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:	***2016.027a-dM***	(to be completed by ICTV officers)

Short title: Four (4) new species in one (1) new genus (*Phasivirus*) in the proposed family *Phenuiviridae* in the proposed order *Bunyavirales*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☒ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Junglen, Sandra (junglen@virology-bonn.de)

Corresponding author with e-mail address:

Junglen, Sandra (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 *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:

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	***2016.027aM***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Phasivirus* (NEW)**
Subfamily:	**unassigned**
Family:	***Phenuiviridae* (NEW, see TP 2016.030M)**
Order:	***Bunyavirales* (NEW, see TP 2016.030M)**

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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Phasi Charoen-like phasivirus	Phasi Charoen-like virus (PCLV) Rio	KR003784–86
Badu phasivirus	Badu virus (BADUV) TS6347	KT693187–89
Wutai mosquito phasivirus	Wǔtái mosquito virus QN3-5	KM817728, KM817700, KM817761
Wuhan fly phasivirus	Wǔhàn fly virus SYY1-9	KM817749, KM817722, KM817689

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

The viruses listed above define a new bunyaviral clade that is equally distant from all currently established bunyaviral genera. This clade branches from a deep node in the family in basal phylogenetic relationship to the accepted genus *Phlebovirus,* and the unassigned "goukoviruses" and "tenuiviruses".

Virions have a uniform size of 130 nm in diameter. Mature virions contain three major structural proteins of approximately 56, 52, and 25 kDa that correspond to the Gc, Gn, and N proteins of bunyaviruses. In contrast to phleboviruses the BADUV Gn protein is post-translationally cleaved by a furin protease. The S and L segments have lengths of 1.1–1.5 and 6.8 kb, respectively. The M segment varies substantially in length (3.4–4.4 kb). No coding regions for additional non-structural proteins have been identified.
The host range of phasiviruses 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	***2016.027bM***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	**unassigned**
Family:	***Phenuiviridae*** **(NEW, see TP 2016.030M)**
Order:	***Bunyavirales*** **(NEW, see TP 2016.030M)**

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

naming a new genus

Code	***2016.027cM***	(assigned by ICTV officers)

To name the new genus: *Phasivirus*

Assigning the type species and other species to a new genus

Code	***2016.027dM***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Badu phasivirus	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:**

4

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 phasi chareon-like virus.

Reasons to justify the choice of type species:

Although phasi chareon-like virus was the first virus that was discovered representing this new bunyaviral phylogenetic lineage, Badu virus is the only virus of this lineage that was isolated in cell culture and which has been characterized phenotypically.

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 phasiviruses are discovered, we propose to use the same species demarcation criteria for this genus as described for the proposed new genera "*Goukovirus*", "*Herbevirus*", "*Orthoferavirus*" and "*Orthojonvirus*" (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 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 phasivirus.

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:

Aguiar E.R., Olmo R.P., Paro S., Ferreira F.V., de Faria I.J., Todjro Y.M., Lobo F.P., Kroon E.G., Meignin C., Gatherer D., Imler J.L., and Marques J.T. (2015). Sequence-independent characterization of viruses based on the pattern of viral small RNAs produced by the host.
Nucleic Acid Res. 43: 6191-6206.

Chandler J.A., Thongsripong P., Green A., Kittayapong P., Wilcox B.A., Schroth G.P., Kapan D.D., and Bennett S.N. (**2014**) Metagenomic shotgun sequencing of a bunyavirus in wild-caught *Aedes aegypti* from Thailand informs the evolutionary and genomic history of the Phleboviruses.
Virology: 464-465:312-9. doi: 10.1016/j.virol.2014.06.036.

Hobson-Peters J., Warrilow D., McLean B.J., Watterson D., Colmant A.M., van den Hurk A.F., Hall-Mendelin S., Hastie M.L., Gorman J.J., Harrison J.J., Prow N.A., Barnard R.T., Allcock R., Johansen C.A., and Hall R.A. (**2016).** Discovery and characterisation of a new insect-specific bunyavirus from *Culex* mosquitoes captured in northern Australia.
Virology: 489:269-81. doi: 10.1016/j.virol.2015.11.003.

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.

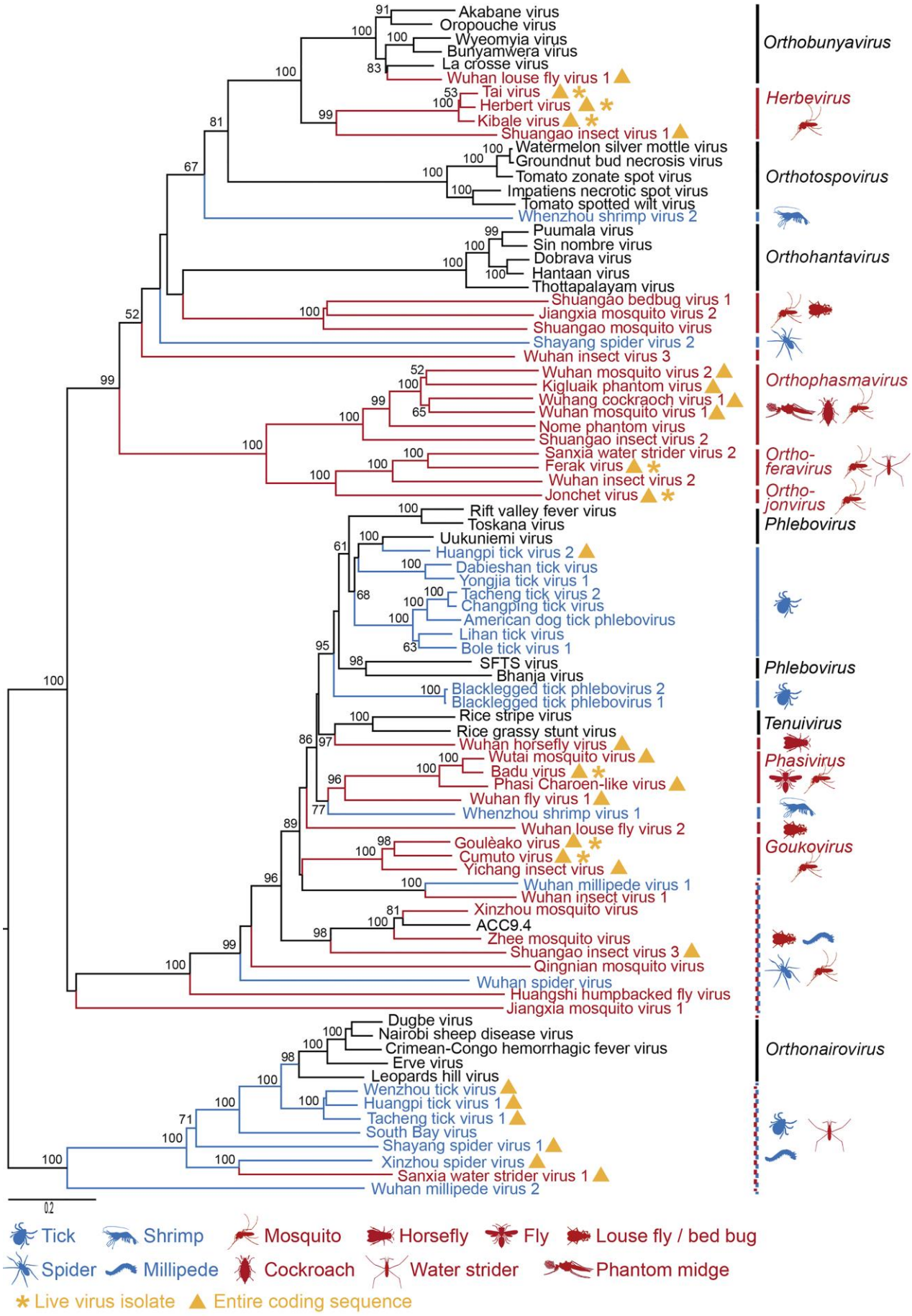
Akabane virus
Oropouche virus
Wyeomyia virus
Bunyamwera virus
La crosse virus
Wuhan louse fly virus 1
Tai virus
Herbert virus
Kibale virus
Shuangao insect virus 1
Watermelon silver mottle virus
Groundnut bud necrosis virus
Tomato zonate spot virus
Impatiens necrotic spot virus
Tomato spotted wilt virus
Whenzhou shrimp virus 2
Puumala virus
Sin nombre virus
Dobrava virus
Hantaan virus
Thottapalayam virus
Shuangao bedbug virus 1
Jiangxia mosquito virus 2
Shuangao mosquito virus
Shayang spider virus 2
Wuhan insect virus 3
Wuhan mosquito virus 2
Kigluaik phantom virus
Wuhang cockroach virus 1
Wuhan mosquito virus 1
Nome phantom virus
Shuangao insect virus 2
Sanxia water strider virus 2
Ferak virus
Wuhan insect virus 2
Jonchet virus
Rift valley fever virus
Toskana virus
Uukuniemi virus
Huangpi tick virus 2
Dabieshan tick virus
Yongjia tick virus 1
Tacheng tick virus 2
Changping tick virus
American dog tick phlebovirus
Lihan tick virus
Bole tick virus 1
SFTS virus
Bhanja virus
Blacklegged tick phlebovirus 2
Blacklegged tick phlebovirus 1
Rice stripe virus
Rice grassy stunt virus
Wuhan horsefly virus
Wutai mosquito virus
Badu virus
Phasi Charoen-like virus
Wuhan fly virus 1
Whenzhou shrimp virus 1
Wuhan louse fly virus 2
Goulèako virus
Cumuto virus
Yichang insect virus
Wuhan millipede virus 1
Wuhan insect virus 1
Xinzhou mosquito virus
ACC9.4
Zhee mosquito virus
Shuangao insect virus 3
Qingnian mosquito virus
Wuhan spider virus
Huangshi humpbacked fly virus
Jiangxia mosquito virus 1
Dugbe virus
Nairobi sheep disease virus
Crimean-Congo hemorrhagic fever virus
Erve virus
Leopards hill virus
Wenzhou tick virus
Huangpi tick virus 1
Tacheng tick virus 1
South Bay virus
Shayang spider virus 1
Xinzhou spider virus
Sanxia water strider virus 1
Wuhan millipede virus 2
0.2
Orthobunyavirus
Herbevirus
Orthotospovirus
Orthohantavirus
Orthophasmavirus
Ortho-feravirus
Ortho-jonvirus
Phlebovirus
Phlebovirus
Tenuivirus
Phasivirus
Goukovirus
Orthonairovirus
Tick
Shrimp
Mosquito
Horsefly
Fly
Louse fly / bed bug
Spider
Millipede
Cockroach
Water strider
Phantom midge
Live virus isolate
Entire coding sequence

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.