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: Mulberry badnavirus-1; Michela Chiumenti, Massimiliano Morelli, Toufic Elbeaino, Livia Stavolone and Angelantonio Minafra

TITLE, AUTHORS, etc

Code assigned:	***2016.015aP***	(to be completed by ICTV officers)

Short title: *Mulberry badnavirus 1*, a new species in the *Badnavirus* genus
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2 X** **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Michela Chiumenti, Massimiliano Morelli, Toufic Elbeaino, Livia Stavolone and Angelantonio Minafra

Corresponding author with e-mail address:

Michela Chiumenti: michela.chiumenti@ipsp.cnr.it

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)	**Plant Viruses Subcommittee** **Caulimoviridae Study Group**

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

Date first submitted to ICTV: July 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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	***2016.015aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Badnavirus***
Subfamily:	
Family:	***Caulimoviridae***
Order:	***Unassigned***

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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Mulberry badnavirus 1	Mulberry badnavirus 1, Lebanon34	NC_026020.2; LN651258.2

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 11

The criteria demarcating species in the genus are:
- Differences in host ranges: To best of our knowledge no other badnavirus has been reported from *Morus* spp. In particular, we found MBV1 either on *Morus alba* or *Morus nigra*.
- Differences in polymerase (RT/RNAse H) nt sequences of more than 20%: BLASTn analysis of RT/RNaseH region evidenced that MBV-1 shares less than 80% nt identity with any closely related badnavirus (CSSV, FBV1, CiMV).
- Differences in gene product sequences: This virus encodes a single main ORF/polyprotein, containing all the functional motifs needed for replication; including the conserved domain of unknown function characteristic of badnaviruses and the smaller ORF I in the other members of the genus. Furthermore, this virus presents the coexistence of an encapsidated defective (less than-full-length) genome, capable to induce infection in healthy plant without the presence of the full-length molecule.
- Differences in vector specificities: the vector has not been identified.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Elbeaino T, Chiumenti M, De Stradis A, Digiaro M, Minafra A, Martelli GP (2013) Identification of a new badnavirus infecting mulberry. J Plant Pathol 95:207-210.

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.

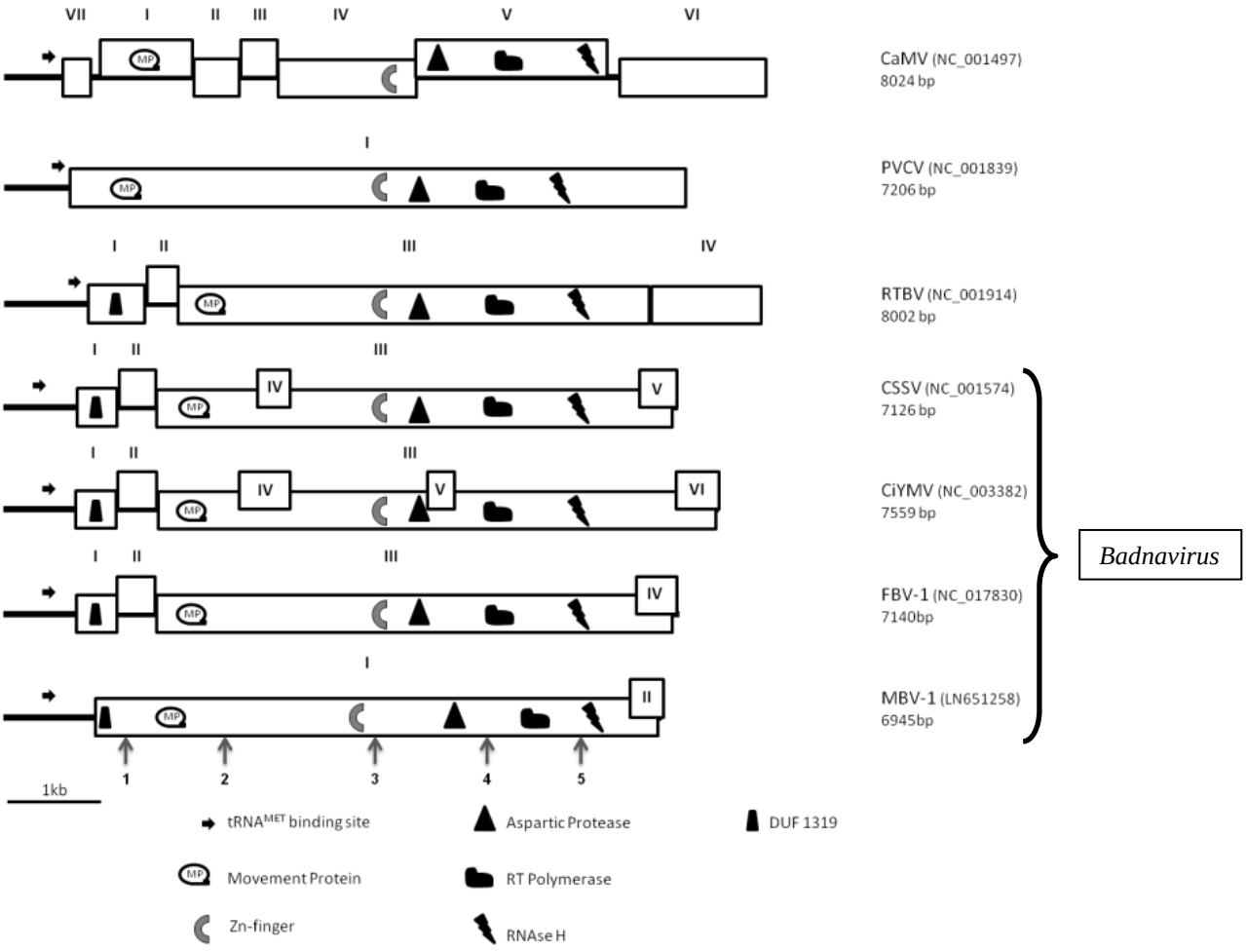

Figure 1. Graphical representation of the genome organisations of selected members of the *Caulimoviridae* family. Boxes represent ORFs, with respective numbers indicated at the top. The position of conserved motifs (described at the bottom) is shown for each genome. Accession numbers and genome lengths are indicated for each virus at the right. Grey numbered arrows below the MBV1 genome indicate the position of predicted coiled coils.

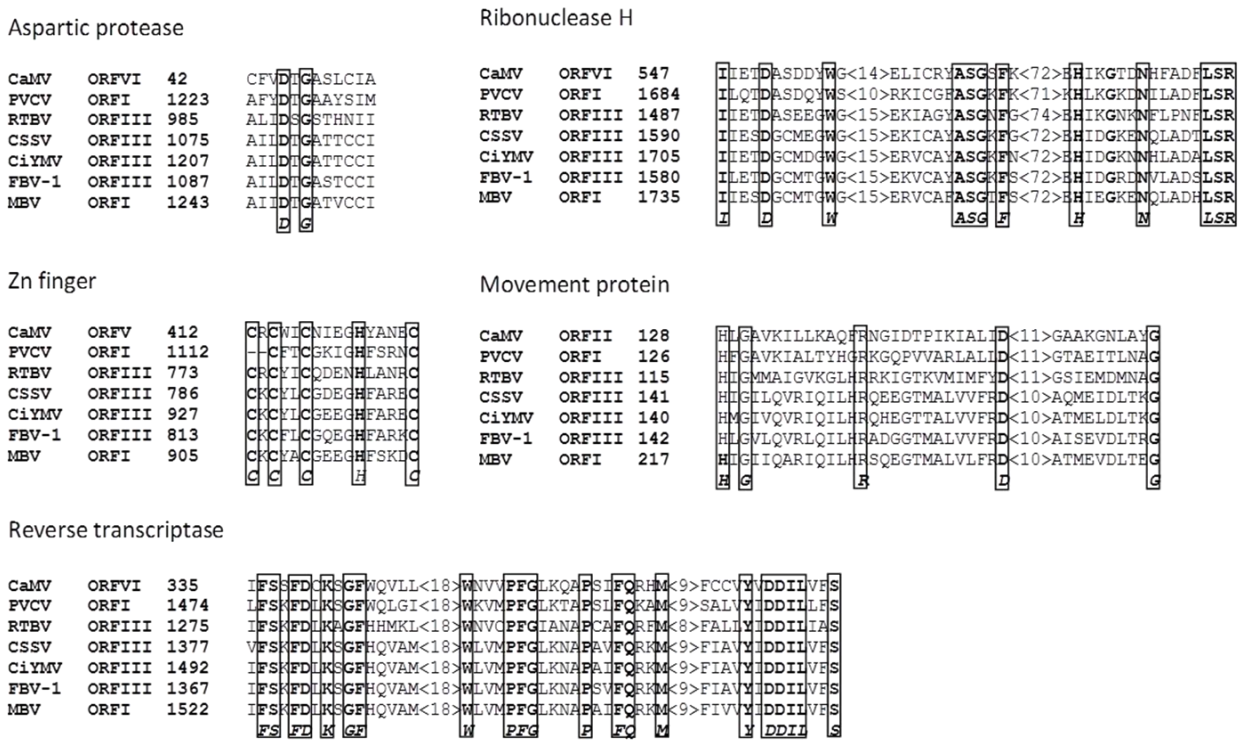

Figure 2. Amino acid alignment of biologically significant homologous regions of proteins encoded by representative members of the *Caulimoviridae* family. Virus acronyms are indicated in front of each sequence, along with ORF designations and the number of residues separating the protein N-termini from the aligned segment. Boxes mark identical amino acids, also reported in italics below the alignment. The spacing between amino acid blocks is given in angle brackets.

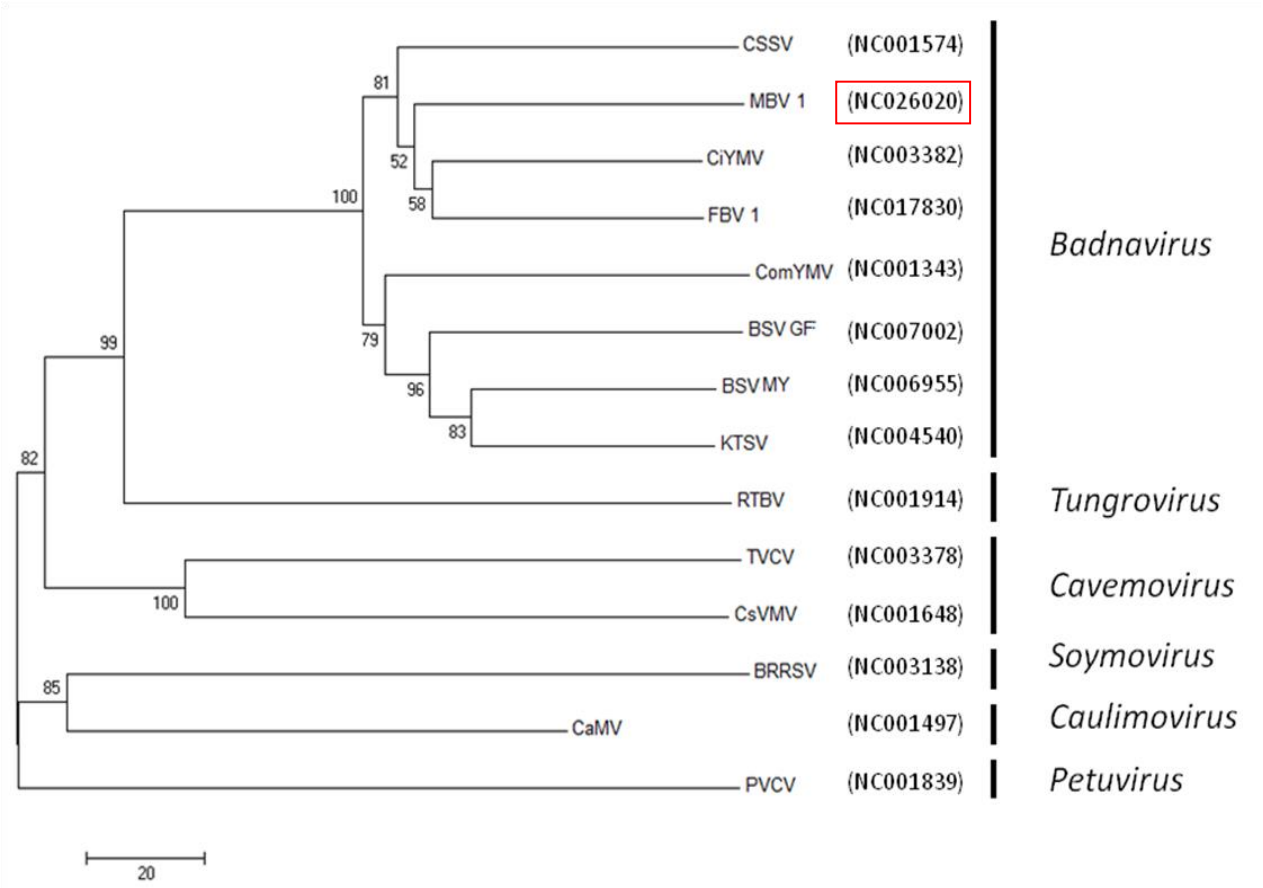

Figure 3. Phylogenetic tree obtained by the Neighbour-Joining method, indicating the distance among members of the *Caulimoviridae* family. Branch lengths are proportional to sequence distances. The scale represents a relative genetic distance of 20 aa changes. Sequences were compared at the amino acid level in the RT-RNAseH region. Validation of branches was performed by bootstrap analysis (1000 replications). Acronyms of the viruses included in the analysis are indicated at the left and their accession numbers are provided. RTBV: *Rice tungro bacilliform virus*; BSGFV: *Banana streak GF virus*; KTSV: *Kalanchoe top-spotting virus;* BSMYV: *Banana streak Mysore virus*; DBV: *Dioscorea bacilliform virus;* ComYMV: *Commelina yellow mottle virus;* CSSV*: Cacao swollen shoot virus*; FBV1: *Fig badnavirus 1*; CiYMV: *Citrus yellow mosaic virus;* MBV1*:* Mulberry badnavirus 1; CaMV: *Cauliflower mosaic virus;* PVCV*: Petunia vein clearing virus;* CsVMV*: Cassava vein mosaic virus*; TVCV: *Tobacco vein clearing virus;* BRRV: *Blueberry red ringspot virus*.

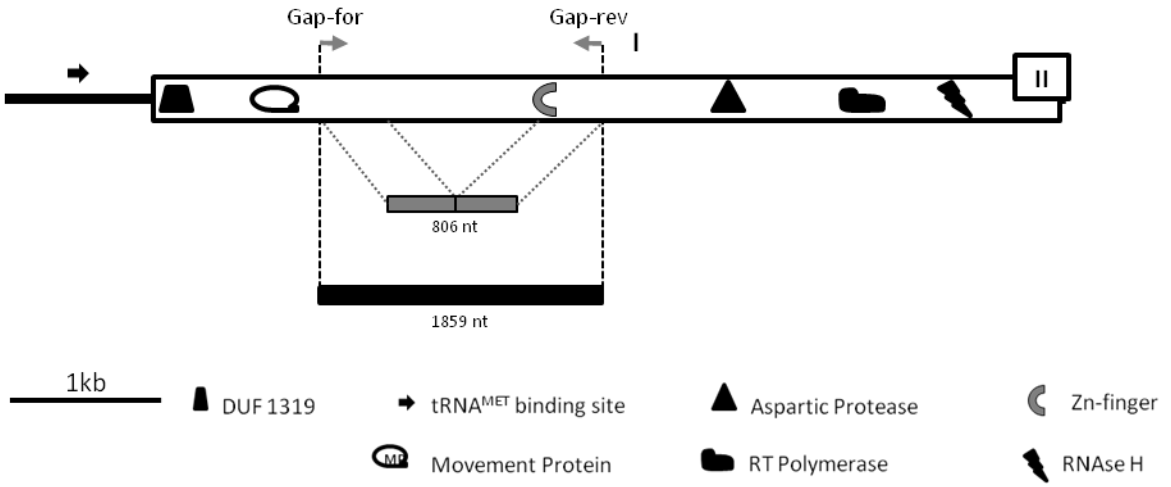

Figure 4. Graphical representation of the MBV1 genome, with its functional domains, described at the bottom. Grey arrows represent the primers flanking the gap region in the defective genome. Black and grey rectangles indicate the different amplicons obtained with the same couple of primers (Gap-for/Gap-rev) from the two genomic templates. Amplicon dimensions are indicated.