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:	***2010.014aP***	(to be completed by ICTV officers)

Short title: A new species in the genus Caulimovirus
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒ **6** ☐	**2** ☒ **7** ☐	**3** ☐ **8** ☐	**4** ☐ **9** ☒	**5** ☐

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	***2010.013aP***	(assigned by ICTV officers)

To create a 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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Lamium leaf distortion virus	EU554423

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.

Lamium leaf distortion virus is clearly a new species within the genus *Caulimovirus* as:

1. The circular, dsDNA genome contains six open reading frames, with gene organization and functions identical to that of the type species, *Cauliflower mosaic virus*.
2. The virus has isometric virions that are 45-52 nm in diameter.
3. Southern blot hybridization results show that the virus is exogenous in nature and not integrated in the host genome.
4. Infected *Lamium maculatum* plants contain cytoplasmic inclusion bodies characteristic of caulimoviruses.
5. In phylogenetic analyses using the ORFV protein (containing aspartic protease, reverse transcriptase and RNase H domains), LLDV groups with CaMV, *Horseradish latent virus* and *Carnation etched ring virus*.
6. The proteins encoded by the six putative ORFs have only 37-67% amino acid identity to all known caulimoviruses.
7. *Lamium maculatum* is the only known host of LLDV and it was unable to be transmitted to *Nicotiana* spp. and other *Lamium maculatum* plants by mechanical and graft inoculation and using the aphid *Myzus persicae*. This is the first record of a natural

infection of a plant species in the family *Lamiaceae* by a caulimovirus.

Zhang et al. (2008) proposed the name Lamium leaf distortion associated virus for this virus because Koch's postulates had not been satisfied. However, the presence of the virus is consistently associated with leaf distortion symptoms and no other virus was observed. As Koch's postulates are rarely satisfied before a virus is named, I recommend that the virus be called Lamium leaf distortion virus for the sake of simplicity and consistency.

GenBank accession EU554423 (= NC_010737).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

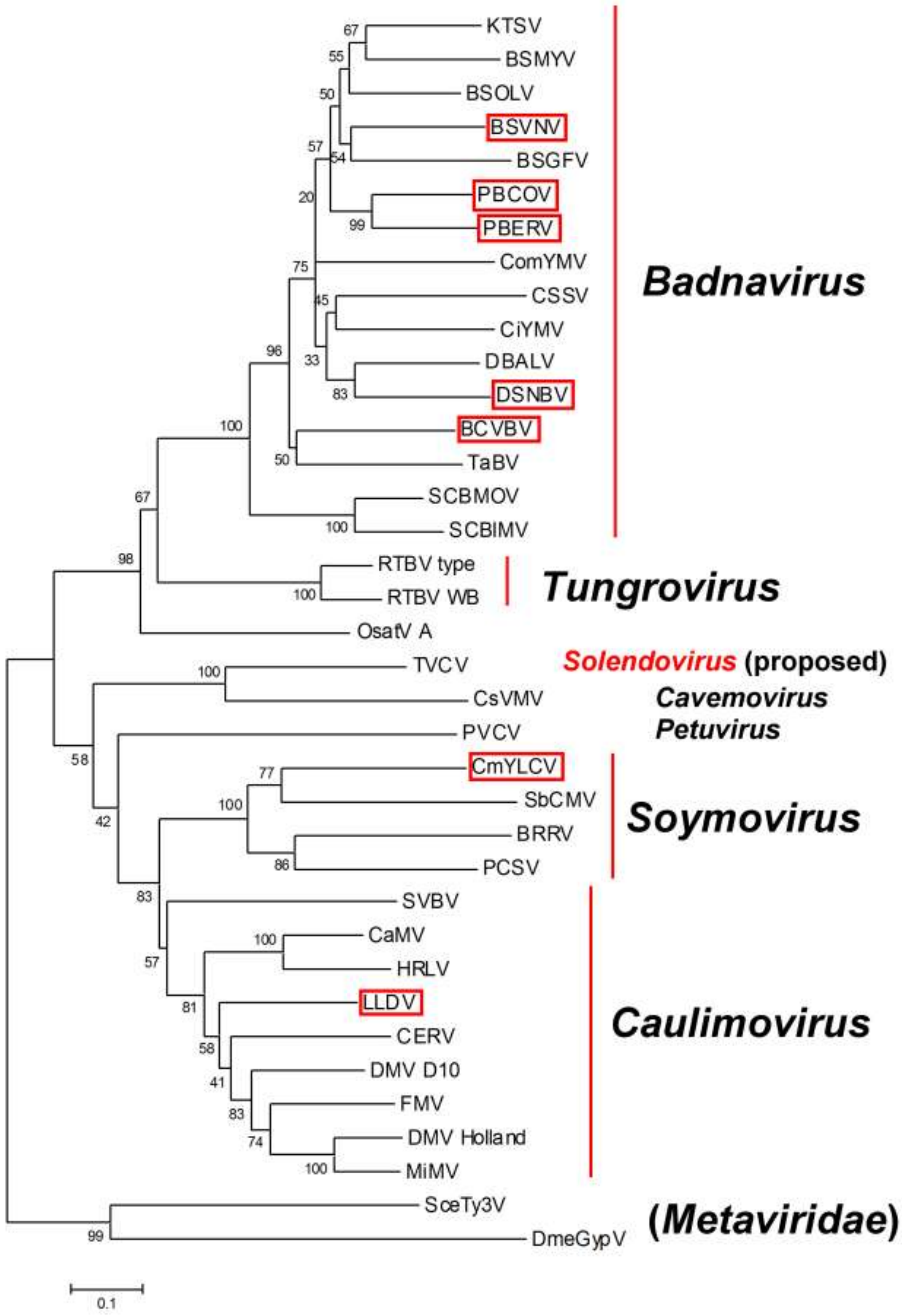
References:

Zhang, L., Lockhart, B., Dahal, G., and Olszewski, N. (2008). Studies on biology and genomic characterization of a caulimo-like virus associated with a leaf distortion disease of Lamium maculatum. Archives of Virology 153, 1181-1184.

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).


67
KTSV
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BSMYV
50
BSOLV
BSVNV
57
54
BSGFV
20
PBCOV
99
PBERV
75
ComYMV
45
CSSV
CiYMV
96
33
DBALV
83
DSNBV
100
BCVBV
50
TaBV
67
SCBMOV
100
SCBIMV
98
RTBV type
100
RTBV WB
OsatV A
100
TVCV
CsVMV
PVCV
58
77
CmYLCV
SbCMV
100
42
BRRV
86
PCSV
83
SVBV
100
CaMV
57
HRLV
81
LLDV
58
CERV
41
DMV D10
83
FMV
74
DMV Holland
100
MiMV
SceTy3V
99
DmeGypV
0.1
Badnavirus
Tungrovirus
Solendovirus (proposed)
Cavemovirus
Petuvirus
Soymovirus
Caulimovirus
(Metaviridae)