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:	***2010.013a,bP***	(to be completed by ICTV officers)				
Short title: Five new species and four nomenclature changes in the genus *Badnavirus* (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	***2010.013aP***	(assigned by ICTV officers)

To create 5 new species within:

Genus:	***Badnavirus***
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:**
Banana streak VN virus	AY750155
Pineapple bacilliform CO virus	EU377664-71 (incomplete)
Pineapple bacilliform ER virus	EU377672-3 (incomplete)
Bougainvillea chlorotic vein banding virus	EU034539
Dioscorea bacilliform SN virus	DQ822073

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.
- Differences in vector specificities

Banana streak VN virus (BSVNV)

Banana streak VN virus can be considered a new badnavirus species for the following reasons:

1. BSVNV is transmitted by the mealybug vector *Planococcus citri* and inoculated plants develop symptoms typical of banana streak disease.
2. Infected plants contain bacilliform-shaped virions with dimensions typical of a badnavirus.
3. A full length viral genome has been PCR-amplified and cloned from purified virions. The virus was propagated in Cavendish bananas (*Musa* AAA genotype), which are not thought to contain any replication-competent endogenous badnaviral sequences, suggesting that the sequence that was cloned is from an exogenous viral genome. The length of the viral genome was 7,801 bp and the genome organization

identical and protein domains characteristic of that of the genus *Badnavirus* (three open reading frames).

4. In phylogenetic analyses using conserved *pol* gene sequences, BSVNV groups within the genus *Badnavirus* and is sister to BSGFV. Within the *pol* gene sequence, BSVNV is 68.1% identical to BSGFV, which is well below the 80% threshold for discrimination of strains and species within the genus *Badnavirus*.

GenBank accessions: AY750155 (= NC_007003), DQ092436

Pineapple bacilliform CO virus (PBCOV) and Pineapple bacilliform ER virus (PBERV)

Pineapple bacilliform CO virus and *Pineapple bacilliform ER virus* can be considered new badnavirus species for the following reasons:

1. PBCOV and PBERV infect both cultivated and wild forms of *Ananas comosus* (pineapple) and infections are always associated with the presence of bacilliform-shaped virions that are typical of a badnavirus.
2. Approximately 1800 nts and 1500 nts of the genome of PBCOV and PBERV, respectively, have been sequenced. These sequences cover the region of the badnavirus genome from the reverse transcriptase domain to the minus-strand primer binding site. Proof that this DNA was amplified from exogenous and not endogenous viral DNA is provided by (i) the DNA that was cloned was PCR-amplified from purified virions that had been treated with DNase I to remove any traces of contaminating plant DNA and (ii) clonal plants of any particular pineapple cultivar do not uniformly contain the DNA, as is normally observed if the DNA is endogenous in nature.
3. Both viruses are transmitted by the mealybug *Dysmicoccus brevipes* and PBCOV also by *Planococcus citri*.
4. PBCOV and PBERV are sister taxa and within the *pol* gene, they have 75.7% nt identity to each other, which is below the 80% nt identity threshold for delimitation of strains and species within the genus *Badnavirus*. All other badnavirus species have less than 70% nucleotide identity to PBCOV and PBERV.

GenBank accessions: incomplete sequences PBERV (EU377673, EU377672), PBCOV (EU377671, EU377670, EU377669, EU377668, EU377667, EU377666, EU377665, EU377664)

Bougainvillea chlorotic vein banding virus (BCVBV)

Bougainvillea chlorotic vein banding virus can be considered a new badnavirus species for the following reasons:

1. *Bougainvillea spectabilis*, *Bougainvillea glabra* and *Bougainvillea buttiana* plants with chlorotic vein-banding symptoms contain bacilliform-shaped virions that are 130–158 × 27–42 nm in size.
2. Fragments of DNA with homology to the *pol* gene of the badnavirus genome have been PCR-amplified from the virions. In phylogenetic analyses using *pol* gene sequences, BCVBV groups within the genus *Badnavirus* and is sister to *Taro*

bacilliform virus.

3. Within the conserved *pol* gene region of the genome, BCVBV has a maximum of 68% nt identity to other badnavirus species and is therefore well below the 80% cut-off for delimitation of strains and species of badnavirus.
4. BCVBV is graft-transmissible between *Bougainvillea* plants. Inoculated plants develop symptoms and are PCR-positive by BCVBV-specific PCR assay, whereas uninoculated plants and plants tested prior to inoculation are PCR-negative. These results suggest that the virus exists only in an exogenous form in *Bougainvillea*.
5. A full length genome sequence of BCVBV has been lodged on GenBank but this sequence has not yet been published in a peer-reviewed journal. The genome organization of this sequence is typical of a badnavirus.

GenBank accessions: EU034539 (=NC_011592) and incomplete sequences AY532653, DQ103759, DQ347841,

Dioscorea bacilliform SN virus (DBSNV)

Dioscorea bacilliform SN virus can be considered a new badnavirus species for the following reasons:

1. *Dioscorea sansibarensis* plants showing mild leaf deformation and chlorosis symptoms contain bacilliform-shaped virions that are 130 × 30 nm. These virions cross-react strongly with a composite polyclonal anti-badnavirus antiserum generated by BEL Lockhart.
2. A full-length viral genome has been amplified from a crude virion preparation. The genome is 7261 nt long and contains three open reading frames. Protein motifs that are typical of the genus *Badnavirus* have been identified.
3. In phylogenetic analyses using each of the predicted proteins encoded by the three ORFs, DBSNV is a sister taxon to *Dioscorea bacilliform virus* (to be renamed *Dioscorea bacilliform AL virus* (DBALV) – see module 8).
4. In pairwise comparisons of the conserved *pol* gene sequence, DBSNV has 70.7% nt identity to DBALV, which is well below the 80% threshold for discrimination of strains and species of badnavirus.
5. In a genetic variability study of badnaviruses infecting *Disocorea* in West Africa, the virus isolates clustered into three distinct clades, one representing DBALV, another DBSNV and the third, a possible undescribed species.

GenBank accession: DQ822073 (= NC_009010)

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	***2010.013bP***	(assigned by ICTV officers)

Title of proposal: Changes to the names of four species in the genus *Badnavirus*

Text of proposal:

Nomenclature change 1: *Citrus mosaic virus* to become *Citrus yellow mosaic virus*. This name change is recommended for the following reasons:

1. There is confusion in the literature because the name citrus mosaic virus is a synonym of *Satsuma dwarf virus*.
2. The name Citrus mosaic virus has never been widely adopted amongst plant virologists and in the majority of relevant publications, the name Citrus yellow mosaic virus has been used.

Nomenclature change 2: *Dioscorea bacilliform virus* to become *Dioscorea bacilliform AL virus*. This name change is recommended because (in module 2) it is proposed that a second badnavirus species be recognized from *Dioscorea* spp. To distinguish the two, an extra descriptor is being added to the virus name in a similar manner to the nomenclature of the badnaviruses infecting *Musa* spp. (banana).

Nomenclature changes 3 and 4: *Banana streak Mysore virus* to become *Banana streak MY virus* and *Sugarcane bacilliform Mor virus* to become *Sugarcane bacilliform MO virus*. These name change are recommended because there has been a lack of a convention on the style of descriptors for badnavirus species that infect the same crop and cause similar symptoms. With this change, I am trying to follow conventions of naming for other badnaviruses (e.g. *Banana streak OL virus*, *Banana streak GF virus*, *Sugarcane bacilliform IM virus*) and also the other new species names proposed in module 2.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Eni, A., Hughes, J.D., Asiedu, R., and Rey, M. (2008). Sequence diversity among badnavirus isolates infecting yam (Dioscorea spp.) in Ghana, Togo, Benin and Nigeria. Archives of Virology 153, 2263-2272.

Gambley, C.F., Geering, A.D.W., Steele, V., and Thomas, J.E. (2008). Identification of viral and non-viral reverse transcribing elements in pineapple (Ananas comosus), including members of two new badnavirus species. Archives of Virology 153, 1599-1604.

Lheureux, F., Laboureau, N., Muller, E., Lockhart, B.E.L., and Iskra-Caruana, M.-L. (2007). Molecular characterization of banana streak acuminata Vietnam virus isolated from Musa acuminata siamea (banana cultivar). Archives of Virology 152, 1409-1416.

Rivas, E.B., Duarte, L.M.L., Alexandre, M.A.V., Fernandes, F.M.C., Harakava, R., and Chagas, C.M. (2005). A new Badnavirus species detected in Bougainvillea in Brazil. Journal of General Plant Pathology 71, 438-440.

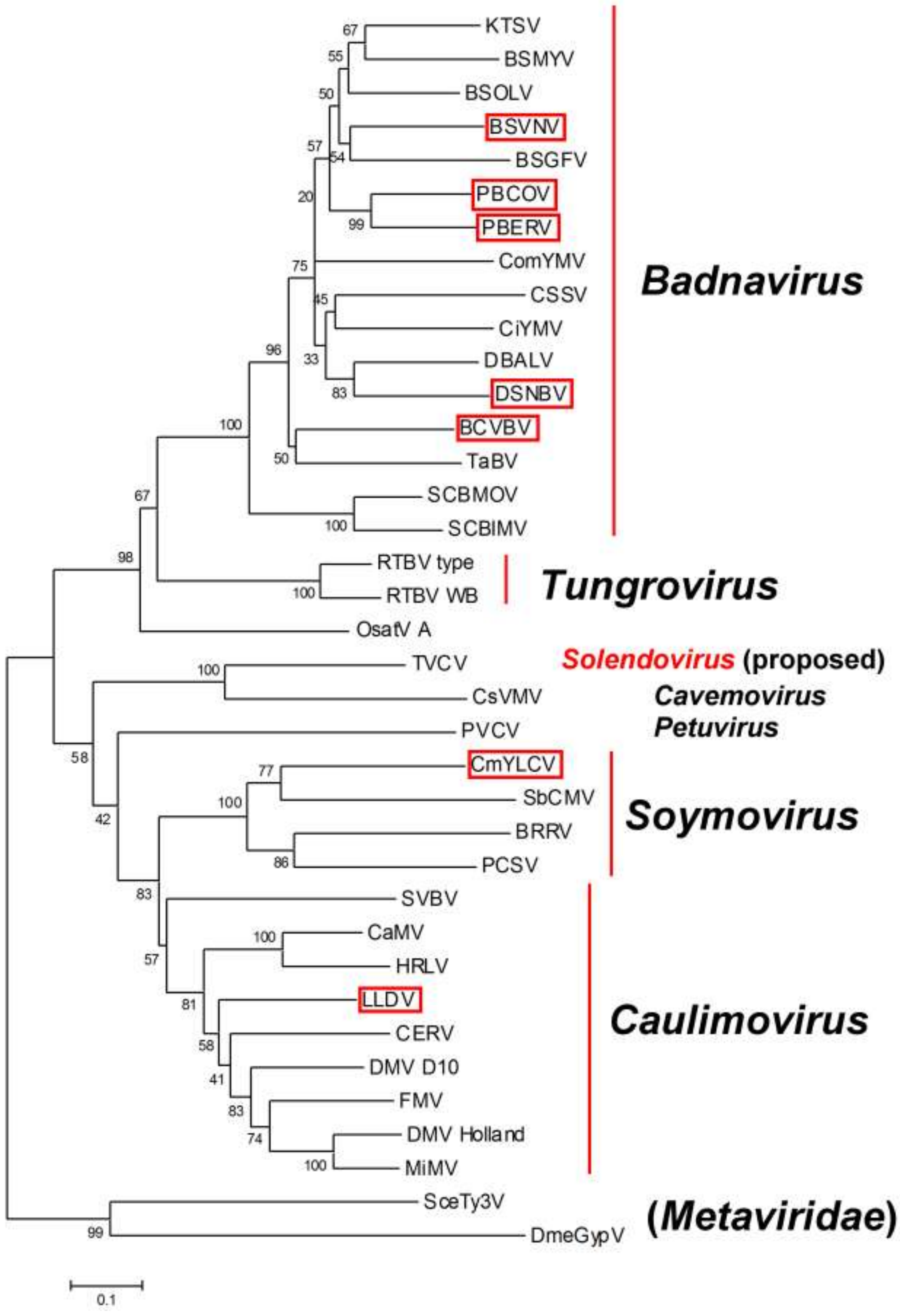
Seal, S., and Muller, E. (2007). Molecular analysis of a full-length sequence of a new yam badnavirus from Dioscorea sansibarensis. Archives of Virology 152, 819-825.

Tsai, C.-H., Su, H.-J., Wu, M.-L., Feng, Y.-C., and Hung, T.-H. (2008). Identification and detection of Bougainvillea spectabilis chlorotic vein-banding virus in different bougainvillea cultivars in Taiwan. Annals of Applied Biology 153, 187-193.

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
55
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
Badnavirus
98
RTBV type
100
RTBV WB
Tungrovirus
OsatV A
100
TVCV
Solendovirus (proposed)
CsVMV
Cavemovirus
58
PVCV
Petuvirus
77
CmYLCV
100
SbCMV
42
BRRV
Soymovirus
86
PCSV
83
SVBV
100
CaMV
57
HRLV
81
LLDV
58
CERV
Caulimovirus
41
DMV D10
83
FMV
74
DMV Holland
100
MiMV
SceTy3V
99
DmeGypV
(Metaviridae)
0.1