



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:	2016.026a,bM	(to be completed by ICTV officers)
Short title: Create five (5) new species in the genus <i>Nairovirus</i> (proposed family <i>Nairoviridae</i> , proposed order <i>Bunyvirales</i>), rename the genus <i>Orthonairovirus</i> , and rename all existing species (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 checked="" type="checkbox"/> 10 <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 *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	2016.026aM	(assigned by ICTV officers)
To create 5 new species within:		
Genus:	<i>Orthonairovirus</i> (renamed in 2016.026bM; former name <i>Nairovirus</i>)	Fill in all that apply. <ul style="list-style-type: none"> • 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>Nairoviridae</i> (formerly <i>Bunyaviridae</i> ; see TP 2016.030M)	
Order:	<i>Bunyavirales</i> (new, formerly unassigned; see TP 2016.030M)	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Burana orthonairovirus</i>	Tăchéng tick virus 1 (TTV-1)	S: KM817743 M: KM817717 L: KM817683
<i>Hazara orthonairovirus</i>	Hazara virus (HAZV)	S: KP406725. M: KP406724 L: KP406723
<i>Keterah orthonairovirus</i>	Keterah virus (KTRV)	S: KR537449 M: KR537448 L: KR537447
<i>Kasokero orthonairovirus</i>	Kasokero virus (KAS(O)V)	S: KR537446 M: KR537445 L: KR537444
<i>Nairobi sheep disease orthonairovirus</i>	Nairobi sheep disease virus (NSDV)	S: KM464724 M: KM464725 L: KM464726.

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

Recently, three separate groups have sequenced numerous putative (ortho)nairoviruses (see all references) and analyzed the entire genus using phylogenetic methods (Walker *et al.* 2015, Walker *et al.* 2016, Kuhn *et al.*). These analyses revealed the need to reorganize the genus to a)

incorporate newly discovered or newly sequenced viruses and b) to properly assign already classified viruses. The three studies (Walker *et al.* 2015, Walker *et al.* 2016, Kuhn *et al.*) are in agreement with each other and authors of all three studies are authors of this taxonomic proposal. For purposes of simplicity, the results of only one study are presented here (Kuhn *et al.*):

A set of (ortho)nairovirus sequences (252 for the N gene of the S segment, 111 for the M segment, and 93 for the L segment) comprising the majority of the nucleotide (nt) sequences from GenBank available on 1 March 2016, were aligned using the CLUSTAL algorithm. Because the nairovirus sequences of all analyzed (ortho)nairoviruses were so different that the alignment reached substitution saturation (no detection of signal), alignments were instead implemented at the amino acid (aa) level (using MEGA Version 5). Non-coding regions of S segments therefore had to be excluded. Additional manual editing was performed to ensure the highest possible quality of alignments. Neighbor-joining (NJ) analysis at the aa level was performed due to the observed high variability of the underlying nt sequences. The statistical significance of tree topology was evaluated by bootstrap re-sampling of the sequences 1000 times. Phylogenetic analyses were performed using MEGA Version 5. The results of these analyses are shown in Figures 1-3. A phylogenetic analysis of the (ortho)nairovirus and (ortho)nairo-like virus core polymerase modules with the corresponding regions of other bunyaviruses ((ortho)hantaviruses, orthobunyaviruses, phleboviruses), mammarenaviruses, and orthomyxoviruses is shown in Figure 4.

Based on the results of these analyses, we propose that (ortho)nairovirus taxonomy ought to be based on sequence analysis of coding-complete regions of all three genomic segments; and that viruses with insufficient genomic sequence information be called “putative (ortho)nairoviruses”. Our analyses indicate the need for a total of 12 (ortho)nairovirus species (5 of them new) with the virus members as outlined in Table 1. Putative (ortho)nairoviruses are listed in Table 2.

MODULE 9: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

Code	2016.026bM	
To rename the following taxon (or taxa):		
Current genus name		Proposed genus name
<i>Nairovirus</i>		<i>Orthonairovirus</i>
Current species name		Proposed species name
<i>Crimean-Congo hemorrhagic fever nairovirus</i>		<i>Crimean-Congo hemorrhagic fever orthonairovirus</i>
<i>Dera Ghazi Khan nairovirus</i>		<i>Dera Ghazi Khan orthonairovirus</i>
<i>Dugbe nairovirus</i>		<i>Dugbe orthonairovirus</i>
<i>Hughes nairovirus</i>		<i>Hughes orthonairovirus</i>
<i>Qalyub nairovirus</i>		<i>Qalyub orthonairovirus</i>
<i>Sakhalin nairovirus</i>		<i>Sakhalin orthonairovirus</i>
<i>Thiafora nairovirus</i>		<i>Thiafora orthonairovirus</i>
Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed		
All species names in the bunyavirus-supergroup follow the Non-Latinized Binomial Species naming format.		

additional material in support of this proposal

References:

1. **Kuhn JH, Wiley MR, Rodriguez SE, Bao Y, Prieto K, Travassos da Rosa AP, Guzman H, Savji N, Ladner JT, Tesh RB, Wada J, Jahrling PB, Bente DA, Palacios G.** 2016. Genomic Characterization of the Genus *Nairovirus* (Family *Bunyaviridae*). *Viruses* **8**:164.
2. **Walker PJ, Widen SG, Firth C, Blasdel KR, Wood TG, Travassos da Rosa AP, Guzman H, Tesh RB, Vasilakis N.** 2015. Genomic Characterization of Yogue, Kasokero, Issyk-Kul, Keterah, Gossas, and Thiafora Viruses: Nairoviruses Naturally Infecting Bats, Shrews, and Ticks. *Am J Trop Med Hyg* **93**:1041-1051.
3. **Walker PJ, Widen SG, Wood TG, Guzman H, Tesh RB, Vasilakis N.** 2016. A Global Genomic Characterization of Nairoviruses Identifies Nine Discrete Genogroups with Distinctive Structural Characteristics and Host-Vector Associations. *Am J Trop Med Hyg* **94**:1107-1122.
4. **Al'khovskii SV, L'Vov D K, Shchelkanov M, Shchetinin AM, Deriabin PG, Gitel'man AK, Botikov AG, Samokhvalov EI, Zakarian VA.** 2014. [Taxonomic status of the Artashat virus (ARTSV) (*Bunyaviridae*, *Nairovirus*) isolated from the ticks *Ornithodoros alactagalis* Issaakjan, 1936 and *O. verrucosus* Olenov, Sassuchin et Fenuk, 1934 (Argasidae Koch, 1844) collected in Transcaucasia]. *Vopr Virusol* **59**:24-28.
5. **Al'khovskii SV, L'Vov D K, Shchelkanov M, Shchetinin AM, Deriabin PG, Samokhvalov EI, Gitel'man AK, Botikov AG.** 2013. [The taxonomy of the Issyk-Kul virus (ISKV, *Bunyaviridae*, *Nairovirus*), the etiologic agent of the Issyk-Kul fever isolated from bats (*Vespertilionidae*) and ticks *Argas (Carios) vespertilionis* (Latreille, 1796)]. *Vopr Virusol* **58**:11-15.
6. **L'Vov D K, Al'khovskii SV, Shchelkanov M, Shchetinin AM, Aristova VA, Gitel'man AK, Deriabin PG, Botikov AG.** 2014. [Taxonomy of previously unclassified Tamdy virus (TAMV) (*Bunyaviridae*, *Nairovirus*) isolated from the *Hyalomma asiaticum asiaticum* Schulze et Schlottke, 1929 (Ixodidae, Hyalomminae) in the Middle East and transcaucasia]. *Vopr Virusol* **59**:15-22.
7. **L'Vov D K, Al'khovskii SV, Shchelkanov M, Shchetinin AM, Aristova VA, Morozova TN, Gitel'man AK, Deriabin PG, Botikov AG.** 2014. [Taxonomic status of the Chim virus (CHIMV) (*Bunyaviridae*, *Nairovirus*, Qalyub group) isolated from the Ixodidae and Argasidae ticks collected in the great gerbil (*Rhombomys opimus* Lichtenstein, 1823) (Muridae, Gerbillinae) burrows in Uzbekistan and Kazakhstan]. *Vopr Virusol* **59**:18-23.
8. **L'Vov D K, Al'khovskii SV, Shchelkanov M, Shchetinin AM, Deriabin PG, Aristova VA, Gitel'man AK, Samokhvalov EI, Botikov AG.** 2014. [Genetic characterization of the Sakhalin virus (SAKV), Paramushir virus (PMRV) (Sakhalin group, *Nairovirus*, *Bunyaviridae*), and Rukutama virus (RUKV) (Uukuniemi group, *Phlebovirus*, *Bunyaviridae*) isolated from the obligate parasites of the colonial seabirds ticks *Ixodes (Ceraticxodes) uriae*, White 1852 and *I. signatus* Birulya, 1895 in the water area of sea of the Okhotsk and Bering sea]. *Vopr Virusol* **59**:11-17.
9. **L'Vov D K, Al'khovskii SV, Shchelkanov M, Shchetinin AM, Deriabin PG, Gitel'man AK, Aristova VA, Botikov AG.** 2014. [Taxonomic status of the Burana virus (BURV) (*Bunyaviridae*, *Nairovirus*, Tamdy group) isolated from the ticks *Haemaphysalis punctata* Canestrini et Fanzago, 1877 and *Haem. concinna* Koch,

additional material in support of this proposal

References:

- 1844 (Ixodidae, Haemaphysalinae) in Kyrgyzstan]. *Vopr Virusol* **59**:10-15.
10. **L'Vov D K, Al'khovskii SV, Shchelkanov M, Shchetinin AM, Deriabin PG, Samokhvalov EI, Gitel'man AK, Botikov AG.** 2014. [Genetic characterization of the Caspiy virus (CASV) (*Bunyaviridae*, *Nairovirus*) isolated from the Laridae (Vigors, 1825) and Sternidae (Bonaparte, 1838) birds and the Argasidae (Koch, 1844) ticks *Ornithodoros capensis* Neumann, 1901, in Western and Eastern coasts of the Caspian Sea]. *Vopr Virusol* **59**:24-29.

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.

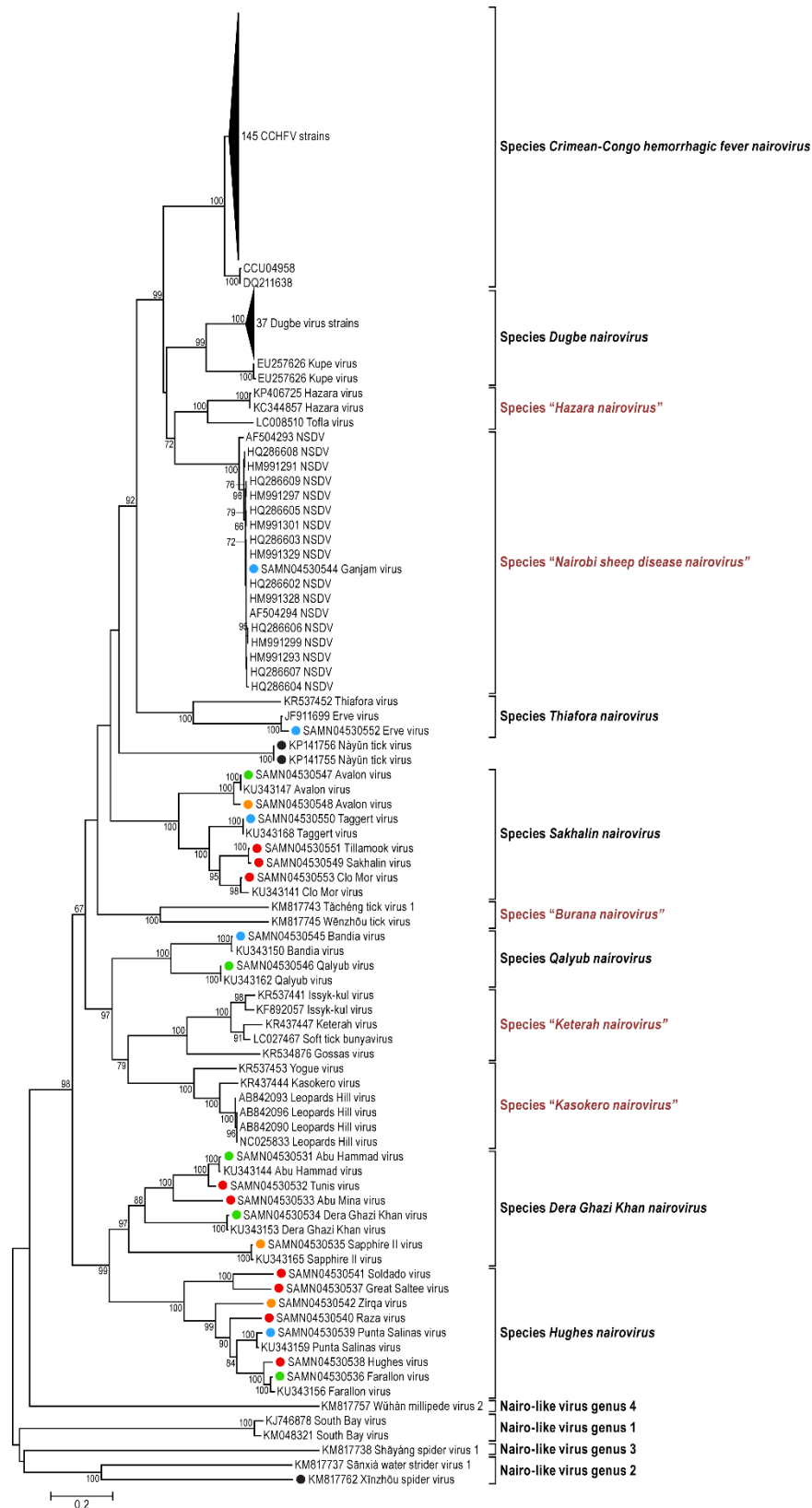


Figure 1. Phylogenetic analysis of (ortho)nairovirus and (ortho)nairo-like virus S segment N gene sequences, including newly determined virus sequences (red dots), newly determined virus isolate sequences (orange dots), re-sequenced genomes (blue dots), and re-sequenced genomes with genomic termini determined for the first time (green dots). Sequences marked with black dots correspond to partial sequences. (Ortho)nairovirus sequences comprise all partial or complete sequences from GenBank

available on 1 March 2016. Proposed new taxa are highlighted in red and placed in quotation marks (Kuhn *et al.*). Note that the names in this figures are those proposed in the publication but differ from those proposed here.

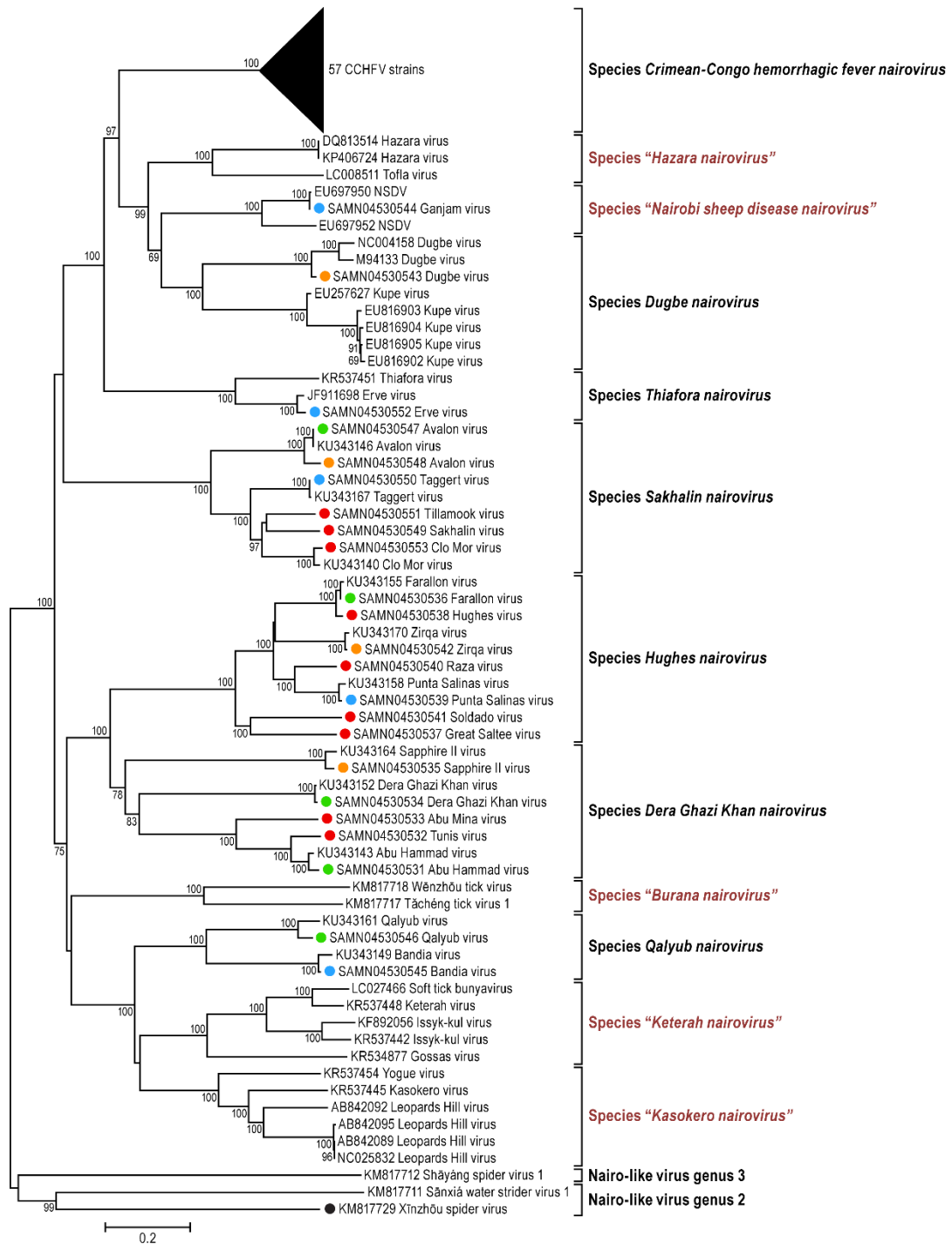


Figure 2. Phylogenetic analysis of (ortho)nairovirus and (ortho)nairo-like virus M segment sequences. Analysis was performed as outlined for Figure 1. Note that the names in this figures are those proposed in the publication but differ from those proposed here.

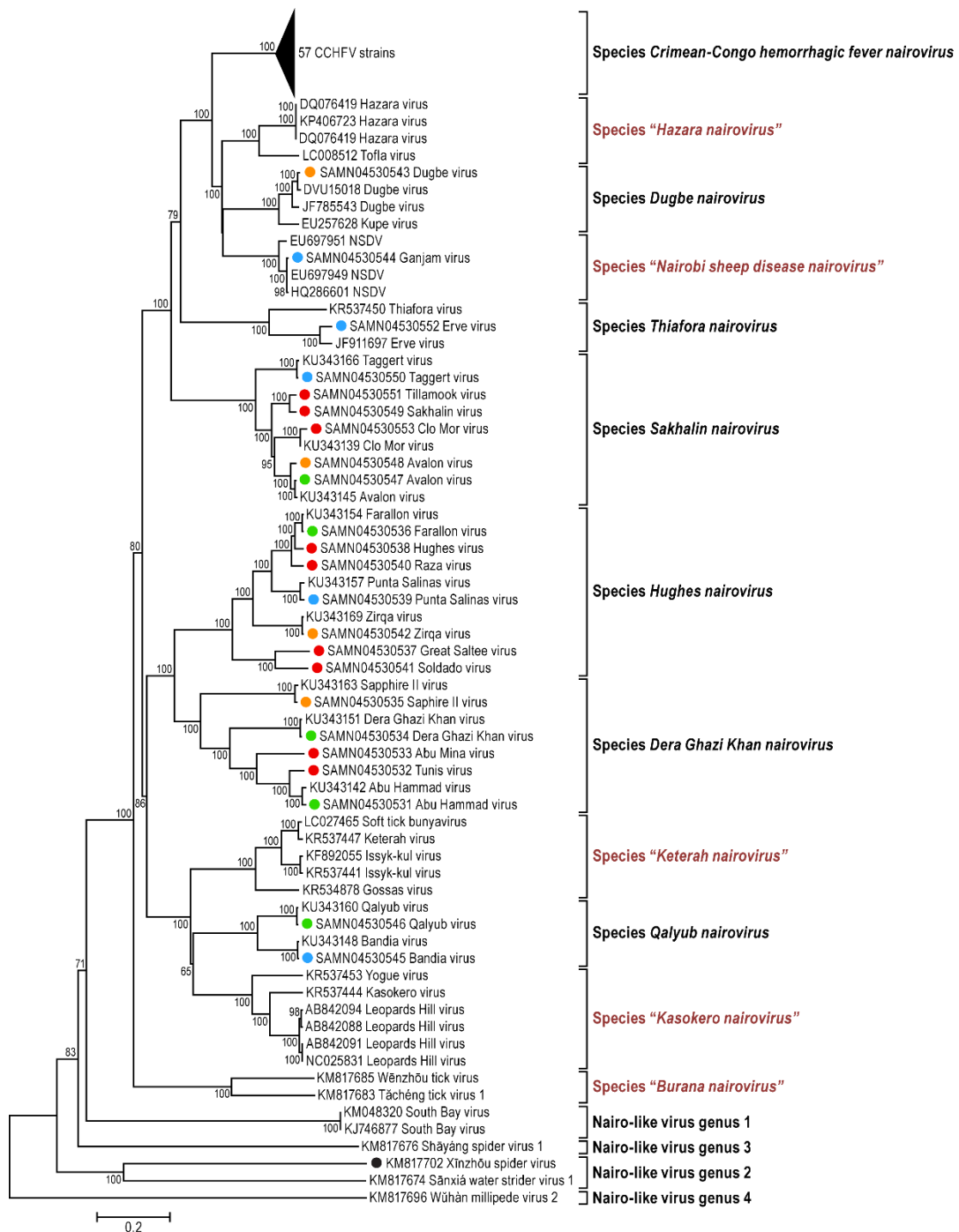


Figure 3. Phylogenetic analysis of (ortho)nairovirus and (ortho)nairo-like virus L segment sequences. Analysis was performed as outlined for Figure 1 (Kuhn *et al.*). Note that the names in this figures are those proposed in the publication but differ from those proposed here.

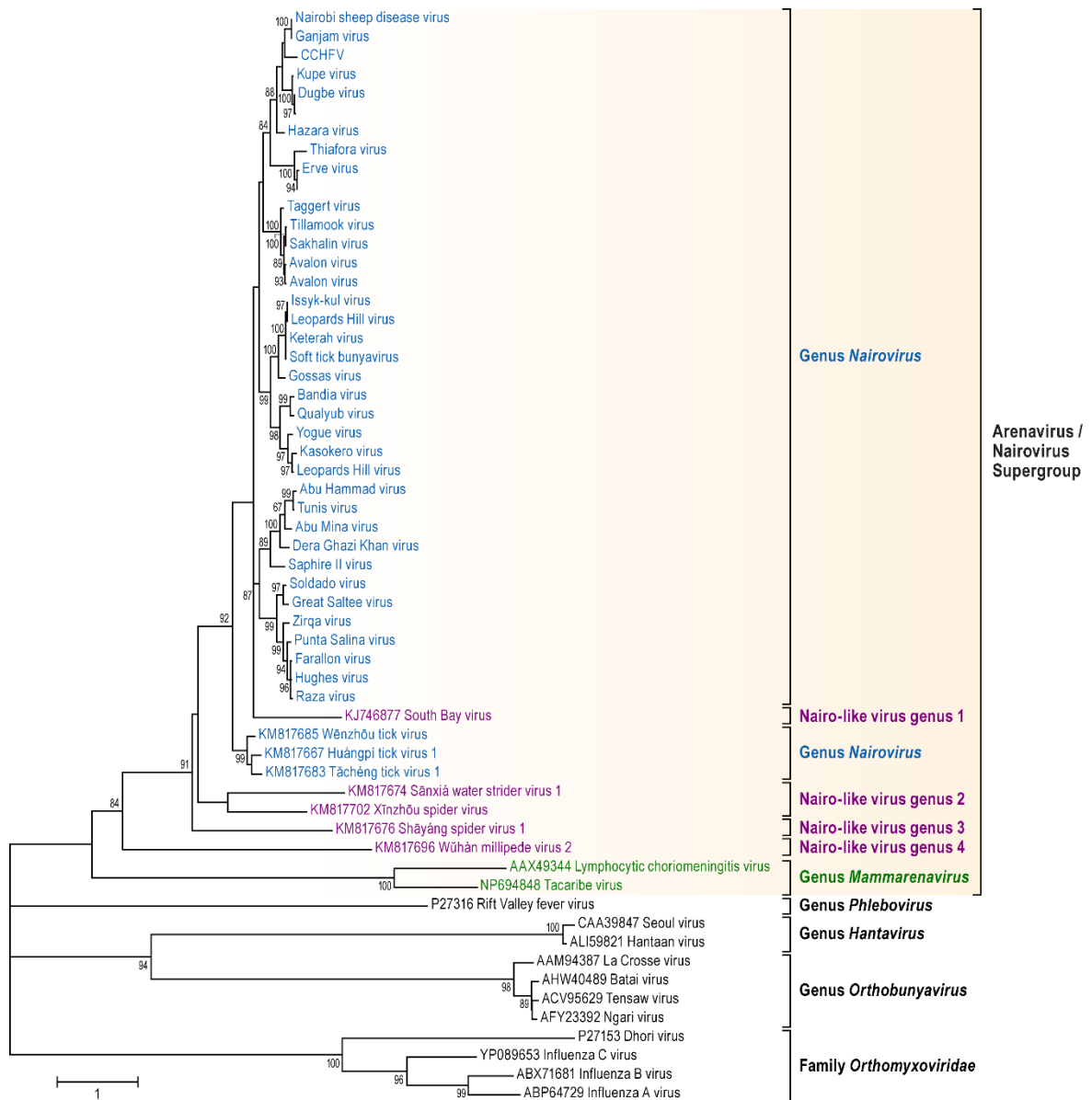


Figure 4. Phylogenetic analysis of the RNA-dependent-RNA polymerase core domain. A set of 58 core domains, comprising motifs A through E for representative viruses were analyzed by maximum likelihood method at the amino acid level using PHYML (Kuhn *et al.*). Note that the names in this figures are those proposed in the publication but differ from those proposed here.

Table 1. Proposed new taxonomy of the genus *Orthoairovirus* based on genomic data. Proposed new taxa are highlighted in red. Viruses mentioned in Table 2 ought to be considered putative orthonairoviruses that based on current data cannot/should not be classified (Kuhn *et al.*).

Species	Virus Members
<i>Burana orthonairovirus</i>	Huángpí tick virus 1 (HTV-1) Tǎchéng tick virus 1 (TTV-1) Wēnzhōu tick virus (WTV)
<i>Crimean-Congo hemorrhagic fever orthonairovirus</i>	Crimean-Congo hemorrhagic fever virus (CCHFV)
<i>Dera Ghazi Khan orthonairovirus</i>	Abu Hammad virus (AHV) including Tunis isolate Abu Mina virus (AMV) Dera Ghazi Khan virus (DGKV) Sapphire II virus (SAPV)
<i>Dugbe orthonairovirus</i>	Dugbe virus (DUGV) Kupe virus (KUPEV)
<i>Hazara orthonairovirus</i>	Hazara virus (HAZV) Tofla virus (TFLV)
<i>Hughes orthonairovirus</i>	Caspiy virus (CASV) Farallon virus (FARV) Great Saltee virus (GRSV) Hughes virus (HUGV) Punta Salinas virus (PSV) Raza virus (RAZAV) Soldado virus (SOLV) Zirqa virus (ZIRV)
<i>Keterah orthonairovirus</i>	Gossas virus (GOSV) Issyk-kul virus (ISKV) Keterah virus (KTRV) including soft tick isolate Uzun-Agach virus (UZAV)
<i>Kasokero orthonairovirus</i>	Kasokero virus (KAS(O)V) Leopards Hill virus (LPHV) Yogue virus (YOGV)
<i>Nairobi sheep disease virus orthonairovirus</i>	Nairobi sheep disease virus (NSDV) including Ganjam isolate
<i>Qalyub orthonairovirus</i>	Bandia virus (BDV) Qalyub virus (QYBV)
<i>Sakhalin orthonairovirus</i>	Avalon virus (AVAV) Clo Mor virus (C(L)MV) Sakhalin virus (SAKV) Taggart virus (TAGB) Tillamook virus (TILLV)
<i>Thiafora orthonairovirus</i>	Erve virus (ERVEV) Thiafora virus (TFAV)

Table 2. Putative nairoviruses that based on current data cannot/should not be classified (Kuhn *et al.*).

Ahun virus
Artashat virus (ARTSV)
Bakel virus (BAKV)
Burana virus (BURV)
Chim virus (CHIMV)
Elliðaeý virus ELL 81-3b
Finch Creek virus (FINCV)
Foula virus F 80-1
Fraser Point virus (FPV)
Garm virus
Geran virus (GERV/GRNV)
Grímsey virus GRIMS82-1b
Inner Farne Island virus IF 80-3, IF80-4
Island of May virus IM81
Kachemak Bay virus (KBV)
Kao Shuan virus (KSV)
Mykines virus M82-2
Nâyũn tick virus
Omo virus (OMOV)
Pathum Thani virus (PTHV)
Pretoria virus (PREV)
Puffin Island virus (PIV)
Sānxiá water strider virus 1 (SWSV-1)
Shāyáng spider virus 1
South Bay virus (SBV)
Tamdy virus (TDYV)
Wũhàn millipede virus 2
Xīnzhōu spider virus (XSV)