



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**

<b>Code assigned:</b>	<b>2016.012aP</b>	(to be completed by ICTV officers)
<b>Short title:</b> Two new species in the genus <i>Badnavirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (modules 1 and 11 are required)	2 <input checked="" type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/> 11 <input checked="" type="checkbox"/>	

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**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* 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	<b>2016.012aP</b>	(assigned by ICTV officers)	
<b>To create two new species within:</b>			
Genus:	<b><i>Badnavirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.	
Subfamily:			
Family:	<b><i>Caulimoviridae</i></b>		
Order:			
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>	
<i>Taro bacilliform CH virus</i>	Taro bacilliform CH virus, isolate TaBCHV-1	KP710178	
<i>Yacon necrotic mottle virus</i>	Yacon necrotic mottle virus, isolate YV1	KM229702	

### 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

*Taro bacilliform CH virus* is considered a new badnavirus species for the following reasons:

1. The complete genome sequences of two isolates of *Taro bacilliform CH virus* (TaBCHV) were assembled from deep sequencing reads and from the sequences of overlapping cloned PCR amplification products. These isolates originate from two separate plants showing mild feathery mosaic symptoms on young leaves and brown spots on matured leaves. Both genomes are 7644 bp long. One large ORF (ORF3) encodes a polyprotein harboring domains homologous to the badnavirus movement protein, aspartic protease, reverse transcriptase, ribonuclease H and zinc finger-like RNA binding domain
2. In phylogenetic analysis using ORF3 nucleotide sequences corresponding to the conserved RT/RNaseH, TaBCHV groups within the genus *Badnavirus* (Fig. 1). TaBCHV most closely related badnavirus is Citrus yellow mosaic virus (CiYMV), with both viruses sharing 69.05% identity (Table 1), which is well below the 80% threshold for discrimination of strains and species within the genus *Badnavirus*.

*Yacon necrotic mottle virus* is considered a new badnavirus species for the following reasons:

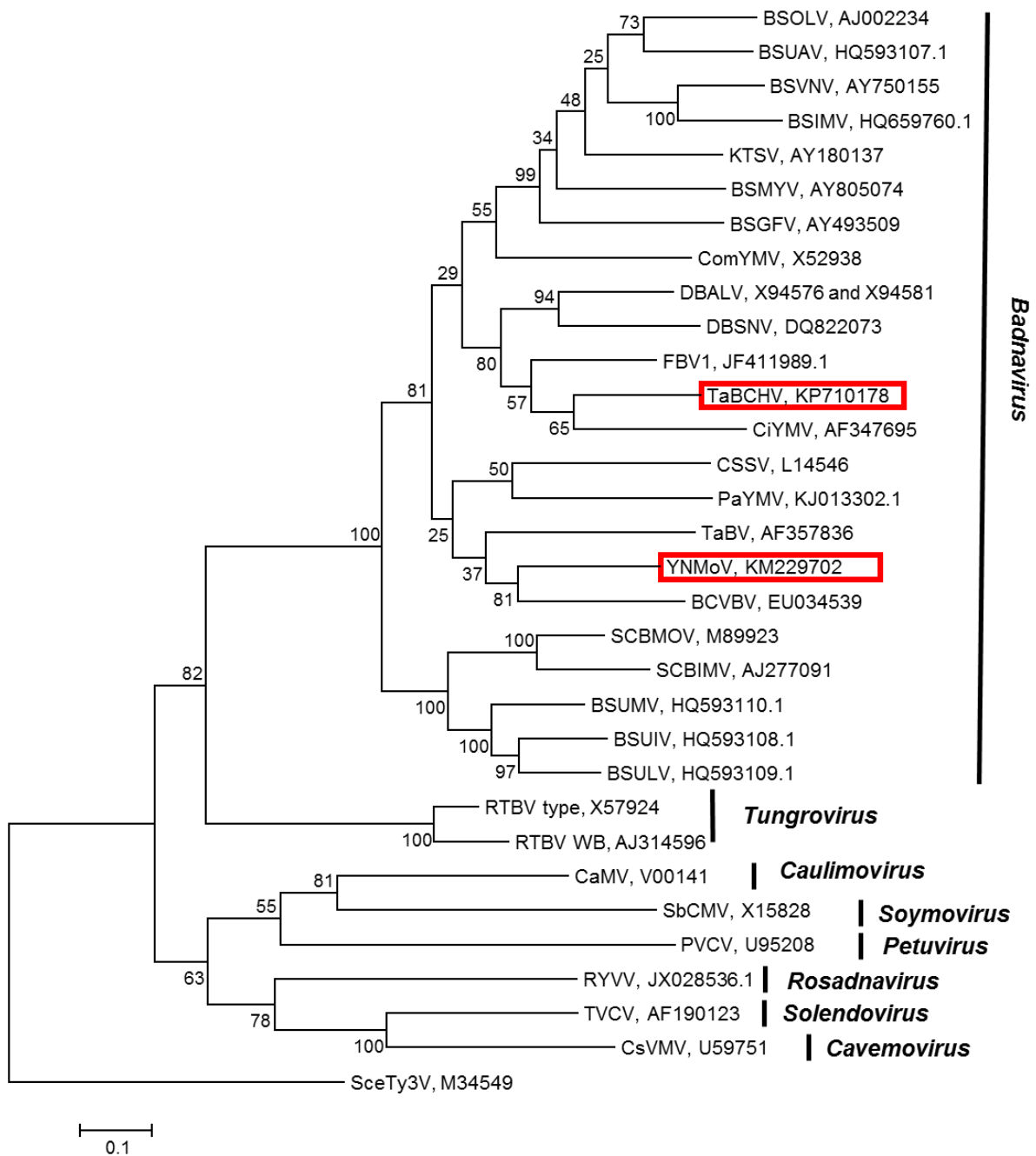
1. A complete genome sequence of Yacon necrotic mottle virus (YNMoV) was assembled from deep sequencing of cDNA obtained from yacon plants (*Smallanthus sonchifolius*) showing systemic necrosis, chlorosis, stunting, and leaf malformation symptoms. PCR amplicons covering the entire circular genome were obtained from symptomatic leaves and sequenced by the Sanger method. The 7661 bp genome displays a typical badnavirus genome organization, with a large ORF (ORF3) putatively encoding a polyprotein precursor of 234 kDa containing conserved MP, CP, viral aspartic protease, RTase, and RNase H domains which are analogous to those of other badnaviruses.
2. YNMoV-specific primers were designed and used for screening yacon plants by PCR. Amplification products were obtained from symptomatic plants but not from asymptomatic ones.
3. In phylogenetic analysis using ORF3 nucleotide sequences corresponding to the conserved RT-RNase H domains, YNMoV groups within the genus *Badnavirus* (Fig. 1). YNMoV is a sister taxon of *Bougainvillea spectabilis chlorotic vein-banding virus* (BCVBV), sharing 68.3% nt identity within the RT-RNase H domains (Table 1), which is well below the 80% demarcation threshold for discrimination of species within the genus *Badnavirus*.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Kazmi SA, Yang Z, Hong N, Wang G, Wang Y (2015) Characterization by small RNA sequencing of Taro bacilliform CH virus (TaBCHV), a novel badnavirus. PLoS ONE 10: E0134147  
Lee YJ, Kwak HR, Lee YK, Kim MK, Choi HS, Seo JK (2015) Complete genome sequence of Yacon necrotic mottle virus, a novel putative member of the genus *Badnavirus*. Arch Virol. 160: 1139-42.



**Fig. 1. Phylogenetic tree showing placement of *Yacon necrotic mottle virus* (YNMoV) and *Taro bacilliform CH virus* (TBCHV) in the genus *Badnavirus*, based on reverse transcriptase-RNase H gene sequences.**

Evolutionary relationships were inferred using the maximum likelihood method, as implemented in MEGA v. 6.06. Bootstrap values from 1000 re-samplings are shown at the nodes of the branches. Type species of other genera in the *Caulimoviridae* are also included. The two proposed new species are highlighted in the red box and accession numbers are provided next to each acronym. BSOLV: *Banana streak OL virus*; BSUAV: *Banana streak UA virus*; BSVNV: *Banana streak VN virus*; BSIMV: *Banana streak IM virus*; KTSV: *Kalanchoe top spotting virus*; BSMYV: *Banana streak MY virus*; BSGFV: *Banana streak GF virus*; ComYMV: *Commelina yellow vein mosaic virus*; DBALV: *Dioscorea bacilliform AL virus*; DBSNV: *Dioscorea bacilliform VN virus*; FBV1: *Fig badnavirus 1*; TaBCHV: *Taro bacilliform CH virus*; CiYMV: *Citrus yellow mosaic virus*; CSSV: *Cacao swollen shoot virus*; PaYMV: *Pagoda yellow mosaic associated virus*; TaBV: *Taro bacilliform virus*; YNMoV: *Yacon necrotic mottle virus*; BCBV: *Bougainvillea spectabilis chlorotic 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*; CaMV: *Cauliflower mosaic virus*; SbCMV: *Soybean chlorotic mottle virus*; PVCV: *Petunia vein clearing virus*; RYV: *Rose yellow vein virus*; TVCV: *Tobacco vein clearing virus*; CsVMV: *Cassava vein mosaic virus*; ScTy3V: *Saccharomyces cerevisiae Ty3 virus*.

**Table 1: Pairwise percent nucleotide identities for members of the genus *Badnavirus* within the conserved reverse transcriptase-RNaseH domains of open reading frame 3.**  
 Data for the two new species are highlighted in yellow. The sequences that were analysed corresponded to nucleotides 4437-5648 of Cauliflower mosaic virus (GenBank V00141.1)

	CaMV	TaBCHV	YNMoV	SbCMV	PVCV	TVCV	CsVMV	CSSV	CIYMV	BSOLV	KTSV	BSVNV	BSGFV	ComYMV	DBALV	DBSNV	BCVBV	TaBV	SCBMOV	SCBIMV	RTBV_typ	RTBV_WE	ScetY3V	RYVV	BSMYV	PaYMV	FBAKV	BSUMV	BSUAV	BSUIV	BSIMV	BSULV				
CaMV																																				
TaBCHV	50,0																																			
YNMoV	49,9	64,7																																		
SbCMV	53,5	46,4	47,2																																	
PVCV	49,5	46,0	45,1	46,4																																
TVCV	53,0	48,8	49,1	50,6	48,7																															
CsVMV	49,0	47,9	47,0	49,8	47,6	62,7																														
CSSV	49,1	62,3	63,4	45,6	45,0	47,0	45,2																													
CIYMV	49,2	69,1	64,8	46,4	44,7	47,9	46,3	63,9																												
BSOLV	49,4	68,5	65,5	46,0	47,7	49,9	48,9	64,3	65,7																											
KTSV	48,4	66,2	64,6	44,6	43,4	45,1	44,9	62,0	63,4	72,5																										
BSVNV	47,4	65,6	63,8	44,1	45,7	48,1	48,2	63,7	62,9	70,9	71,1																									
BSGFV	48,1	64,5	64,3	45,3	46,1	49,8	48,0	61,6	61,8	67,8	68,5	69,9																								
ComYMV	48,2	64,5	63,8	46,5	45,6	47,0	46,8	62,0	62,1	66,6	63,8	66,3	64,7																							
DBALV	49,5	69,9	65,7	45,5	45,2	48,4	46,3	63,6	65,8	68,2	66,5	66,1	63,9	64,5																						
DBSNV	50,0	68,2	64,2	43,5	43,8	48,0	45,0	62,5	66,6	66,1	65,2	65,9	63,8	64,1	72,0																					
BCVBV	49,1	65,2	68,3	46,3	46,3	47,1	46,8	59,7	62,1	63,9	63,2	63,6	62,7	62,3	63,9	65,7																				
TaBV	49,1	64,5	64,6	47,1	45,9	47,5	47,3	62,5	60,7	62,2	59,6	62,3	61,1	61,6	64,5	63,1	64,8																			
SCBMOV	48,7	61,2	63,2	45,7	46,2	48,9	47,9	59,5	58,1	62,9	60,3	61,6	61,8	62,2	63,0	61,7	61,6	61,3																		
SCBIMV	49,5	60,2	61,0	45,8	44,1	48,7	44,5	58,1	59,0	61,9	58,7	59,1	60,1	62,4	61,3	61,8	61,5	59,9	79,5																	
RTBV_typ	50,1	53,0	53,2	48,8	47,3	53,5	52,4	49,8	51,0	53,8	50,5	52,4	53,1	50,4	52,6	50,0	51,7	52,8	53,3	51,5																
RTBV_WE	49,4	51,2	52,3	49,1	46,4	53,0	51,3	50,0	51,0	53,4	49,0	50,9	52,1	51,1	52,8	49,9	50,8	52,0	52,7	52,2	86,0															
ScetY3V	45,3	44,1	44,2	44,4	43,5	43,0	43,5	43,1	43,1	44,8	44,4	44,6	43,9	45,0	44,7	43,9	43,7	45,6	46,0	43,0	45,4	44,4														
RYVV	49,4	48,8	48,4	47,6	47,3	53,1	53,6	47,1	49,3	50,6	45,4	49,1	48,8	48,2	48,2	48,8	48,6	47,4	49,5	48,5	50,5	49,2	46,0													
BSMYV	48,8	65,8	62,2	44,4	45,7	48,7	46,9	59,8	62,9	70,4	68,7	69,8	66,5	63,4	66,4	66,8	64,3	59,8	62,0	59,2	52,1	51,4	43,7	49,1												
PaYMV	47,7	61,8	63,2	44,1	44,3	47,9	44,9	62,1	61,4	62,1	61,8	62,0	59,3	60,4	63,4	62,3	62,7	62,1	58,1	59,3	49,9	49,1	45,0	47,7	61,4											
FBAKV	48,7	69,6	68,4	45,0	46,5	47,7	46,8	64,9	68,6	67,7	65,0	66,3	64,1	63,9	70,2	66,9	66,1	64,1	61,6	60,6	53,6	52,3	43,9	48,8	64,8	63,3										
BSUMV	48,2	64,5	65,1	45,3	44,6	51,0	47,9	60,1	60,9	65,6	63,3	65,5	65,3	63,3	64,5	64,0	63,4	63,3	72,1	68,1	54,7	54,0	46,1	47,2	64,3	60,1	63,7									
BSUAV	47,9	66,1	66,7	46,0	46,6	50,2	50,1	62,4	64,4	75,2	71,0	73,3	69,8	65,4	68,3	67,7	64,8	62,0	62,9	63,2	53,6	53,1	44,0	50,4	70,4	62,4	67,9	64,8								
BSUIV	49,2	64,5	64,3	46,3	45,0	50,4	47,6	59,3	62,6	68,9	63,5	64,3	64,3	62,1	63,5	64,1	62,4	62,1	73,1	70,1	54,6	53,5	45,5	49,4	65,0	59,2	65,0	77,5	66,8							
BSIMV	47,9	65,1	63,6	46,6	45,7	47,4	48,4	62,1	62,0	72,3	70,6	77,7	69,1	64,1	66,6	65,3	63,9	63,1	61,5	60,3	52,6	50,8	45,4	48,7	67,0	61,5	66,4	64,4	72,4	63,0						
BSULV	48,8	64,5	64,5	46,9	46,1	51,5	49,2	59,4	61,4	64,7	62,3	63,5	65,6	62,9	64,5	64,9	63,8	62,1	72,0	69,7	54,3	53,4	45,1	50,1	64,8	59,6	64,5	78,3	66,2	80,6	63,7					