



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:	2016.011a-dP	(to be completed by ICTV officers)
Short title: 1 new species in the new genus <i>Blunervirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input type="checkbox"/>	
2 <input checked="" type="checkbox"/> 3 <input checked="" type="checkbox"/> 4 <input type="checkbox"/> 5 <input 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)

Cilevirus SG

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

Date first submitted to ICTV: July 18, 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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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	2016.011aP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Blunervirus</i> (new)	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.
Subfamily:	<i>unassigned</i>	
Family:	<i>unassigned</i>	
Order:	<i>unassigned</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Blueberry necrotic ring blotch virus</i>	Georgia	JN651148 JN651149 JN651150 JN651151

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

In 2006, a new disease was observed in blueberry in southeastern states of the USA (Martin et al., 2012). The discovery of a new virus infecting blueberry was published by Quito-Avila et al. in 2013. Symptomatic blueberry leaves infected with blueberry necrotic ring blotch virus (BNRBV) had symptoms of irregularly shaped green centric circular spots, and blotches. The genome of BNRBV was composed of four RNAs. RNA1 was 5906 nt length and possessed one ORF that encoded a polyprotein with methyltransferase, protease, and helicase domains. RNA2 was 3935 nt in length and encoded a 130kDa polyprotein with a second helicase domain and an RNA-dependent RNA polymerase (RdRp) domain. RNA3 was 2588 nt in length and consisted of five ORFs but the functions of these hypothetical proteins (p7, p9, p22, p28 and p31) remain unknown. RNA4 was 1724 nt in length and the single ORF encoded a protein with conserved motifs present in the 3A movement proteins. Secondary structures were present in the 3' non-translated region of all 4 RNAs but none of the RNAs were polyadenylated. To date, there is no conclusive experimentation that identifies an arthropod vector of BNRBV (Robinson et al., 2016)

Phylogenetic relationships based on the helicase and RdRp domains were established and confirmed that BNRBV is distantly related to members of the plant virus genera *Cilevirus* and *Higrevirus*. As with members of these two genera, BNRBV produces only localized infection (Robinson et al., 2016). However BNRBV is clearly not a strain of an existing species in these genera due differences in genome organization, number of helicase domains, number of

genomic segments, the presence or absence of poly(A) tail on the genomic segments, and overall low sequence homology. For example, the RdRp domain of BNRBV is only 31-32 and 33% identical to members of the genera *Cilevirus* and *Higrevirus*, respectively. This domain has slightly higher identity (up to 37%) to recently described insect viruses designated as “negeviruses” by some or “sandewaviruses” and “nelorpiviruses” by others (see Kallies et al 2014, Roy et al 2015, Vasilakis et al 2013). However, these primarily mosquito-borne viruses and taxa are not yet recognized by the ICTV. Overall, based on these characteristics, BNRBV clearly represents a new virus species.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	2016.011bP	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	<i>Unassigned</i>	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 family is specified, enter “ unassigned ” in the family box
Family:	<i>Unassigned</i>	
Order:	<i>unassigned</i>	

naming a new genus

Code	2016.011cP	(assigned by ICTV officers)
To name the new genus: <i>Blunervirus</i>		

Assigning the type species and other species to a new genus

Code	2016.011dP	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Blueberry necrotic ring blotch virus</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
<i>One</i>		

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 11

Biologically and genetically, BNRBV is distantly related to members of the genera *Cilevirus* and *Higrevirus*. However, its genome organization, number of RNA segments, lack of a polyadenylated 3' terminus on RNA segments, and unique protein products make it distinct from these and other viral genera.

Origin of the new genus name:

Blunervirus - Blueberry necrotic ring blotch virus

Reasons to justify the choice of type species:

BNLBV represents the only member of the proposed genus

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

n/a

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

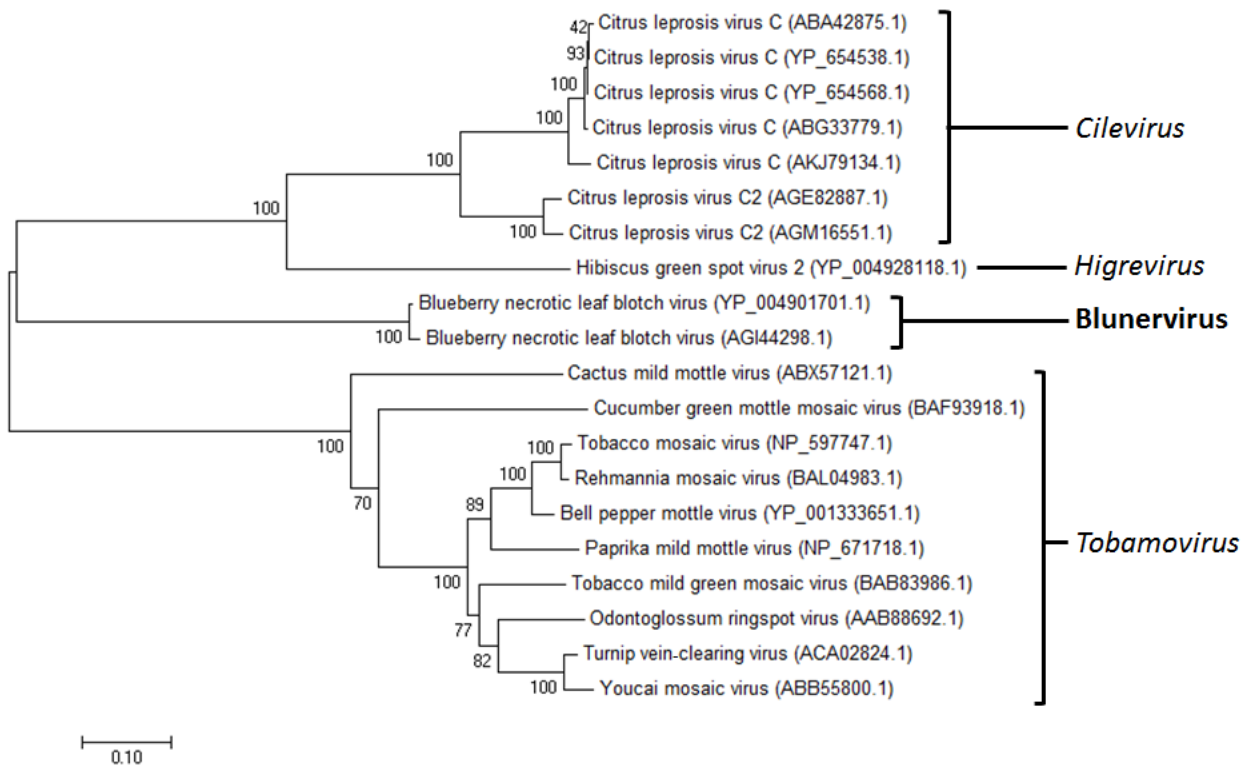
References:

- Kallies, R, Kopp, A, Zirkel, F, Estrada, A, Gillespie, TR, Drosten, C, and Junglen, S. 2014/ Genetic characterization of goutnap virus, a novel virus related to negevirus, cileviruses, and higreviruses. *Viruses* 6:4346-4357.
- Martin, RR, Polashock, JJ, Tzanetakis, IE. 2012. New and emerging viruses of blueberry and cranberry. *Viruses* 4:2831-2852.
- Quito-Avila, DF, Brannen, PM, Cline, WO, Harmon, PF, and Martin, RR. 2013. Genetic characterization of blueberry necrotic ring blotch virus, a novel RNA virus with unique genetic features. *Journal of General Virology* 94:1426-1434
- Robinson, TS, Scherm, H, Brannen, PM, Allen, R, and Deom, CM. 2016. Blueberry necrotic ring blotch virus in southern highbush blueberry: insights into in planta and in-field movement. *Plant Disease*. 100 (8): 1575-1579
- Roy, A., Hartung, JS., Schneider, WL., Shao, J., León, MG., Melzer, M. J., Otero-Colina, G., Beard, JJ., Bauchan, GR., Ochoa, R., and Brlansky, RH. 2015. Role bending: complex relationships between viruses, hosts and mite vectors related to citrus leprosis, an emerging disease. *Phytopathology*. 105:1013-1025.
- Vasilakis, N, Forrester, NL, Palacios, G, Nasar, F, Savji, N, Rossi, SL, Guzman, H, Wood, TG, Popov, V, Gorchakov, R, Gonzalez, AV, Haddow, AD, Watts, DM, da Rosa, AP, Weaver, SC, Lipkin, WI, Tesh, RB. 2013. Negevirus: a proposed new taxon of insect-specific viruses with wide geographic distribution. *Journal of Virology* 87:2475-2488.

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.

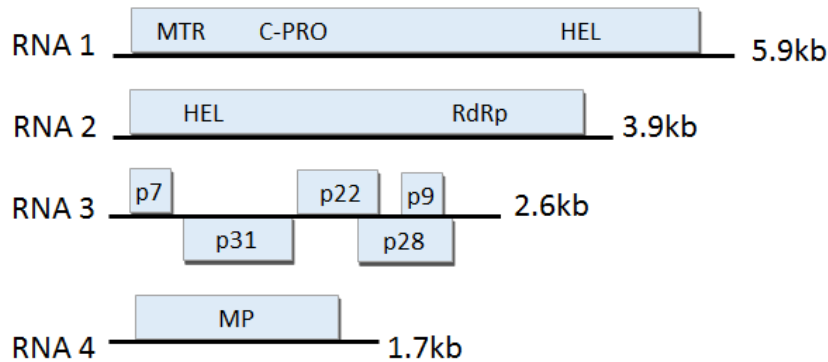
Phylogenetic Analysis



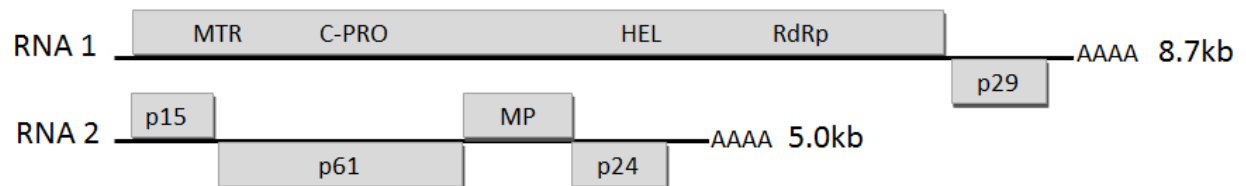
Unrooted phylogenetic tree depicting the placement of the proposed blueberry necrotic ring blotch virus and Blunervirus genus. This tree is based on the RNA-dependent RNA polymerase domain encoded on RNA 2 using a neighbor joining algorithm with 1000 bootstrap replications. The proposed Blunervirus genus is placed between the *Tobamovirus* genus and *Higrevirus*/*Cilevirus* genera with strong branch support. GenBank accession numbers are provided after the virus species name. In some cases, several accession numbers are used for the same species that correspond to individual isolates. The scale on the bottom left represents the number of substitutions for the given branch length.

Genome Organization

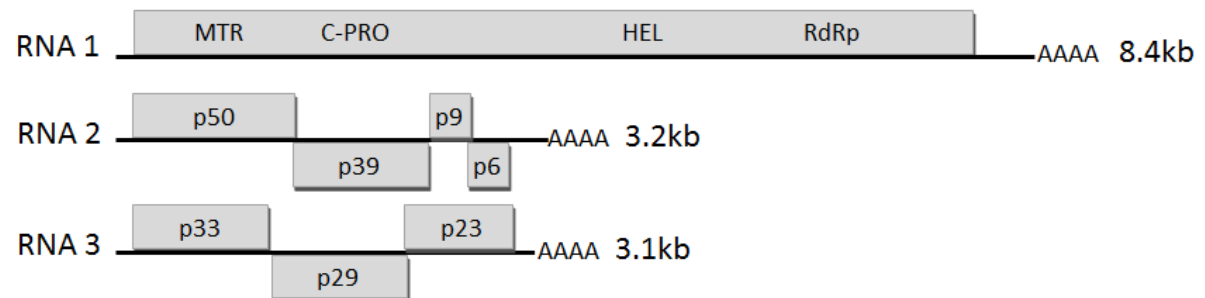
Blueberry necrotic ring blotch virus, proposed genus *Blunervirus*



Citrus leprosis virus C, genus *Cilevirus*



Hibiscus green spot virus 2, genus *Higrevirus*



Genome organization of blueberry necrotic ring blotch virus of the proposed genus *Blunervirus* in comparison to that of *Citrus leprosis virus C* and *Hibiscus green spot virus 2*, the type members of the genera *Cilevirus* and *Higrevirus*, respectively. MTR – methyltransferase; C-PRO – cysteine like protease; HEL – helicase; RdRp – RNA dependent RNA polymerase; MP – movement protein