This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

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.

Part 1: **TITLE, AUTHORS, etc**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.017P*** | | | | (to be completed by ICTV officers) |
| **Short title:** 6 new species in the genus *Badnavirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Andrew Geering, Moritz Bömer, Aliyu A. Turaki, Susan E. Seal, Pierre-Yves Teycheney | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Pierre-Yves Teycheney, teycheney@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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | [*Caulimoviridae*](https://talk.ictvonline.org/information/w/members/466/caulimoviridae-study-group)  Teycheney, Pierre-Yves (Chair) | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 2017 | |
| Date of this revision (if different to above): | | | |  | |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.017P.N.v1.Badnavirus\_6sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 3:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

|  |
| --- |
| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
|  |

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| Bömer M, Turaki A, Silva G, Kumar P, Seal SA (2016) Sequence-independent strategy for amplification and characterisation of episomal Badnavirus sequences reveals three previously uncharacterised yam badnaviruses. *Viruses* 8: 188.  Chingandu N, Zia-Ur-Rehman M, Sreenivasan TN, Surujd. eo-Maharaj S, Umaharan P, Gutierrez OA, Brown JK (2017) Molecular characterization of previously elusive badnaviruses associated with symptomatic cacao in the New World. *Arch Virol*. 162(5):1363-1371.  Li Y, Deng C, Qiao Y, Zhao X, Zhou Q (2017) Characterization of a new badnavirus from *Wisteria sinensis*. *Arch Virol* doi: 10.1007/s00705-017-3322-4.  Umber M, Gomez RM, Gélabale S, Bonheur L, Pavis C, Teycheney PY (2017) The genome sequence of Dioscorea bacilliform TR virus, a member of the genus *Badnavirus* infecting *Dioscorea* spp., sheds light on the possible function of endogenous Dioscorea bacilliform viruses. *Arch Virol* 162(2):517-521. |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**The following has been extracted from the above references to support this proposal:**

Cacao mild mosaic virus(CaMMV) and Cacao yellow vein banding virus (CYVBV) can be considered new badnavirus species for the following reasons:

1. CaMMV and CYVBV have circular dsDNA genomes with four putative ORFs (ORFs 1 to 4). A large ORF (ORF3) encodes a putative polyprotein with conserved aspartic protease, reverse transcriptase and ribonuclease H domains analogous to those of other badnaviruses.
2. Both genomes have a tRNAMet primer binding site at positions 1-18.
3. In phylogenetic analyses using badnavirus RT/RNAseH domain nucleotide sequence, CaMMV and CYVBV group within the genus *Badnavirus*. Their closest relative is Bougainvillea chlorotic vein banding virus (Fig. 1).
4. CaMMV and CYVBV RT/RNase H domains and complete genome sequences share 61.8% and 60% nt identity, respectively.
5. CaMMV and CYVBV nucleotide sequences corresponding to the RT/RNAse H domain share 59-71% and 59-62% identity with those of other badnaviruses, respectively, which is below the 80% threshold for discrimination of strains and species within the genus *Badnavirus* (Table 1).

Dioscorea bacilliform RT virus 1 (DBRTV1), Dioscorea bacilliform RT virus 2 (DBRTV2) and Dioscorea bacilliform TR virus (DBTRV) can be considered new badnavirus species for the following reasons:

1. The circular dsDNA genomes of DBRTV1 (7702bp), DBRTV2 (7438bp) and DBTRV (7333 bp) have 3 ORFs, including a large ORF (ORF3) encoding a putative polyprotein with conserved movement protein, coat protein, aspartic protease, reverse transcriptase and ribonuclease H domains analogous to those of other badnaviruses.
2. All three genomes have a tRNAMet primer binding site at positions 1-18.
3. In phylogenetic analyses using badnavirus nucleotide sequences corresponding to the conserved RT/RNAseH domain, DBRTV1, DBRTV2 and DBTRV group within the genus *Badnavirus*, in a monophyletic group comprising all known badnaviruses infecting yams. DBRTV1 and DBTRV closest relative is Dioscorea bacilliform AL virus (DBALV), whereas DBRTV2 closest relative is Dioscorea bacilliform SN virus (DBSNV) (Fig. 1).
4. DBRTV1, DBRTV2 and DBTRV nucleotide sequences corresponding to the RT/RNAse H domain share 58.5-75.2% nt sequence identity with similar regions of other badnaviruses, which is below the 80% threshold for discrimination of strains and species within the genus *Badnavirus*.

Wisteria badnavirus 1 (WBV1) can be considered a new badnavirus species for the following reasons:

1. The circular dsDNA genome of WBV1 (7362 bp) has 4 ORFs, including a large ORF (ORF3) encoding a putative polyprotein with conserved movement protein, aspartic protease, reverse transcriptase and ribonuclease H domains analogous to those of other badnaviruses.
2. The genome of WBV1 has a tRNAMet primer binding site at positions 1-18.
3. In phylogenetic analyses using badnavirus nucleotide sequences corresponding to the RT/RNAseH domain, WBV1 groups within the genus *Badnavirus* (Fig. 1). WBV1 closest relative isPagoda yellow mosaic associated virus (PaYMV), with which it shares 75.6% identity in the RT/RNAseH domain.

****

**Fig. 1. Phylogenetic tree showing placement of cacao mild mosaic virus (CaMMV), cacao yellow vein banding virus (CYVBV), Dioscorea bacilliform RT virus 1 (DBRTV1), Dioscorea bacilliform RT virus 2 (DBRTV2), Dioscorea bacilliform TR virus (DBTRV) and Wisteria badnavirus 1 (WBV1) in genus *Badnavirus*.**

Maximum likelihood analysis with 1000 bootstrap sets was performed on nucleotide sequences corresponding to the RT-RNase H domains. Virus isolates corresponding to species in other genera in the *Caulimoviridae* family are also included. Virus sequences corresponding to the proposed new species are shown in red boxes.

Acronyms are: DBRTV1: Dioscorea bacilliform RT virus 1; DBTRV: Dioscorea bacilliform TR virus; DBRTV2: Dioscorea bacilliform RT virus 2; DBALV: Dioscorea bacilliform AL virus; DBSNV: Dioscorea bacilliform SN virus; MBV1: mulberry badnavirus 1;FBAKV: fig badnavirus; TaBCHV: taro bacilliform CH virus; CiYMV: Citrus yellow mosaic virus; ComYMV: Commelina yellow vein mosaic virus; BSGFV: banana streak GF virus; BSMYV: banana streak MY virus; KTSV: Kalanchoe top-spotting virus; BSOLV: banana streak OL virus; BSUAV: banana streak UA virus; BSVNV: banana streak VN virus; BSIMV: banana streak IM virus; CSSV: cacao swollen shoot virus; WBV1: Wisteria badnavirus 1; PaYM: Pagoda yellow mosaic associated virus; TaBV: taro bacilliform virus; YNMoV: Yacon necrotic mottle virus; BVCBV Bougainvillea chlorotic vein banding virus; CaMMV: cacao mild mosaic virus; CYVBV: cacao yellow vein banding virus; ScBMOV: sugarcane bacilliform MO virus; SCBIMV: sugarcane bacilliform IM virus; BSUMV: banana streak UM virus; BSUIV: banana streak UI virus; BSULV: banana streak UL virus; RTBV: rice tungro bacilliform virus; SceTy3V: Saccharomyces cerevisiae Ty3 virus; DmeGypV: Drosophila melanogaster Gypsy virus; PVCV: Petunia vein clearing virus; TVCV: tobacco vein clearing virus; CsVMV: cassava vein mosaic virus; RYVV: rose yellow vein virus; CmYLCV: Cestrum yellow leaf curling virus; SbCMV: soybean chlorotic mottle virus; BRRV: blueberry red ringspot virus; PCSV: peanut chlorotic streak virus; SVBV: strawberry vein banding virus; CaMV: cauliflower mosaic virus; HRLV: horseradish latent virus; CERV: Carnation etched ring virus; AMMV: Atractylodes mild mottle virus; SPuV: soybean Putnam virus; LLDV: Lamium leaf distortion virus; DMV: Dahlia mosaic virus; MiMV: Mirabilis mosaic virus; FMV: figwort mosaic virus.

**Table 1: Percent nucleotide identities for the *Caulimoviridae* in ORF3 nucleotide sequences corresponding to the conserved RT/RNAseH domain.**

Identities for the proposed new species are highlighted in yellow.

