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:	***2011.013aP***	(to be completed by ICTV officers)

Short title: Two new species in the genus *Badnavirus*, 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:

Jan Kreuze (J.KREUZE@CGIAR.ORG) and Andrew 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:

Approved by the group. No comments.

Date first submitted to ICTV: 22 August 2011
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	***2011.013aP***	(assigned by ICTV officers)

To create 2 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:**
Sweet potato pakakuy virus	FJ560943 = NC_015655
Grapevine vein clearing virus	JF301669 = NC_015784

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 suggested species, Sweet potato pakakuy virus (SPPV) and Grapevine vein clearing virus (GVCV), have the genome organization of other species in the genus *Badnavirus* except that ORF3 is divided into two ORFs containing the movement protein and coat protein (ORF3a) and aspartic protease, reverse transcriptase (RT) and RNaseH (ORF3b) domains, respectively. Evolution of this genome organization appears to have evolved on two occasions and is not considered a significant enough difference to warrant separation of these viruses from the genus *Badnavirus*. GVCV and SPPV are more closely related to badnaviruses with a more typical genome organization (movement protein, coat protein, aspartic protease, reverse transcriptase and RNase H domains in one polyprotein encoded by ORF3) than they are to each other.

Within the reverse transcriptase and RNase H domains, SPPV and GVCV have less than 70% nucleotide identity with any other badnavirus species and therefore clearly exceed the 80% threshold used to demarcate badnavirus species. Two different strains of SPPV exist and these are 82.3% identical in the abovementioned region of the genome.

The grapevine genome has been sequenced and it is clear that the GVCV sequence derives from an exogenous virus (one that is not integrated in the genome of its host). SPPV occurs in very low titers in sweetpotato, does not cause obvious symptoms and can be graft-transmitted to the indicator plant *Ipomoea setosa*. SPPV is only detectable by PCR and siRNA deep sequencing and because it cannot be detected by nucleic acid hybridization in either a dot-blot or Southern blot assay it is assumed that the virus is not integrated in the genome of the host.

The name ‘Grapevine vein clearing virus’ refers to the symptoms associated with infection. The word ‘pakakuy’ in ‘Sweet potato pakakuy virus’ means ‘hidden’ in the native Quechua language of Peru and refers to its symptomless and low titer nature.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

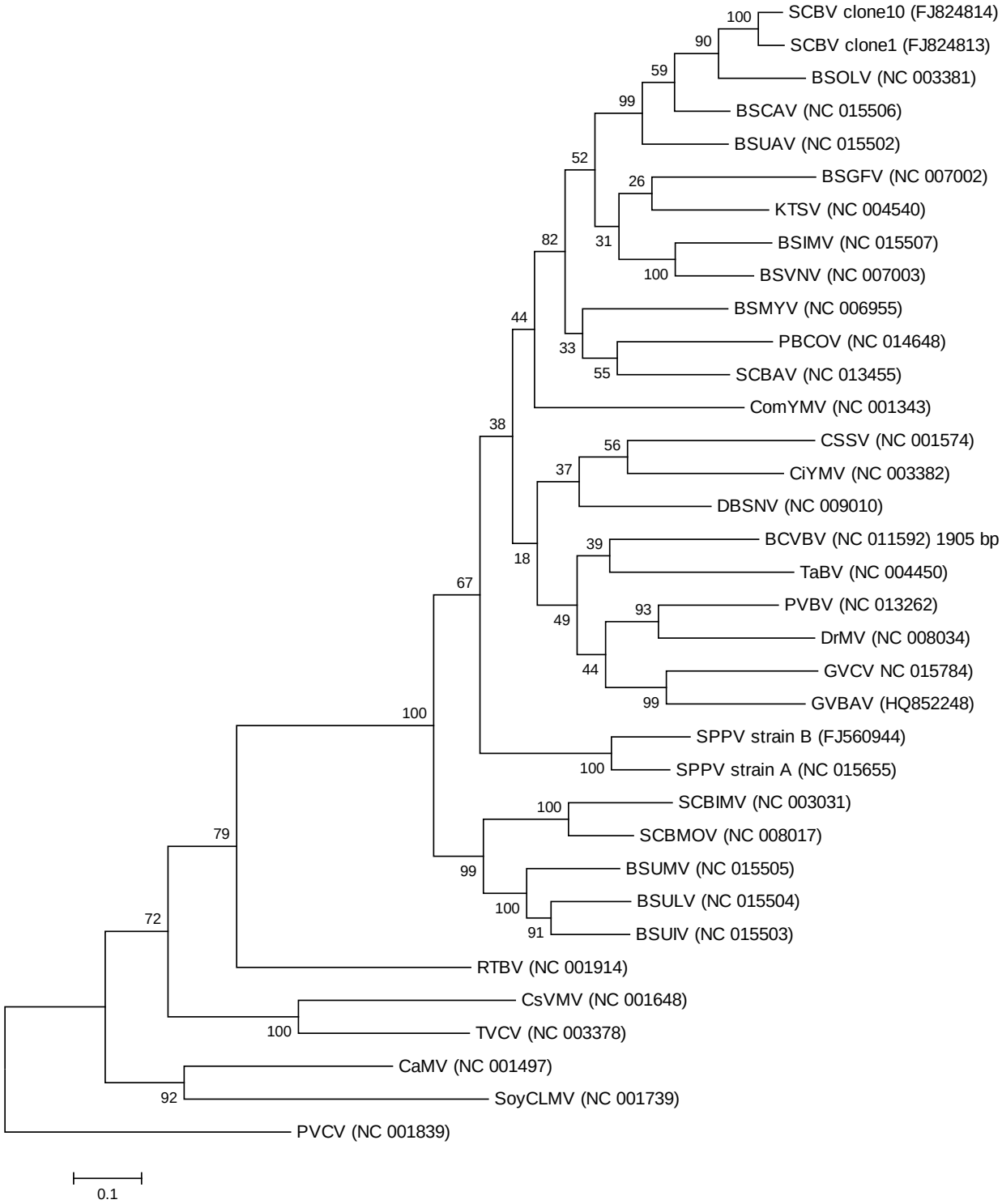
References:

1. Kreuze, J. F., Perez, A., Untiveros, M., Quispe, D., Fuentes, S., Barker, I., et al. 2009. Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: A generic method for diagnosis, discovery and sequencing of viruses. Virology. 388:1-7
2. Zhang Y, Singh K, Kaur R, Qiu W (2011) Association of a novel DNA virus with the grapevine vein-clearing and vine decline syndrome. *Phytopathology* **101**, 1081-1090.

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. Maximum likelihood phylogram depicting relationships within the genus *Badnavirus*. The phylogram was inferred from an alignment of nucleotide sequences within ORF3 that encode for the reverse transcriptase and RNaseH domains. GenBank accessions are provided in brackets after the virus acronyms. The badnaviruses are: *Banana streak OL virus* (BSOLV), Banana streak CA virus (BSCAV), Banana streak UA virus (BSUAV), Banana streak GF virus (BSGFV), Banana streak IM virus (BSIMV), *Banana streak MY virus* (BSMYV), Banana streak VN virus (BSVNV), Banana streak UI virus (BSUIV), Banana streak UL virus (BSULV), Banana streak UM virus (BSUMV), *Kalanchoë top spotting virus* (KTSV), *Pineapple bacilliform CO virus* (PBCOV), Cacao swollen shoot virus (CSSV), *Commelina yellow mottle virus* (ComYMV), Dioscorea bacilliform SN virus (DBSNV), *Citrus yellow mosaic virus* (CiYMV), Pelargonium vein banding virus (PVBV), Dracaena mottle virus (DrMV), Grapevine vein clearing virus (GVCV), Sweet potato pakakuy virus (SPPV), *Gooseberry vein banding associated virus* (GVBAV), *Sugarcane bacilliform MO virus* (SCBMOV) and Sugarcane *bacilliform IM virus* (SCBIMV). Outgroups are: *Rice tungro bacilliform* (RTBV), *Cassava vein mosaic virus* (CsVMV), *Tobacco vein clearing virus* (TVCV), *Cauliflower mosaic virus* (CaMV), *Soybean chlorotic mottle virus* (SoyCMV) and *Petunia vein clearing virus* (PVCV)


SCBV clone10 (FJ824814)
SCBV clone1 (FJ824813)
BSOLV (NC 003381)
BSCAV (NC 015506)
BSUAV (NC 015502)
BSGFV (NC 007002)
KTSV (NC 004540)
BSIMV (NC 015507)
BSVNV (NC 007003)
BSMYV (NC 006955)
PBCOV (NC 014648)
SCBAV (NC 013455)
ComYMV (NC 001343)
CSSV (NC 001574)
CiYMV (NC 003382)
DBSNV (NC 009010)
BCVBV (NC 011592) 1905 bp
TaBV (NC 004450)
PVBV (NC 013262)
DrMV (NC 008034)
GVCV NC 015784)
GVBAV (HQ852248)
SPPV strain B (FJ560944)
SPPV strain A (NC 015655)
SCBIMV (NC 003031)
SCBMOV (NC 008017)
BSUMV (NC 015505)
BSULV (NC 015504)
BSUIV (NC 015503)
RTBV (NC 001914)
CsVMV (NC 001648)
TVCV (NC 003378)
CaMV (NC 001497)
SoyCLMV (NC 001739)
PVCV (NC 001839)
0.1