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:	***2015.026aP***	(to be completed by ICTV officers)

Short title: Creation of 4 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):

MULLER Emmanuelle, CIRAD, UMR BGPI, Campus International de Baillarguet, TA A54/K 34398 Montpellier cedex 5

Corresponding author with e-mail address:

Emmanuelle Muller emmanuelle.muller@cirad.fr

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 Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: 15-06-2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

EC Comments: In view of the likely ratification of a general proposal prohibiting the use of diacritics characters in species name, the words *Côte d'Ivoire* pose problems with the accent grave and the apostrophy. Because it may not be a good idea to misspell the name of a country, it was suggested that an alternative name could be adopted. One possibility that was suggested was to use the abbreviation CI instead of spelling out *Côte d'Ivoire*. Other options could also be considered. Please also correct the table on page 2 where species name are misaligned with the isolate names and GenBank numbers.

Response: The name Cacao swollen shoot CD virus was adopted.

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	***2015.026aP***	(assigned by ICTV officers)

To create 4 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)**
Sugarcane bacilliform Guadeloupe A virus	SCBV-R570	FJ824813
Sugarcane bacilliform Guadeloupe D virus	SCBV-Ba3	FJ439817
Cacao swollen shoot Togo A virus	CSSV-Wobe12	AJ781003
Cacao swollen shoot CD virus	CSSV-CI152	JN606110

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

Sugarcane bacilliform Guadeloupe A virus (SCBGAV) and *Sugarcane bacilliform Guadeloupe D virus (SCBGDV)* are viruses that infect sugarcane. They were found in Guadeloupe. They 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 7.3-7.4 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, both viruses group within the genus *Badnavirus* and differ by more than 20% in the RT-RH region from previously recognized badnavirus species infecting sugarcane Sugarcane bacilliform Mor virus (SCBMOV) and Sugarcane bacilliform IM virus (SCBIMV) thus being below the 80% nt threshold for demarcation of species. In the RT-RH region, SCBGAV and SCBGDV share 68.2% nucleotide identity; SCBGAV shares 63% nucleotide identity with SCBMOV and 62.2% nucleotide identity with SCBIMV; SCBGDV shares 62% nucleotide identity with SCBMOV and 61.5% nucleotide identity with SCBIMV.
3. Both genome sequences have been generated from full length copies of viral genomes amplified by long range PCR performed on total DNA extracted from infected plants, using a Taq DNA polymerase with proofreading activity and a low error rate. There is no evidence of endogenous badnavirus sequence in the genome of sugarcane.

Cacao swollen shoot Togo A virus (CSSTAV) and *Cacao swollen shoot CD virus (CSSCDV)* are viruses that infect cacao. They were found in Togo and Côte d'Ivoire, respectively. They 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 7.0-7.3 kbp with five open reading frames (ORF). ORFIII encodes a large polyprotein containing movement protein, capsid protein, aspartic protease, reverse transcriptase and RNaseH.
2. In phylogenetic analyses, both viruses group within the genus *Badnavirus* and differ by more than 20% in the RT-RH region from previously recognized species Cacao swollen shoot virus thus being below the 80% nt threshold for demarcation of species. In the RT-RH region, CSSTAV (Wobe 12) and CSSCDV (CI152) share 75.2% nucleotide identity. In the RT-RH region, CSSTAV (Wobe 12) and CSSCDV (CI152) share 76.1% and 72% nucleotide identity with CSSV-Agou1, respectively.
3. Both genome sequences have been generated from full length copies of viral genomes amplified by long range PCR performed on total DNA extracted from infected plants, using a Taq DNA polymerase with proofreading activity and a low error rate. There is no evidence of endogenous badnavirus sequence in the fully sequenced genome of cacao.

additional material in support of this proposal

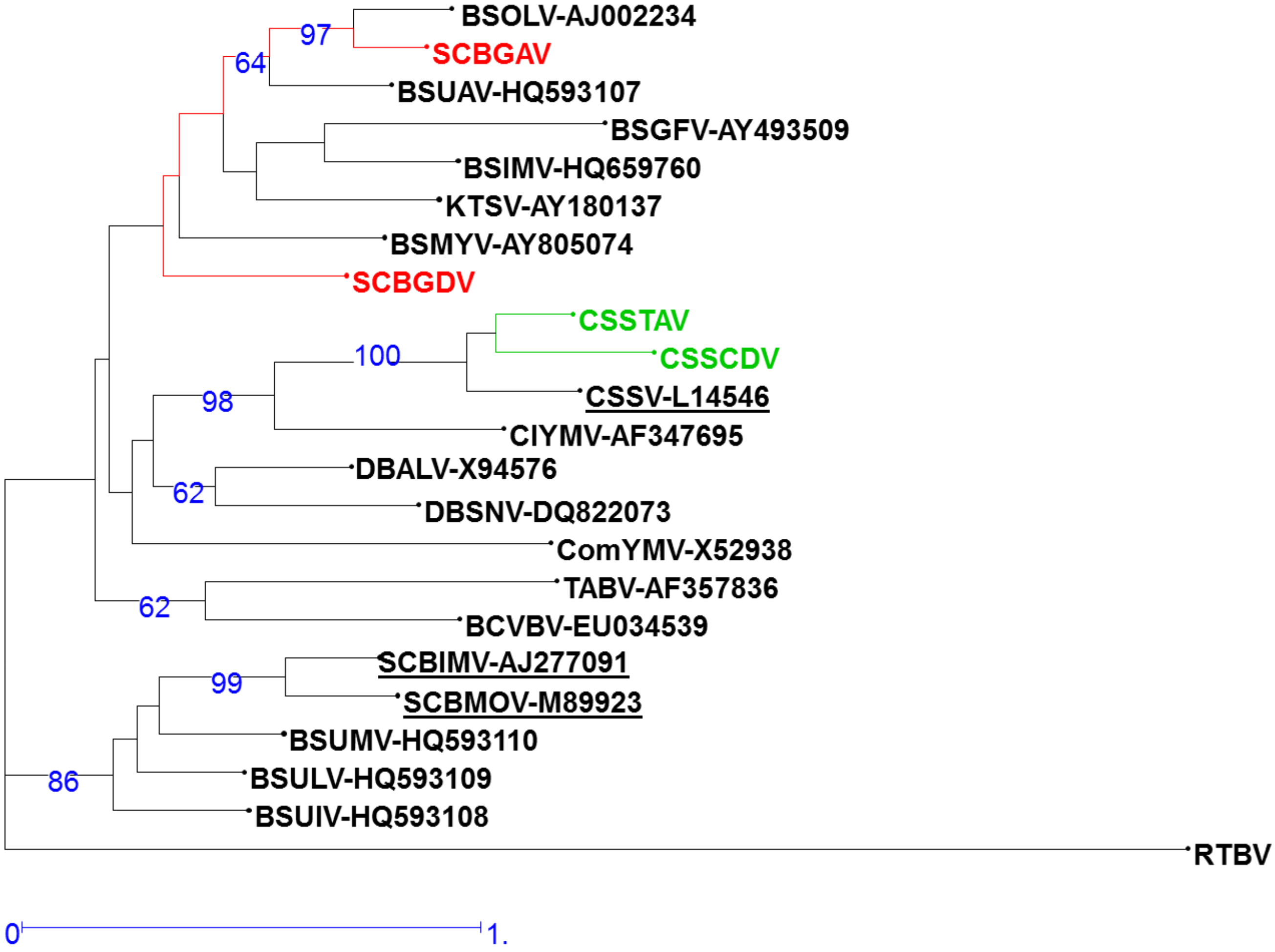
References:

Kouakou K, Kebe I, Kouassi N, Aké S, Cilas C and Muller E. 2012. Geographical distribution of Cacao swollen shoot virus (CSSV) molecular variability in Côte d'Ivoire. Plant Disease 96: 1445-1450.

Muller E, Sackey S. 2005. Molecular variability analysis of five new complete Cacao swollen shoot virus genomic sequences. Archives of Virology 150: 53-66.

Muller E., Dupuy V., Blondin L., Bauffe F., Daugrois J.-H., Laboureau N. and Iskra-Caruana M.-L. 2011. High molecular variability of sugarcane bacilliform viruses in Guadeloupe implying the existence of at least three new species. Virus Research 160: 414-419

Annex



Maximum likelihood phylogeny of badnaviruses RTase/RNaseH sequences constructed with PhyML software (100 bootstraps repeats, values less than 60% have been excluded). Sequences have been aligned with Muscle algorithm and filtered by the Gblock software to eliminate poorly aligned positions from the multiple alignments. Proposed new virus species infecting sugarcane and cacao are shown in red and green, respectively. Previously approved badnavirus species infecting cacao (*Cacao swollen shoot virus*, CSSV) and sugarcane (*Sugarcane bacilliform IM virus*, SCBIMV) and *Sugarcane bacilliform MO virus*, SCBMOV) are underlined. Abbreviations of badnaviruses are: BSOLV, *Banana streak OL virus*; BSMYV, *Banana streak MY virus*; KTSV, *Kalanchoe top-spotting virus*; BSUAV, *Banana streak UA 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*; DBALV, *Dioscorea bacilliform AL virus*; SCBIMV, *Sugarcane bacilliform IM virus*; SCBMOV, *Sugarcane bacilliform MO virus*; TaBV, *Taro bacilliform virus*. *Rice tungro bacilliform virus* (RTBV) is a tungrovirus species.