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:	***2015.025aP***	(to be completed by ICTV officers)

Short title: Creation of 1 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):

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pierre-yves.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 (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:

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	***2015.025aP***	(assigned by ICTV officers)

To create 1 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)**
Grapevine Roditis leaf discoloration-associated virus	GRLDaV-w4	HG940503

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

Grapevine Roditis leaf discoloration-associated virus (GRLDaV) should be considered a new species in the genus *Badnavirus* for the following reasons:

1. GLRDaV was discovered as part of a high throughput RNA-Seq survey of a symptomatic grape sampled in Crete (Greece). It was characterized from a single source plant. A complete virus genome was assembled from RNA-Seq data and confirmed by Sanger sequencing of PCR-amplified overlapping fragments covering the entire viral genome.
2. GLRDaV is clearly an exogenous virus as it was successfully graft transmitted to grape and mechanically inoculated to indicator plant *Physalis floridana*. Small scale survey showed that GLRDaV is present in grape in two other distant Greek provinces.
3. GLRDaV genome is 6988 nt; it has four open reading frames (ORF) and an identical genome organization to that of *Fig badnavirus 1* (FBV-1), *Cacao swollen shoot virus* (CSSV) and *Pagoda yellow mosaic associated virus* (PYMAV). GLRDaV ORF3 encodes a large polyprotein which harbors the motifs for the movement protein (MP), coat protein (CP), aspartic protease, reverse transcriptase (RT) and RNaseH domains commonly found in the equivalent proteins of badnaviruses.
4. In a phylogenetic analysis using conserved RT-RH gene sequences, GLRDaV groups within the genus *Badnavirus* (Figure 1, Annex).
5. Phylogenetic analyses show that GLRDaV is most closely related to FBV-1, with which it shares 79.7% nucleotide identity in the RT-RH region; this value is very slightly above the 20% cut-off value used as the species demarcation criterion in the genus *Badnavirus*.

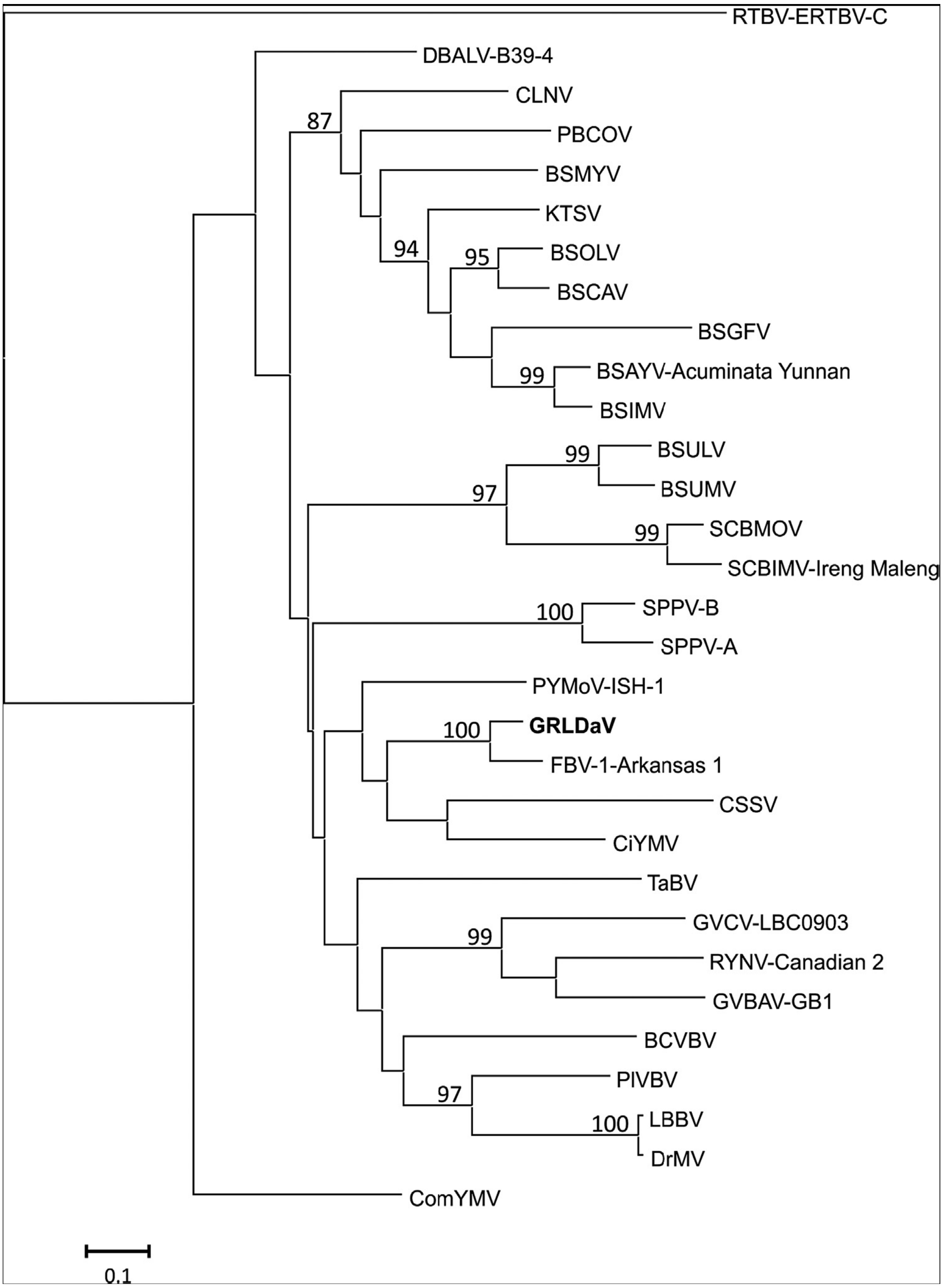
MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Maliogka,V.I., Olmos,A., Pappi,P.G., Lotos,L., Efthimiou,K., Grammatikaki,G., Candresse,T., Katis,N.I. and Avgelis,A.D.(2015) A novel grapevine badnavirus is associated with the Roditis leaf discoloration disease. Virus Res. 203, 47-55

Annex



Phylogenetic tree constructed using the amino acid sequence of the RT-RNaseH region from members of the genus *Badnavirus*. Abbreviations in the genus *Badnavirus* are (with approved species in italics and unclassified viruses in normal font): BSAYV-Acuminata Yunnan: Banana streak AY virus (DQ092436), BSCAV : Banana streak CA virus (HQ593111), BSGFV : *Banana streak GF virus* (AY805074), BSMYV : *Banana streak MY virus* (AY805074), BSIMV : *Banana streak IM virus* (HQ593111), BSOLV : *Banana streak OL virus* (AJ002234), BSULV : *Banana streak UL virus* (HQ593109), BSUMV : *Banana streak UM virus* (HQ593110), BCVBV : *Bougainvillea chlorotic vein banding virus* (EU034539), CSSV: *Cacao swollen shoot virus* (L14546), CiYMV : *Citrus yellow mosaic virus* (AF347695), ComYMV : *Commelina yellow mottle virus* (X52938), CLNV : Cycad leaf necrosis virus (EU853709), DBALV : *Dioscorea bacilliform AL virus* (DQ822073), DrMV : Dracaena mottle virus (DQ473478), FBV-1: *Fig badnavirus 1* (JF411989), GVBAV : *Gooseberry vein banding associated virus* (HQ852248), **GRLDaV : *Grapevine Roditis leaf discoloration associated virus* (HG940503)**, GVCV : *Grapevine vein clearing virus* (JF301669), KTSV : *Kalanchoë top-spotting virus* (AY180137), LBBV : Lucky bamboo bacilliform virus (EF494181), PlVBV : Pelargonium vein banding virus (GQ428155), PBCOV : *Pineapple bacilliform CO virus* (GU121676) , PYMoV : *Piper yellow mottle virus* (KC808712), RYNV : *Rubus yellow net virus* (KF241951), SCBIMV : *Sugarcane bacilliform IM virus* (AJ277091), SCBMOV : *Sugarcane bacilliform MO virus* (NC 008017), SPPV : *Sweet potato pakakuy virus* (SPPV-A/FJ560943, SPPV-B/FJ560944), and TaBV : *Taro bacilliform virus* (NC 004450). RTBV : *Rice tungro bacilliform virus* (BR000031) is a species in the genus *Tungrovirus.*