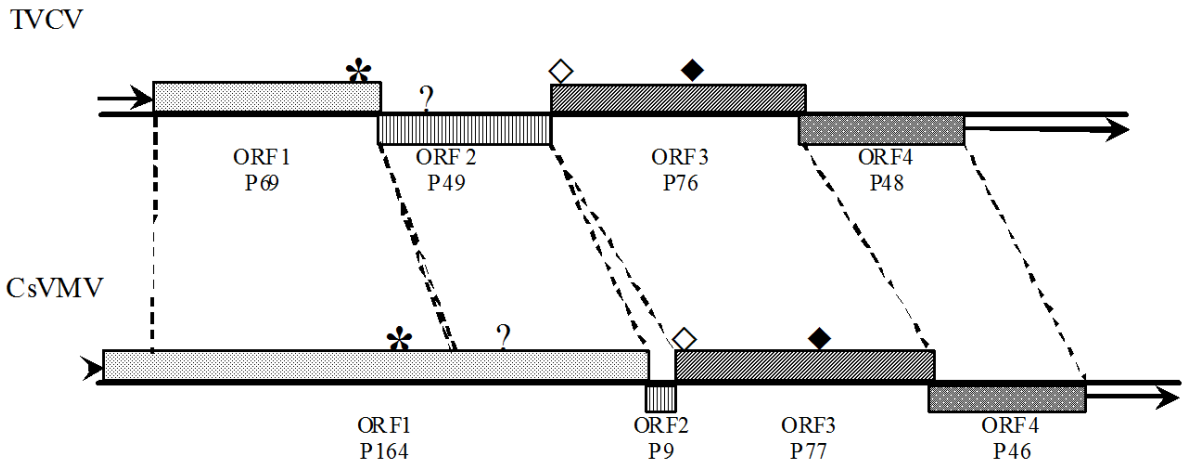

Fig. 1. Comparison of the genome organisation of *Tobacco vein clearing virus* and *Cassava vein mosaic virus*. Genome maps are linearised and following convention, numbering begun at the first nucleotide of the $tRNA^{met}$ binding site. Conserved motifs are marked with the following symbols: movement protein (♣), zinc finger (*), aspartic protease active site (◇) and reverse transcriptase active site (◆). Dotted lines mark homologous parts of the different virus genomes. Protein molecular weights (kDa) are provided under each ORF label. Arrows denote untranslated regions.

Fig. 2. 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 – proposed new genus *Solendovirus*),** *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).

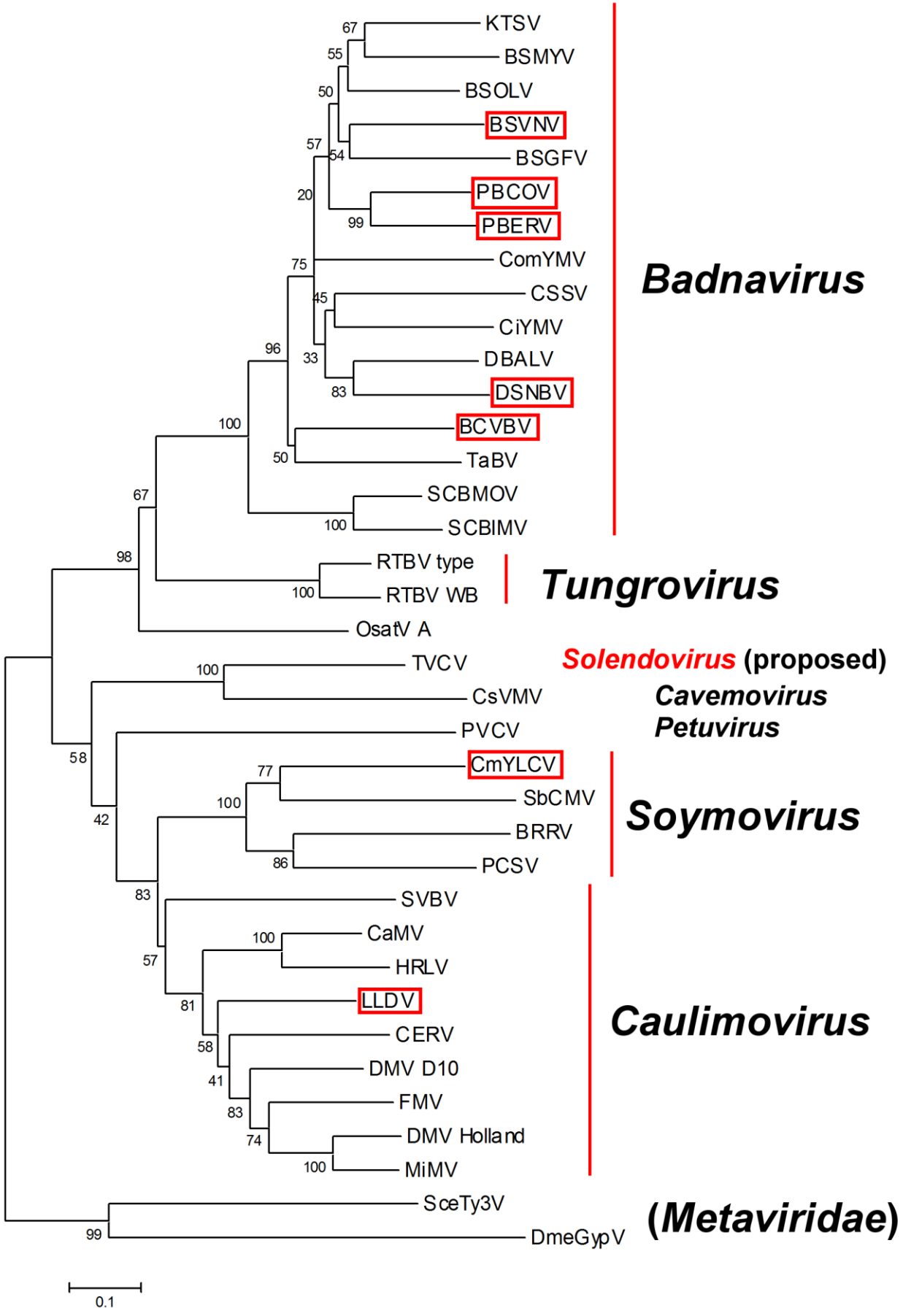
KTSV
BSMYV
BSOLV
BSVNV
BSGFV
PBCOV
PBERV
ComYMV
CSSV
CiYMV
DBALV
DSNBV
BCVBV
TaBV
SCBMOV
SCBIMV
RTBV type
RTBV WB
OsatV A
TVCV
CsVMV
PVCV
CmYLCV
SbCMV
BRRV
PCSV
SVBV
CaMV
HRLV
LLDV
CERV
DMV D10
FMV
DMV Holland
MiMV
SceTy3V
DmeGypV
0.1
Badnavirus
Tungrovirus
Solendovirus (proposed)
Cavemovirus
Petuvirus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

Table 1. Mean nucleotide (below diagonal) and amino acid (above diagonal) distances between virus genera in the family *Caulimoviridae*. Figures provided are the number of nucleotide substitutions per site (Kimura two-parameter distance; plain font), percent nucleotide difference (bold font in brackets), number of amino acid substitutions per site (Poisson correction distance; plain font) and percent amino acid difference (bold font in brackets).

	Orendovirus	*Tungrovirus*	*Badnavirus*	*Soymovirus*	*Caulimovirus*	Solendovirus	*Cavemovirus*	*Petuvirus*
Orendovirus		0.653 (**48.0**)	0.671 (**48.9**)	0.995 (**63.0**)	0.772 (**53.7**)	0.843 (**57.0**)	0.896 (**59.2**)	0.974 (**62.3**)
Tungrovirus	0.619 (**41.7**)		0.798 (**55.0**)	1.124 (**67.5**)	0.968 (**62.0**)	0.978 (**62.4**)	1.087 (**66.3**)	1.091 (**66.4**)
Badnavirus	0.706 (**45.5**)	0.761 (**47.6**)		1.075 (**65.8**)	0.928 (**60.4**)	1.014 (**63.7**)	1.028 (**64.2**)	1.119 (**67.3**)
Soymovirus	0.795 (**48.9**)	0.883 (**51.8**)	0.975 (**54.4**)		0.764 (**53.4**)	1.053 (**65.1**)	1.104 (**66.8**)	1.076 (**65.9**)
Caulimovirus	0.691 (**45.2**)	0.837 (**50.3**)	0.881 (**51.6**)	0.718 (**46.0**)		0.884 (**58.7**)	0.924 (**60.3**)	0.932 (**60.2**)
Solendovirus	0.721 (**46.3**)	0.765 (**47.9**)	0.926 (**52.9**)	0.778 (**48.3**)	0.775 (**48.2**)		0.702 (**50.5**)	1.127 (**67.6**)
Cavemovirus	0.694 (**45.3**)	0.802 (**49.2**)	0.948 (**53.7**)	0.827 (**50.0**)	0.783 (**48.5**)	0.545 (**38.7**)		1.099 (**66.7**)
Petuvirus	0.832 (**50.2**)	0.925 (**53.1**)	0.976 (**54.3**)	0.919 (**52.9**)	0.831 (**50.1**)	0.938 (**53.5**)	0.891 (**52.1**)	

Note: The region of comparison is the conserved reverse transcriptase and RNase H1 domains of the virus replicase and comparisons used a representative of each recognised (or proposed) species in each genus. The entry ‘Orendovirus’ is for sequences that are probably replication-defective endogenous copies of DNA in the rice genome. The study group is still discussing whether to propose this as a new genus.