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:	***2014.012aP***	(to be completed by ICTV officers)

Short title: Creation of 7 new species 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:

ADW 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

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

EC comments: This proposal was conditionally approved. Please clarify the wording in the figure legend of the phylogenetic tree to state that the tree was built using the maximum likelihood method. Please 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: For Pagoda yellow mosaic associated virus, please provide evidence for the existence of an exogenous virus. If it is not possible, consider removing the creation of this particular species from the proposal.

AG comments: Evidence for the existence of an exogenous virus has now been provided in the taxonomic justification.

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	***2014.012aP***	(assigned by ICTV officers)

To create 7 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.

Name of new species:	**Representative isolate:**	**GenBank sequence accession number(s)**
Banana streak IM virus	IRFA 910	HQ659760.1
Banana streak UA virus	Likhako	HQ593107.1
Banana streak UI virus	Kisansa	HQ593108.1
Banana streak UL virus	Kibuzi	HQ593109.1
Banana streak UM virus	Mbwazirume	HQ593110.1
Fig badnavirus 1	Arkansas 1	JF411989.1
Pagoda yellow mosaic associated virus	pymav-01	KJ013302.1

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

Fig badnavirus 1 (FBV 1) should be recognized as a new badnavirus species for the following reasons:

1. The genome of FBV 1 is typical of the genus *Badnavirus*, and consists of a circular double-stranded DNA molecule of 7.1 kbp with three open reading frames (ORF). ORFIII encodes a large polyprotein containing movement protein, capsid protein, aspartic protease, reverse transcriptase (RT) and RNaseH (RH).
2. Although present in an endogenous form, there is strong evidence that the virus also exists in an exogenous form, as the virus is mechanically transmissible to seven other herbaceous plant species from different families. The genomic DNA is also amplifiable by rolling circle amplification (TempliPhi).
3. In a phylogenetic analysis, FBV 1 groups within the genus *Badnavirus* (see Fig. 1, Annex) and has ≤64% nucleotide sequence identity in the RT-RH region of the genome with other recognized badnavirus species, thus being far below the 80% nt threshold for demarcation of species.
4. Fig (*Ficus carica*) is a previously unreported host for a badnavirus.

Pagoda yellow mosaic associated virus (PYMaV) should be recognized as a new badnavirus species for the following reasons:

1. The genome of PYMaV is typical of the genus *Badnavirus*, and consists of a circular double-stranded DNA molecule of 7.4 kbp with three ORFs. ORFIII encodes a large polyprotein containing movement protein, capsid protein, aspartic protease, RT and RH.
2. In a phylogenetic analysis, PYMaV groups within the genus *Badnavirus* (see Fig. 1, Annex) and has ≤71% nucleotide sequence identity in the RT-RH region of the genome with other recognized badnavirus species, thus being far below the 80% nt threshold for demarcation of species.
3. Pagoda (*Styphnolobium japonicum*) is a previously unreported host for a badnavirus.
4. Available evidence suggests that this virus only exists in an exogenous form as viral DNA could only be PCR-amplified from pagoda leaves with yellow and mosaic leaves and not from healthy pagoda leaves.

Banana streak IM virus, Banana streak UA virus, Banana streak UI virus, Banana streak UL virus and Banana streak UM virus are all viruses that infect banana (*Musa* spp.). They all should be recognized as new badnavirus species for the following reasons:

1. Their genomes are typical of the genus *Badnavirus*, and consist of circular double-stranded DNA molecules of 7.4-7.8 kbp with three open reading frames (ORF). ORFIII encodes a large polyprotein containing movement protein, capsid protein, aspartic protease, reverse transcriptase and RNaseH.
2. In phylogenetic analyses, all viruses group within the genus *Badnavirus* and have ≤80.6% nucleotide sequence identity in the RT-RH region of the genome with each other and other recognized badnavirus species, thus being on or below the 80% nt threshold for demarcation of species.
3. All genome sequences have been generated by rolling circle amplification (TempliPhi), a technique that distinguishes exogenous from endogenous badnaviruses, or by cloning DNA from a purified virus preparation.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Geering ADW, Parry JN, Thomas JE (2011) Complete genome sequence of a novel badnavirus, Banana streak IM virus. Archives of Virology 156: 733-737.
James AP, Geijskes RJ, Dale JL, Harding RM (2011) Molecular characterisation of six badnavirus species associated with leaf streak disease of banana in East Africa. Annals of Applied Biology 158: 346-353.
Laney AG, Hassan M, Tzanetakis IE (2012) An integrated badnavirus is prevalent in fig germplasm. Phytopathology 102: 1182-1189.
Wang Y, Cheng X, Wu XM, Wang A, Wu X (2014) Characterization of complete genome and small RNA profile of pagoda yellow mosaic associated virus, a novel badnavirus in China. Virus Research 188: 103-108.

Annex:

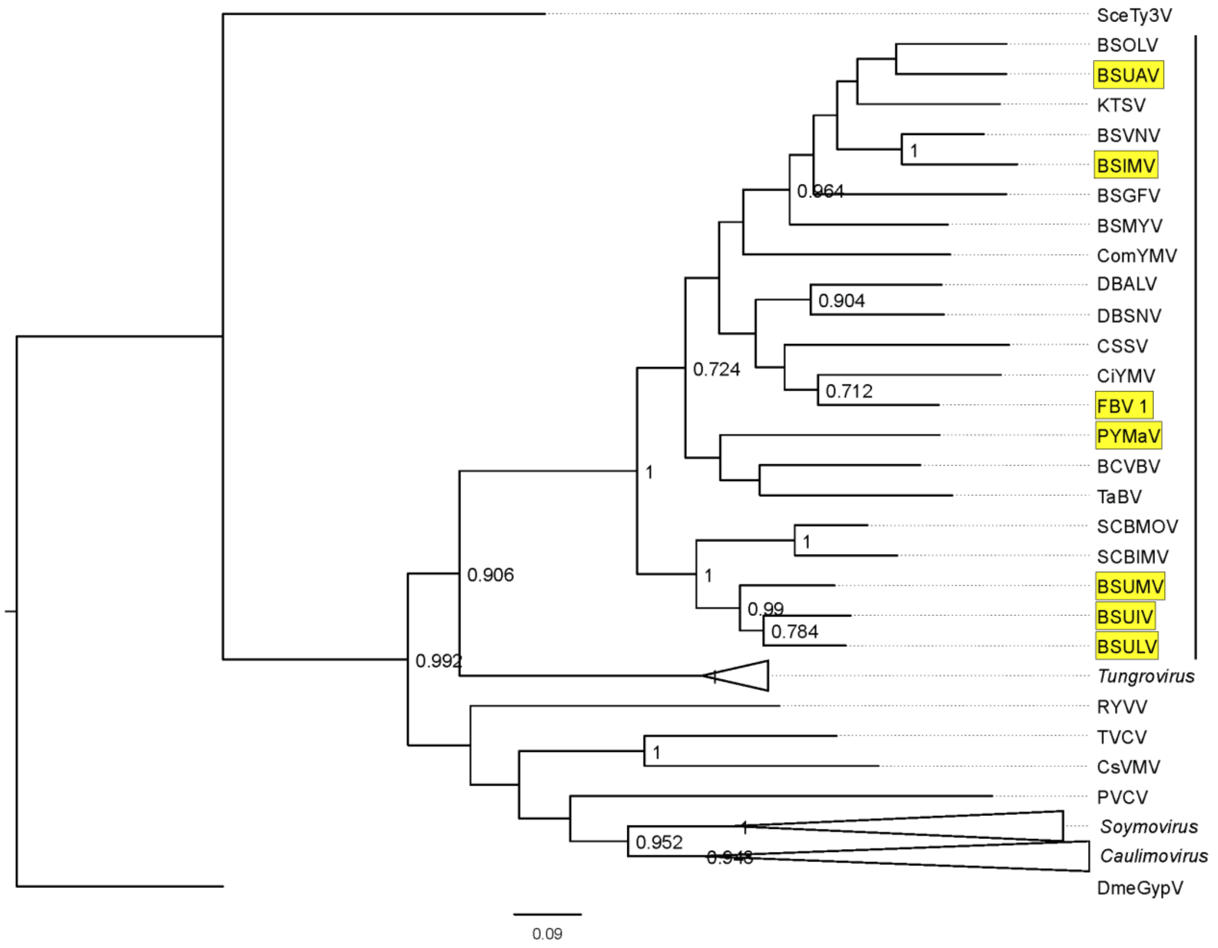

Figure 1. Phylogram of the *Caulimoviridae* built using the maximum likelihood method provided in the MEGA 6.06 suite of software. Reverse transcriptase-RNase H1 gene sequences, equivalent to nucleotides 4449-5648 of the cauliflower mosaic virus genome (NCBI accession NC_001497.1), were used for phylogenetic inference. Abbreviations of badnaviruses are: BSOLV, *Banana streak* OL *virus*; BSMYV, *Banana streak MY virus*; KTSV, *Kalanchoe top-spotting virus*; BSUAV, Banana streak UA virus; BSVNV, *Banana streak VN virus*; BSGFV, *Banana streak GF virus*; BSIMV, Banana streak IM virus; BSUIV, Banana streak UI virus; BSULV, Banana streak UL virus; BSUMV, Banana streak UM virus; BCVBV, *Bougainvillea chlorotic vein banding virus*; ComYMV, *Commelina yellow mottle virus*; CSSV, *Cacao swollen shoot virus*; CiYMV, *Citrus yellow mosaic virus*; DBSNV, *Dioscorea bacilliform SN virus*; PaYMV; FBAKV, Fig badnavirus 1; PYMaV, Pagoda yellow mosaic associated virus; SCBIMV, *Sugarcane bacilliform IM virus*; SBMOV, *Sugarcane bacilliform* MO *virus*; TaBV, *Taro bacilliform virus*. Proposed new badnavirus species are highlighted in yellow. Abbreviations of other virus species 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 caulimovirus, soymovirus and tungrovirus species have been collapsed. Bootstrap values for 500 replicates are shown in the nodes of the branches (values less than 0.7 have been excluded).