MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	*2016.021a-dM*	(to be completed by ICTV officers)

Short title: One (1) new species in one new genus (*Orthoferavirus*), to be included in the proposed family *Feraviridae* 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 ☐

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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:

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	*2016.021aM*		(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Orthoferavirus* (NEW)**	Fill in all that apply.
Subfamily:	**unassigned**	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Family:	***Feraviridae* (NEW, see TP 2016.030M)**	
Order:	***Bunyavirales* (NEW, see TP 2016.030M)**	• 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)
Ferak orthoferavirus	ferak virus (FERV) C51-CI-2004	KP710264, KP710246, KP710267

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

Ferak virus (FERV) is equally distant from all genera and branches from a deep node in the proposed order *Bunyavirales* in basal phylogenetic relationship to the accepted genera *Hantavirus* (proposed *Orthohantavirus*), *Orthobunyavirus, Tospovirus* (proposed *Orthotospovirus*), and the unassigned "herbeviruses".

FERV virions are pleomorphic and are similar in morphology to those produced by the unassigned "goukoviruses". The FERV genome consists of the bunyavirus-typical S, M, and L segments, which are 1.5, 4.3, and 6.9 kb in length, respectively. The S segment encodes a putative NSs ORF that precedes the nucleoprotein ORF, a coding strategy also found in the unassigned "jonviruses" and "phasmaviruses". Interestingly, the FERV M segment also encodes an ORF that is upstream of the glycoprotein precursor gene and may code for an NSm protein. Mature ferak virions contain prominent proteins of 80, 75, and 40 kDa representing the Gn, Gc, and N proteins, respectively.

MODULE 3: **NEW GENUS**

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

Code	*2016.021bM*	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	**unassigned**	Fill in all that apply.
Family:	*Feraviridae* **(NEW, see TP 2016.030M)**	• If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
Order:	*Bunyavirales* **(NEW, see TP 2016.030M**	• If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	*2016.021cM*	(assigned by ICTV officers)

To name the new genus: *Orthoferavirus*

Assigning the type species and other species to a new genus

Code	*2016.021dM*	(assigned by ICTV officers)

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

Ferak orthoferavirus	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:**

1

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 <u>ferak</u> <u>virus</u>.

Reasons to justify the choice of type species:

Ferak virus was the first virus that was discovered representing this new bunyaviral phylogenetic lineage. It is the only virus of this lineage that was isolated in cell culture and from which a complete genome sequence is available.

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

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.

Tick Shrimp Mosquito Horsefly Fly Louse fly / bed bug
Spider Millipede Cockroach Water strider Phantom midge
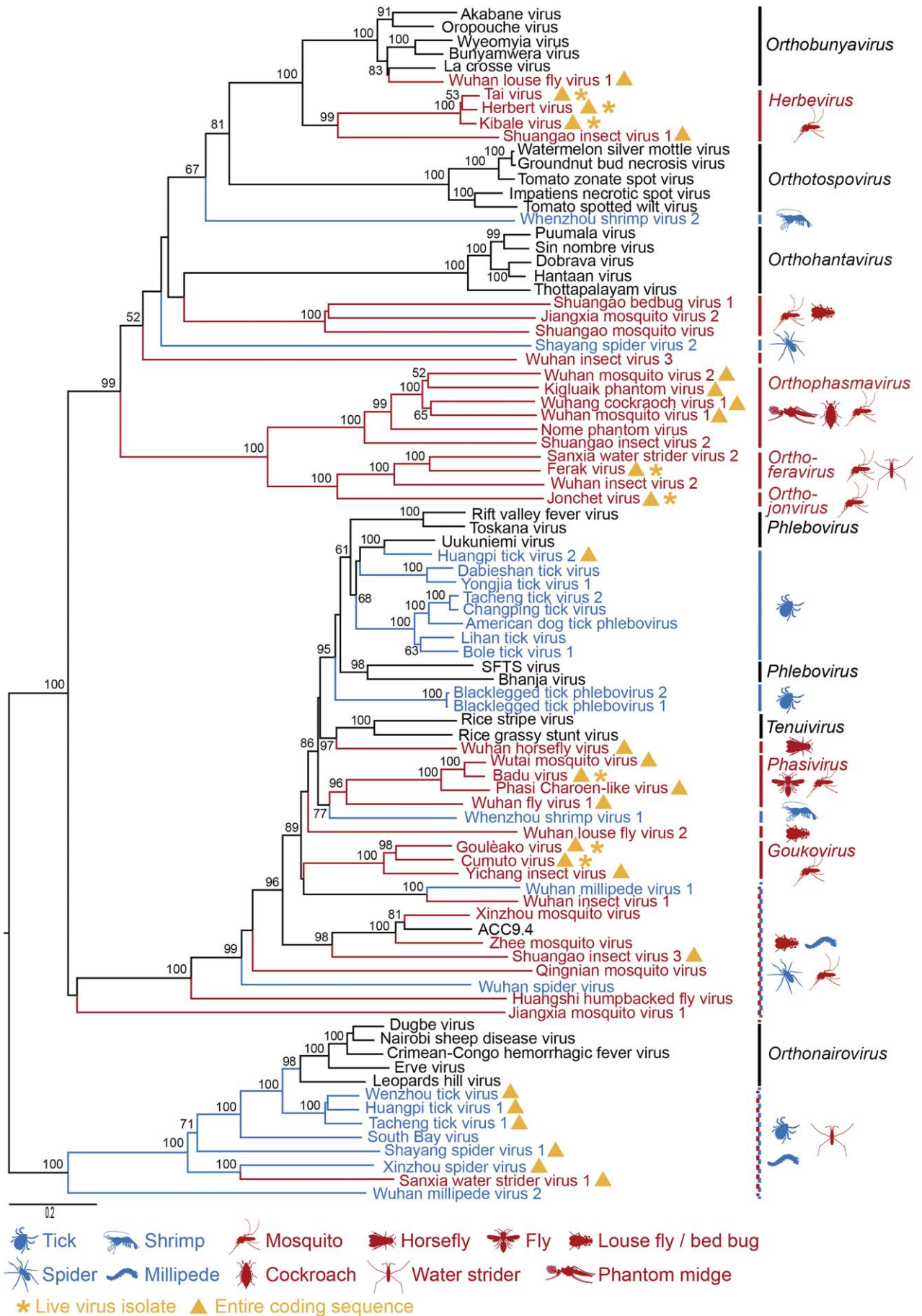* Live virus isolate ▲ Entire coding sequence

Figure: Phylogenetic relationship of bunyaviruses (Junglen). 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.