



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>2016.025a-dM</b>	(to be completed by ICTV officers)
<b>Short title:</b> One (1) new species in one new genus ( <i>Orthojonvirus</i> ) to be included in the new family <i>Jonviridae</i> in the new order <i>Bunyvirales</i> (family and order proposed in 2016.030M) (e.g. 6 new species in the genus <i>Zetavirus</i> )		
<b>Modules attached</b> (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 checked="" type="checkbox"/>

**Author(s):**

Junglen, Sandra ([junglen@virology-bonn.de](mailto:junglen@virology-bonn.de))  
Marklewitz, Marco ([marklewitz@virology-bonn.de](mailto:marklewitz@virology-bonn.de))  
Zirkel, Florian ([zirkel@virology-bonn.de](mailto:zirkel@virology-bonn.de))  
Drosten, Christian ([drosten@virology-bonn.de](mailto:drosten@virology-bonn.de))

**Corresponding author with e-mail address:**

Junglen, Sandra ([junglen@virology-bonn.de](mailto:junglen@virology-bonn.de))

**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)

ICTV *Bunyviridae* Study Group

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

The ICTV *Bunyviridae* Study Group has seen and discussed this proposal, and agreed to its submission to the ICTV Executive Committee based on votes of support by individual Study Group members or the absence of dissenting votes.

Date first submitted to ICTV:

July 18, 2016

Date of this revision (if different to above):

September 21, 2016

**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	<b>2016.025aM</b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Orthojonvirus</i> (NEW)</b>	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:	<b>unassigned</b>	
Family:	<b><i>Jonviridae</i> (NEW, see TP 2016.030M)</b>	
Order:	<b><i>Bunyvirales</i> (NEW, see TP 2016.030M)</b>	
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Jonchet orthojonvirus</i>	jonchet virus (JONV) B81-CI-2004	KP710240, KP710243, KP710232

**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

Jonchet virus (JONV) is equally distant from all genera and branches from a deep node in the proposed order *Bunyvirales* in basal phylogenetic relationship to the genera *Hantavirus* (proposed *Orthohantavirus*), *Orthobunyavirus*, *Tospovirus* (proposed *Orthotospovirus*) and to the unassigned clade of “herbevirus”. JONV shares a most common recent ancestor (MRCA) with ferak virus (unassigned clade of “feraviruses”) but the genetic distance as well as the differences in virion morphology and genome organisation indicate that both viruses belong to different genera.

The enveloped JONV virions have two types of morphologies. One is atypical for bunyaviruses: virions form tubules of 60 nm in diameter and up to 600 nm in length. Bunyavirus-typical virions are spherical 80 nm in diameter. The L segment of JONV is 6.9 kb in length and the L protein is predicted to contain a putative endonuclease domain at its N-terminus. At 5.5 kb, JONV has the longest bunyavirus M segment observed to date. The M segment is predicted to encode a glycoprotein precursor protein that is post-translationally cleaved into NSm, Gn, and Gc proteins. The S segment is 1.7 kb in size and encodes a nucleoprotein and an NSs protein that is encoded upstream of the nucleoprotein ORF. Six proteins of about 250, 200, 100, 80, 50, and 15 kDa were identified in mature virions corresponding to the RdRp, GPC, Gn, Gc, and N genes, as well as to the putative NSs ORF, respectively.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	<b>2016.025bM</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
Subfamily:	<b>unassigned</b>	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:	<b>Jonviridae (NEW, see TP 2016.030M)</b>	
Order:	<b>Bunyavirales (NEW, see TP 2016.030M)</b>	

naming a new genus

Code	<b>2016.025cM</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Orthojonvirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2016.025dM</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<b><i>Jonchet orthojonvirus</i></b>		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). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b>		
<b>1</b>		

**Reasons to justify the creation of a new genus:**

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

See justification for new species.
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**Origin of the new genus name:**

Derived from <u>jonchet</u> virus (jonchet means Mikado in French and is derived from the morphology of the virions).
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**Reasons to justify the choice of type species:**

Jonchet virus was the first virus that was discovered in this new phylogenetic lineage. It is the only virus that was isolated in cell culture and for which a complete genome sequence is available.
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**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
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MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

**Marklewitz M., Handrick S., Grasse W., Kurth A., Lukashev A., Drosten C., Ellerbrok H., Leendertz F.H., Pauli G., Junglen S.** 2011. Gouleako virus isolated from West African mosquitoes constitutes a proposed novel genus in the family Bunyaviridae. *Journal of Virology* 85: 9227-9234.

**Marklewitz M., Zirkel F., Rwego I.B., Heidemann H., Trippner P., Kurth A., Kallies R., Briese T., Lipkin W.I., Drosten C., Gillespie T.R., Junglen S.** 2013. Discovery of a Unique Novel Clade of Mosquito-Associated Bunyaviruses. *Journal of Virology* 87: 12850-12865.

**Marklewitz M., Zirkel F., Kurth A., Drosten C., Junglen S.** 2015. Evolutionary and phenotypic analysis of live virus isolates suggests arthropod origin of a pathogenic RNA virus family. *Proceedings of the National Academy of Sciences* 112: 7536-41.

**Junglen S. (2016).** Evolutionary origin of pathogenic arthropod-borne viruses — a case study in the family *Bunyaviridae*. *Current Opinion in Insect Science* 16: 81-86.

**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.

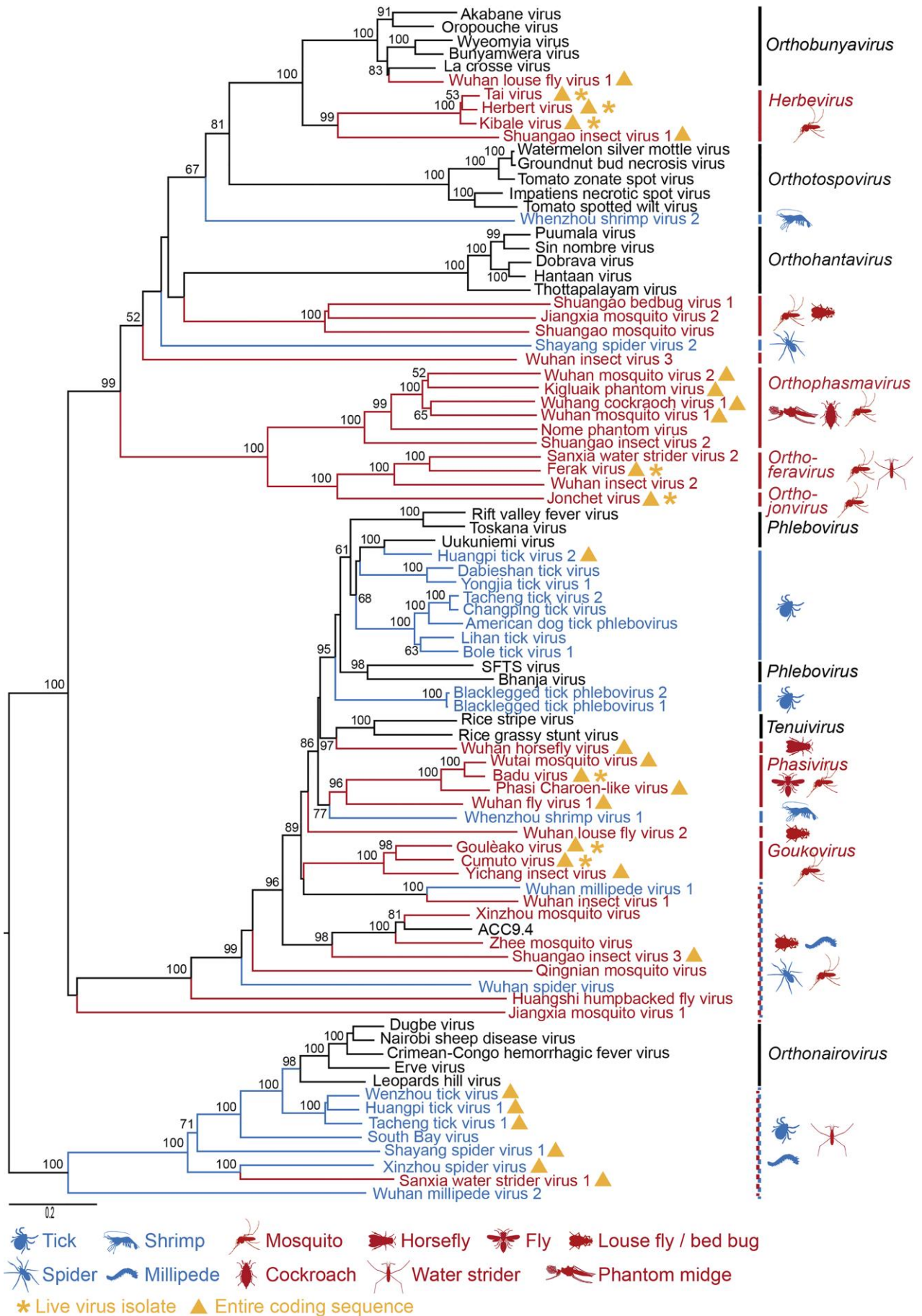


Figure: Phylogenetic relationship of bunyaviruses. Phylogenetic analyses were based on RdRp proteins. Complete RdRp proteins were aligned using MAFFT (E-INS-I algorithm). Alignment columns were stripped to 10% gaps in Geneious. Maximum likelihood (ML) analyses were performed on a 508 amino acid alignment guided by the Blosum62 amino acid substitution matrix with 4 gamma categories and a gamma shape parameter of 1. Confidence testing was performed by 1000 bootstrap replicates. Only bootstrap values over 50 are shown.