



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:	2016.028a-dM	(to be completed by ICTV officers)
Short title: Six (6) new species in one (1) new genus (<i>Orthophasmavirus</i>) to be included in the proposed family <i>Phasmaviridae</i> in the proposed order <i>Bunyavirales</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)

ICTV *Bunyaviridae* Study Group

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

The ICTV *Bunyaviridae* 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	2016.028aM	(assigned by ICTV officers)
To create 6 new species within:		
Genus:	<i>Orthophasmavirus</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:	unassigned	
Family:	<i>Phasmaviridae</i> (NEW, see TP 2016.030M)	
Order:	<i>Bunyvirales</i> (NEW, see TP 2016.030M)	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Kigluaik phantom orthophasmavirus</i>	Kigluaik phantom virus G10N	KJ434182–84
<i>Nome phantom orthophasmavirus</i>	Nome phantom virus TE13	KJ434185–87
<i>Wuhan mosquito orthophasmavirus 2</i>	Wūhàn mosquito virus 2 QN2-7	KM817759, KM817698, KM817727
<i>Wuchang cockroach orthophasmavirus 1</i>	Wūchāng cockroach virus 1 ECZL-5	KM817688, KM817721, KM817748
<i>Wuhan mosquito orthophasmavirus 1</i>	Wūhàn mosquito virus 1 WT3-15	KM817726, KM817697, KM817758
<i>Shuangao insect orthophasmavirus 2</i>	Shuāngào insect virus 2 QSA03	KM817741, KM817740, KM817680, KM817741

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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 <p>The viruses listed above define a new bunyaviral clade that is equally distant from all established bunyaviral genera. This clade branches from a deep node in the proposed order <i>Bunyvirales</i> in basal phylogenetic relationship to the accepted genera <i>Hantavirus</i> (proposed <i>Orthohantavirus</i>), <i>Orthobunyavirus</i>, <i>Tospovirus</i> (proposed <i>Orthotospovirus</i>), and the unassigned “herbevirususes”. Phasmaviruses define a sister clade to the clade formed by the unassigned “feraviruses” and “jonviruses”.</p>

The genome segments show a great variety in length that is comparable to the high level of genetic diversity observed in the phylogenetic analyses. The S, M, and L segments are 1.8–2.2, 2.1–2.8, and 6.5–6.6 kb in length. Phasmaviruses are predicted to encode NSs and NSm proteins in a similar coding strategy as observed for jonchet virus (JONV, proposed new genus *Orthojonvirus*). The host range of phasmaviruses is likely to be restricted to insects.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2016.028bM	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:	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 family is specified, enter “unassigned” in the family box
Family:	<i>Phasmaviridae</i> (NEW, see TP 2016.030M)	
Order:	<i>Bunyavirales</i> (NEW, see TP 2016.030M)	

naming a new genus

Code	2016.028cM	(assigned by ICTV officers)
To name the new genus: <i>Orthophasmavirus</i>		

Assigning the type species and other species to a new genus

Code	2016.028dM	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Kigluaik phantom orthophasmavirus</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:		
6		

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.

Origin of the new genus name:

Derived from the hosts, phantom midges.

Reasons to justify the choice of type species:

Kigluaik phantom virus was the first virus that was discovered (together with Nome phantom virus) representing this new bunyaviral phylogenetic lineage.
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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.

Until further phasmaviruses are discovered, we propose to use the same species demarcation criteria for this genus as described for the proposed new genera “ <i>Goukovirus</i> ”, “ <i>Herbevirus</i> ”, “ <i>Orthoferavirus</i> ”, and “ <i>Orthojonvirus</i> ” (see separate co-submitted proposals). Species demarcation criteria should be based on a ≈1 kb sequence fragment containing the core polymerase domain (premotif A to motif E) of the third conserved region of the L protein. These motifs can be aligned
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between all members of the proposed order *Bunyavirales* and would allow comparative species demarcation criteria for all genera of the entire family. Moreover, as the motifs are highly conserved between all bunyaviruses, amplification of this genome region from new viruses is facilitated. Species demarcation criteria of other viral families are also based on the replicative genes/domains and have been shown to be suitable criteria.

Species should be defined on the criterion that the ≈ 1 kb sequence fragment containing the core polymerase domain (premotif A to motif E) of the third conserved region of the L protein should be less than 90% identical on the amino acid level compared to that of any other described phasmavirus.

This <90% aa identity threshold for the core polymerase domain is in agreement with the aa identity values for established bunyavirus species within the five established genera.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Ballinger M.J., Bruenn J.A., Hay J., Czechowski D., and Taylor D.J. (2014). Discovery and evolution of bunyavirids in arctic phantom midges and ancient bunyavirid-like sequences in insect genomes.
Journal of Virology 88: 8783-8794.

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.

Li C.X., Shi M., Tian J.H., Lin X.D., Kang Y.J., Chen L.J., Qin X.C. Xu J., Holmes E.C. and Zhang Y.Z. (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses.
Elife 4: e05378.

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.

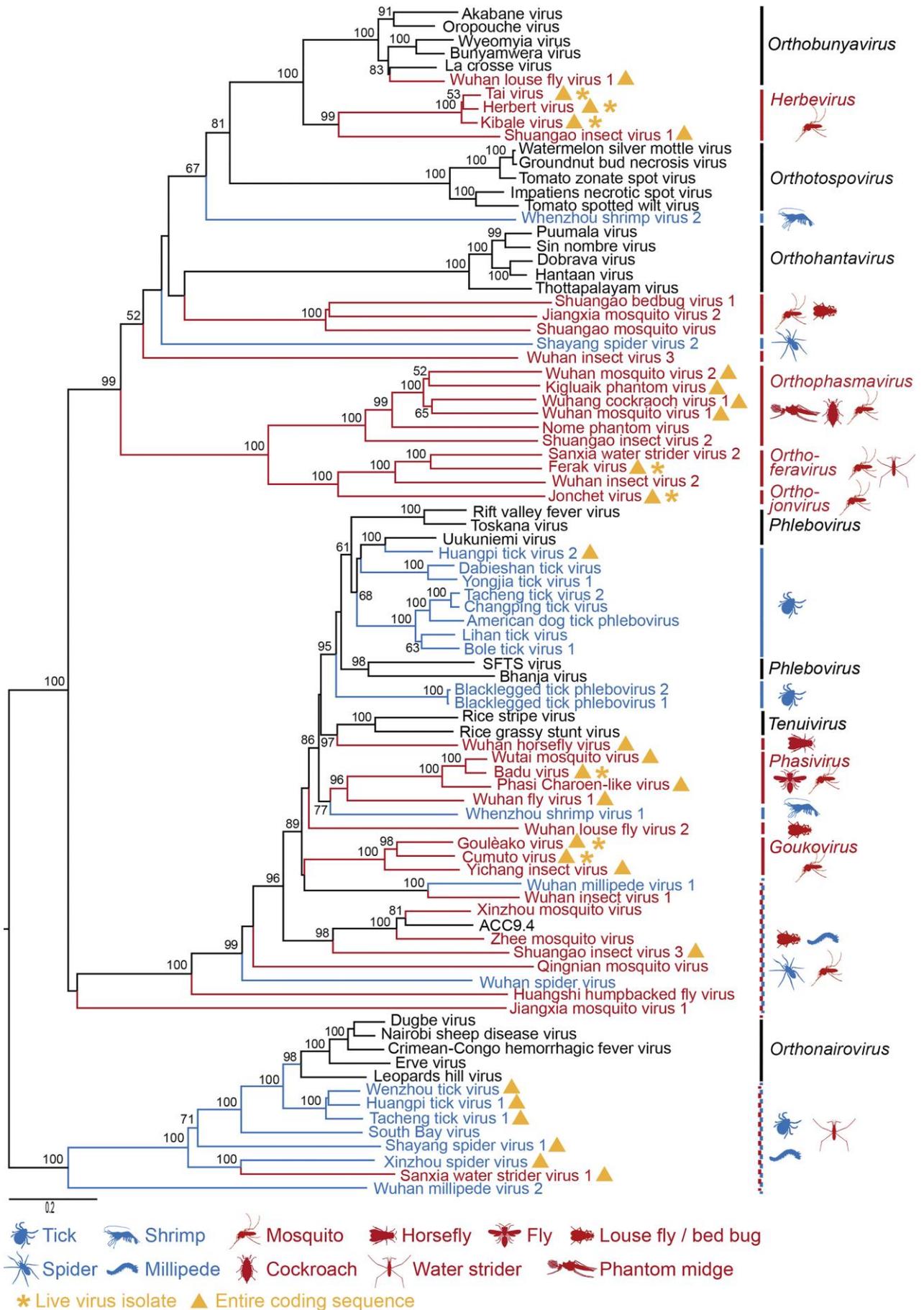


Figure: Phylogenetic relationship of bunyaviruses. Phylogenetic analyses were based on RdRp proteins. Complete RdRp proteins were aligned using MAFFT (E-INS-I algorithm). Alignment columns were stripped to 10% gaps in Geneious. Maximum likelihood (ML) analyses were performed on a 508 amino acid alignment 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.