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:	***2016.023a-cM***	(to be completed by ICTV officers)

Short title: In the genus *Hantavirus* (proposed family *Hantaviridae*, proposed order *Bunyavirales*), create 24 new species, abolish 7 species, change the demarcation criteria, and change the name of the genus to *Orthohantavirus*; likewise, rename its constituent species.
(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. The Study Group reserves the possibility to switch hantavirus classification to an S+M+L sequence analysis requirement in the future.

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	***2016.023aM***	(assigned by ICTV officers)

To create 24 new species within:

Genus:	***Orthohantavirus*** (renamed in 2016.023cM; former name *Hantavirus*)
Subfamily:	**unassigned**
Family:	***Hantaviridae*** (formerly *Bunyaviridae*; see TP 2016.030M)
Order:	***Bunyavirales*** (new, formerly unassigned; 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)**
Amga orthohantavirus	Amga virus (MGAV) AH301	KF974360, KF974359
Asama orthohantavirus	Asama virus (ASAV) N10	EU929072, EU929075
Asikkala orthohantavirus	Asikkala virus (ASIV) CZ/Beskydy/412/2010/Sm	KC880341, KC880344, KC880347
Bowe orthohantavirus	Bowé virus (BOWV) VN1512	KC631782-KC631784
Bruges orthohantavirus	Bruges virus (BRGV) BE/Vieux-Genappe/TE/2013/1	KX551960-KX551962
Cao Bang orthohantavirus	Cao Bang virus (CBNV) 3	EF543524-EF543526
Choclo orthohantavirus	Choclo virus (CHOV) MSB96073	DQ285046-DQ285047
Dabieshan orthohantavirus	Dabieshan virus (DBSV) Yongjia-Nc-58	JF796022, JF796036
Fugong orthohantavirus	Fugong virus (FUGV) FG10	KT899701-KT899703
Fusong orthohantavirus	Fusong virus (FUSV) Fusong-Mf-682	EU072480, EU072488
Imjin orthohantavirus	Imjin virus (MJNV) Cixi-Cl-23	KJ420559, KJ420541, KJ420567
Jeju orthohantavirus	Jeju virus (JJUV) 10-11	HQ834695-HQ834697
Kenkeme orthohantavirus	Kenkeme virus (KKMV) Fuyuan-Sr-326	KJ857341, KJ857337, KJ857320
Laibin orthohantavirus	Laibin virus (LAIV) BT20	KM102247- KM102249
Longquan orthohantavirus	Longquan virus (LQUV) Longquan-Rs-32	JX465422, JX465402

Luxi orthohantavirus	Luxi virus (LUXV) LX309	HM756286, HM756287, HQ404253
Maporal orthohantavirus	Maporal virus (MAPV) HV-97021050	AB689164, AY363179, EU788002
Montano orthohantavirus	Montano virus (MTNV) 104/2006	AB620100-AB620102
Necocli orthohantavirus	Necocli virus (NECV) HV-O0020002	KF481954, KF494345
Nova orthohantavirus	Nova virus (NVAV) 3483 (Te34)	KR072621-KR072623
Oxbow orthohantavirus	Oxbow virus (OXBV) Ng1453	FJ539166, FJ539167
Quezon orthohantavirus	Quezon virus (QZNV)	KU950713-KU950715
Rockport orthohantavirus	Rockport virus (RKPV) MSB57412	HM015223, HM015219, HM015221
Yakeshi orthohantavirus	Yakeshi virus (YKSV) Yakeshi-Si-210	JX465423, JX465403

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

We used a recently introduced computational approach to hierarchically classify the current genus *Hantavirus* (proposed to be renamed *Orthohantavirus*) by relying solely on genetic data, DEmARC or 'DivErsity pArtitioning by hierarchical Clustering' introduced by Chris Lauber and Alexander Gorbalenya (Lauber and Gorbalenya, 2012a; Lauber and Gorbalenya, 2012b). Briefly, in DEmARC virus clusters are delimited by devising a threshold on the maximum intra-cluster (intra-taxon) divergence of viruses. This is done separately for each level of the hierarchical classification, all of which are selected using a cost function that measures the quality of virus clustering. The approach was extensively evaluated in a case study of picornaviruses (Lauber and Gorbalenya, 2012b) and filoviruses (Lauber and Gorbalenya, 2012a).

Many sequences of hantaviruses are available online (e.g., through NCBI GenBank), but only a limited number of coding-complete genome sequences (full S, M, and L segment sequences of the same hantavirus) are available. A single segment sequence renders insufficient information; an all-segments analysis is limited by the availability of coding-complete sequences (especially the L segment). A concatenated multiple alignment of the nucleocapsid protein (S) segment, and the Gn and Gc glycoprotein ORFs (M segment) was used. PED (pairwise evolutionary distances) values were calculated based on the WAG amino acid substitution model by applying a maximum likelihood approach as implemented in the Tree-Puzzle program (v5.2). Based on this matrix, species demarcation was calculated (see also Figure 1 and Figure 2) and a species cutoff was defined.

- Make an amino acid concatenated multiple alignment containing the coding-complete regions of the nucleocapsid protein (S segment) and glycoproteins (M segment);

- Calculate PED values using WAG amino acid substitution matrix (Tree-Puzzle, maximum likelihood parameter);
- A species of the genus *Hantavirus* (proposed *Orthohantavirus*) is defined by a PED value for its member greater than 0.1.

All 24 proposed species meet the criteria to be demarcated as distinct *Hantavirus* (proposed *Orthohantavirus*) species of a 0.1 PED threshold for each member virus (Figure 1).

MODULE 8: **REMOVE (ABOLISH)**

Use this module if an existing taxon needs to be completely removed (abolished). Use module 9 if there is simply a change of name.

removing (abolishing a taxon)

Code	***2016.023bM***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Isla Vista hantavirus
Muleshoe hantavirus
New York hantavirus
Rio Mamore hantavirus
Rio Segundo hantavirus
Saaremaa hantavirus
Topografov hantavirus

The present taxonomic position of these taxon/taxa:

Genus:	***Orthohantavirus*** (renamed in 2016.023cM; former name *Hantavirus*)	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	***Hantaviridae*** (new, formerly *Bunyaviridae*; see TP 2016.030M)	
Order:	***Bunyavirales*** (new, formerly unassigned; see TP 2016.030M)	

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

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

Isla vista hantavirus: Only 1 complete S segment sequence, partial M (max. length 337 bp), and no L segment sequences are available of Isla vista virus (ISLAV). Therefore this virus was not considered for the DEmARC analysis. For this reason (incomplete sequencing data available) this species should be abolished.

Muleshoe hantavirus: Only 1 complete S segment sequence available of Muleshoe virus (MULV). No M or L segment sequences are available. Therefore this virus was not considered for the DEmARC analysis. For this reason (incomplete sequencing data available) this species should be abolished.

New York hantavirus: New York virus (NYV), which has been associated with typical hantavirus cardio-pulmonary syndrome (HCPS) was isolated from a white-footed deermouse (*Peromyscus leucopus*) caught at an island off the coast of New York. This virus, demarcated as belonging to a separate *Hantavirus* species by ICTV, shows high similarity with Sin Nombre virus on both the M and S segment amino acid sequences. Although New York virus can be distinguished undoubtedly by using neutralization tests, the virus does not meet the other ICTV criteria to be demarcated into a distinct hantavirus species. In the DEmARC analysis, NYV is considered as a strain of Sin Nombre virus (species *Sin Nombre hantavirus*).

Rio Mamore hantavirus: Rio Mamoré virus (RIOMV) shares high similarity on both S and M segments with Laguna Negra virus (species *Laguna Negra hantavirus*). In the DEmARC analysis, RMV is considered as a strain of Laguna Negra virus.

Rio Segundo hantavirus: Only 1 complete S segment sequence is available of Río Segundo virus (RIOSV). No M or L segment sequences are available. Therefore this virus was not considered for the DEmARC analysis. For this reason (incomplete sequencing data available) this species should be abolished.

Saaremaa hantavirus: Saaremaa virus (SAAV) shows high similarity with Dobrava-Belgrade virus (species *Dobrava-Belgrade hantavirus*) in the DEmARC analysis and can be considered as a representative virus of the Dobrava-Belgrade virus. In 2013, the international research community working on SAAV and Dobrava-Belgrade virus suggested to classify SAAV as a virus of the *Dobrava-Belgrade hantavirus* species together with Dobrava virus, Kurkino virus, and Sochi virus (Klempa et al, 2013).

Topografov hantavirus: Khabarovsk virus (KHAV) was isolated from a reed vole (*Microtus fortis*) caught in the Khabarovsk region in far-eastern Russia, whereas Topogravof virus (TOPV) was isolated from a Siberian brown lemming (*Lemmus sibiricus*) caught near the Topografov River in the Taymyr Peninsula, Siberia, Russia. TOPV shows high similarity with KHAV in the DEmARC analysis and can be considered as a strain of KHAV.
Although the viruses are carried by two distinct arvicolines, the viruses have a high similarity in their M segment- and especially in their S segment-encoded amino acid sequences, suggesting a likely host switching event from the ancestor of *Myodes* which could have been the donor of an ancestral virus that became the common evolutionary origin of both viruses. Long deletions in the S and M segment 3’ noncoding regions of KHAV compared with TOPV virus suggest that TOPV could represent a more ancestral virus than KHAV. Currently KHAV and TOPV virus are defined by ICTV as members of two separate species based on the fact that KHAV and TOPV virus are carried by clearly distinct hosts in which they are constantly maintained. However, these viruses cannot be distinguished using neutralization tests.

None of the above-mentioned viruses meet the criteria of a PED-value of at least 0.1 to be demarcated in distinct *Hantavirus* (proposed *Orthohantavirus*) species. (PED species demarcation threshold >0.1).

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	***2016.023cM***

To rename the following taxon (or taxa):

Current genus name	**Proposed genus name**
Hantavirus	*Orthohantavirus*
Current species name	**Proposed species name**
Andes hantavirus	*Andes orthohantavirus*
Bayou hantavirus	*Bayou orthohantavirus*
Black Creek Canal hantavirus	*Black Creek Canal orthohantavirus*
Cano Delgadito hantavirus	*Cano Delgadito orthohantavirus*
Dobrava-Belgrade hantavirus	*Dobrava-Belgrade orthohantavirus*
El Moro Canyon hantavirus	*El Moro Canyon orthohantavirus*
Hantaan hantavirus	*Hantaan orthohantavirus*
Khabarovsk hantavirus	*Khabarovsk orthohantavirus*
Laguna Negra hantavirus	*Laguna Negra orthohantavirus*
Prospect Hill hantavirus	*Prospect Hill orthohantavirus*
Puumala hantavirus	*Puumala orthohantavirus*
Sangassou hantavirus	*Sangassou orthohantavirus*
Seoul hantavirus	*Seoul orthohantavirus*
Sin Nombre hantavirus	*Sin Nombre orthohantavirus*
Thailand hantavirus	*Thailand orthohantavirus*
Thottapalayam hantavirus	*Thottapalayam orthohantavirus*
Tula hantavirus	*Tula orthohantavirus*

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.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Klempa B, Avsic-Zupanc T, Clement J, Dzagurova TK, Henttonen H, Heyman P, Jakab F, Kruger DH, Maes P, Papa A, Tkachenko EA, Ulrich RG, Vapalahti O, Vaheri A. Complex evolution and epidemiology of Dobrava-Belgrade hantavirus: definition of genotypes and their characteristics. Arch Virol. 2013, 158(3):521-9. doi: 10.1007/s00705-012-1514-5.

Lauber C, Gorbalenya AE. Genetics-based classification of filoviruses calls for expanded sampling of genomic sequences. Viruses. 2012a, 4(9):1425-37. doi: 10.3390/v4091425.

Lauber C, Gorbalenya AE. Partitioning the genetic diversity of a virus family: approach and evaluation through a case study of picornaviruses. J Virol. 2012b, 86(7):3890-904. doi: 10.1128/JVI.07173-11.

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: (Ortho)hantavirus classification according to DEmARC by using a concatenated S+M complete coding region (amino acid) dataset. Box- and whisker graphs are used to plot level-specific PED distributions for the 41 clusters of the lowest classification level. The 41 orange clusters correspond to the 41 original or new ICTV species of the genus *Hantavirus* (proposed *Orthohantavirus*). The *Hantavirus* (proposed *Orthohantavirus*) species are grouped vertically according to a Bayesian MCMC phylogeny shown at the left. Internal nodes of the tree that correspond to *Hantavirus* (proposed *Orthohantavirus*) species are collapsed; all of them have bootstrap support values of 1.

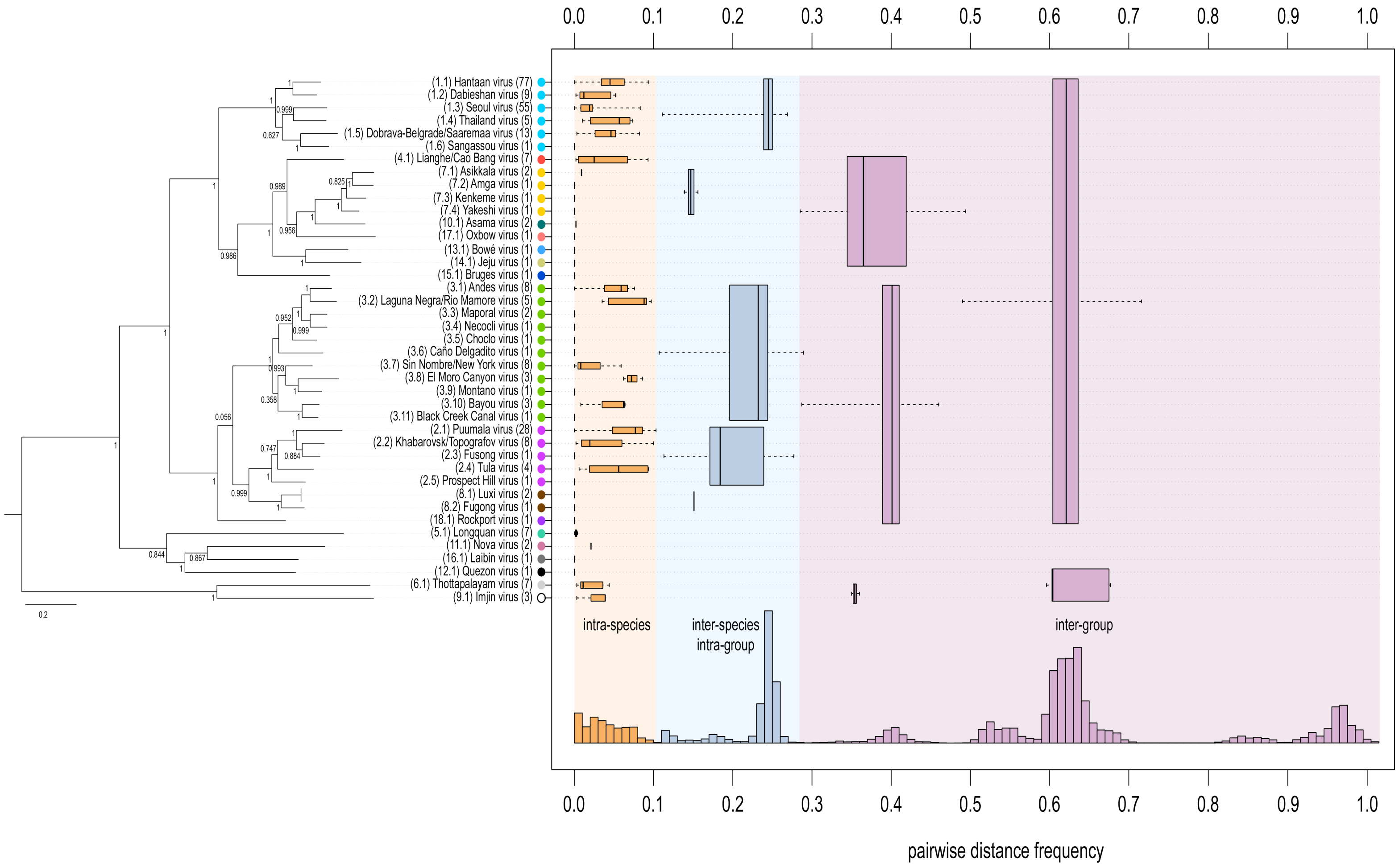
(1.1) Hantaan virus (77)
(1.2) Dabieshan virus (9)
(1.3) Seoul virus (55)
(1.4) Thailand virus (5)
(1.5) Dobrava-Belgrade/Saaremaa virus (13)
(1.6) Sangassou virus (1)
(4.1) Lianghe/Cao Bang virus (7)
(7.1) Asikkala virus (2)
(7.2) Amga virus (1)
(7.3) Kenkeme virus (1)
(7.4) Yakeshi virus (1)
(10.1) Asama virus (2)
(17.1) Oxbow virus (1)
(13.1) Bowé virus (1)
(14.1) Jeju virus (1)
(15.1) Bruges virus (1)
(3.1) Andes virus (8)
(3.2) Laguna Negra/Rio Mamore virus (5)
(3.3) Maporal virus (2)
(3.4) Necocli virus (1)
(3.5) Choclo virus (1)
(3.6) Caño Delgadito virus (1)
(3.7) Sin Nombre/New York virus (8)
(3.8) El Moro Canyon virus (3)
(3.9) Montano virus (1)
(3.10) Bayou virus (3)
(3.11) Black Creek Canal virus (1)
(2.1) Puumala virus (28)
(2.2) Khabarovsk/Topografov virus (8)
(2.3) Fusong virus (1)
(2.4) Tula virus (4)
(2.5) Prospect Hill virus (1)
(8.1) Luxi virus (2)
(8.2) Fugong virus (1)
(18.1) Rockport virus (1)
(5.1) Longquan virus (7)
(11.1) Nova virus (2)
(16.1) Laibin virus (1)
(12.1) Quezon virus (1)
(6.1) Thottapalayam virus (7)
(9.1) Imjin virus (3)
0.999
0.627
0.825
0.989
0.956
0.986
0.952
0.999
0.993
0.358
0.056
0.747
0.884
0.999
0.844
0.867
0.2
intra-species
inter-species
intra-group
inter-group
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
pairwise distance frequency

Figure 2: Frequency distribution of PED values is shown for the complete S+M amino acid dataset. In a first stage, peaks in the distribution were approximated using a mixture of normal distribution (red curves) together with an estimation of noise (purple horizontal line), with a goodness-of-fit of 0.962. For discrete distance along the distance range, TSM values (green bins) are shown. This measure is proportional to the probability of a particular distance not to be originated from one of the peak distributions. Consecutive distances with high TSM values provide candidate regions of distance discontinuity, which can be used for partitioning the distribution and to infer levels of the hierarchical classification.

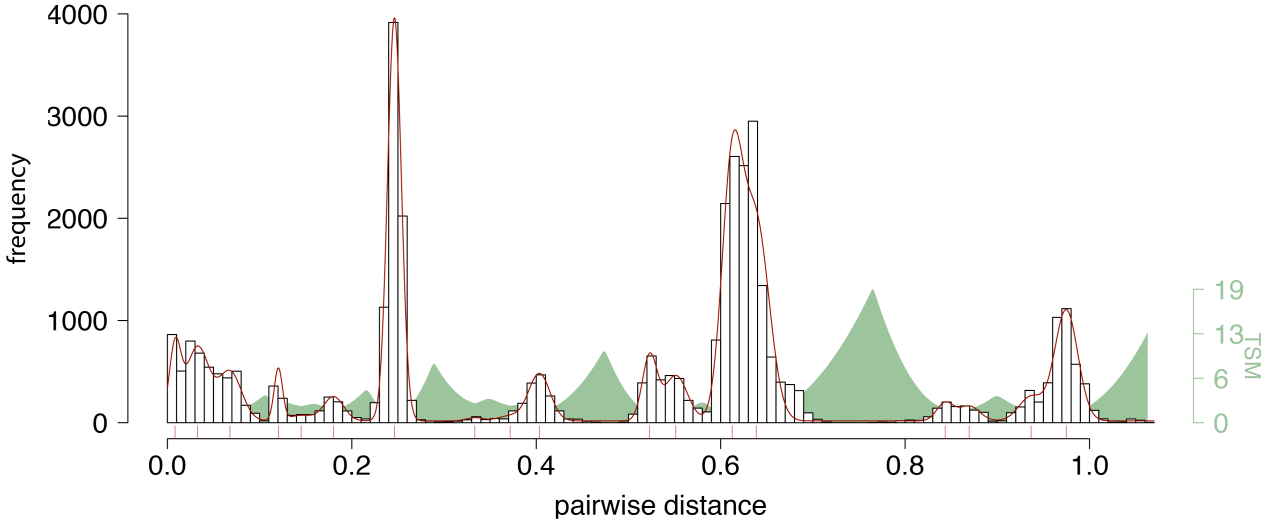

Figure 3: Bayesian MCMC phylogenetic tree of a concatenated S+M full coding region (amino acid) dataset. Internal nodes of the tree that correspond to *Hantavirus* species are collapsed (triangles); all of them have bootstrap support values of 1. Note that all species names in this table would be changed to the format "*Xxx orthohantavirus*" if this taxonomic proposal is accepted in its entirety

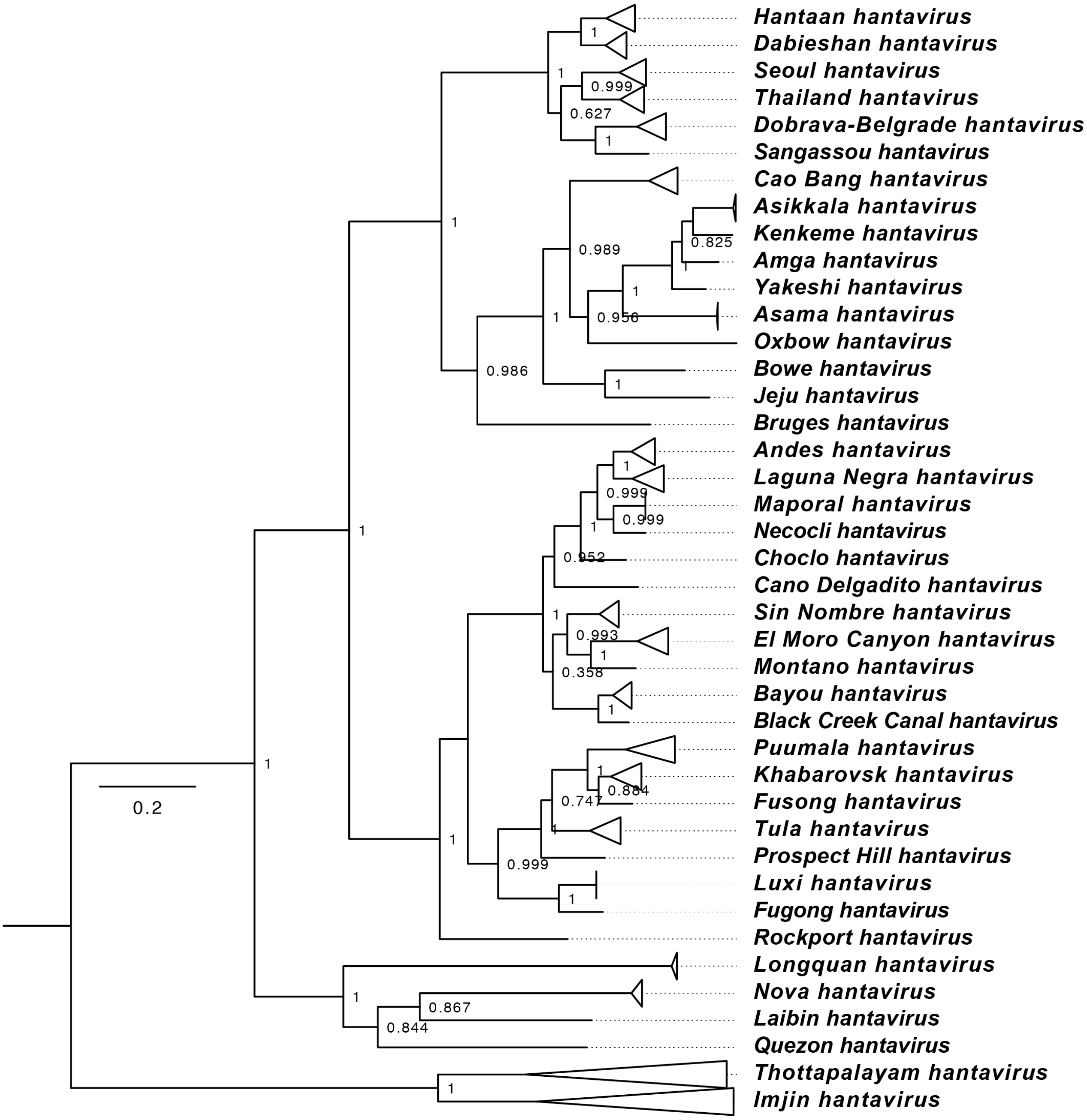

Table 1. New complete species list in the genus.

	Species	Representative virus(es)	Virus abbreviation
1	*Amga orthohantavirus*	Amga virus AH301	MGAV
2	*Andes orthohantavirus*	Andes virus Chile-9717869 Lechiguanas virus Oran virus Castelo dos Sonhos virus	ANDV
3	*Asama orthohantavirus*	Asama virus N10	ASAV
4	*Asikkala orthohantavirus*	Asikkala virus CZ/Beskydy/412/2010/Sm	ASIV
5	*Bayou orthohantavirus*	Bayou virus Louisiana Catacamas virus	BAYV
6	*Black Creek Canal orthohantavirus*	Black Creek Canal virus	BCCV
7	*Bowe orthohantavirus*	Bowé virus VN1512	BOWV
8	*Bruges orthohantavirus*	Bruges virus BE/Vieux-Genappe/TE/2013/1	BRGV
9	*Cano Delgadito orthohantavirus*	Caño Delgadito virus	CADV
10	*Cao Bang orthohantavirus*	Cao Bang virus 3 Lianghe virus	CBNV
11	*Choclo orthohantavirus*	Choclo virus MSB96073	CHOV
12	*Dabieshan orthohantavirus*	Dabieshan virus Yongjia-Nc-58	DBSV
13	*Dobrava-Belgrade orthohantavirus*	Dobrava virus Kurkino virus Saaremaa virus Sochi virus	DOBV
14	*El Moro Canyon orthohantavirus*	El Moro Canyon virus Carrizal virus Huitzilac virus	ELMCV
15	*Fugong orthohantavirus*	Fugong virus FG10	FUSV
16	*Fusong orthohantavirus*	Fusong virus Fusong-Mf-682	FUGV
17	*Hantaan orthohantavirus*	Hantaan virus 76-118 Amur virus Soochong virus	HTNV
18	*Imjin orthohantavirus*	Imjin virus Cixi-Cl-23	MJNV
19	*Jeju orthohantavirus*	Jeju virus 10-11	JJUV
20	*Kenkeme orthohantavirus*	Kenkeme virus Fuyuan-Sr-326	KKMV
21	*Khabarovsk orthohantavirus*	Khabarovsk virus Topografov virus	KHAV
22	*Laguna Negra orthohantavirus*	Laguna Negra virus Maripa virus Rio Mamore virus	LANV
23	*Laibin orthohantavirus*	Laibin virus BT20	LAIV
24	*Longquan orthohantavirus*	Longquan virus Longquan-Rs-32	LQUV
25	*Luxi orthohantavirus*	Luxi virus LX309	LUXV
26	*Maporal orthohantavirus*	Maporal virus HV-97021050	MAPV
27	*Montano orthohantavirus*	Montano virus 104/2006	MTNV
28	*Necocli orthohantavirus*	Necocli virus HV-O0020002	NECV
29	*Nova orthohantavirus*	Nova virus 3483 (Te34)	NVAV
30	*Oxbow orthohantavirus*	Oxbow virus Ng1453	OXBV
31	*Prospect Hill orthohantavirus*	Prospect Hill virus	PHV

32	*Puumala orthohantavirus*	Puumala virus Hokkaido virus Muju virus	PUUV
33	*Quezon orthohantavirus*	Quezon virus	QZNV
34	*Rockport orthohantavirus*	Rockport virus MSB57412	RKPV
35	*Sangassou orthohantavirus*	Sangassou virus	SANGV
36	*Seoul orthohantavirus*	Seoul virus HR80-39 Gou virus	SEOV
37	*Sin Nombre orthohantavirus*	Sin Nombre virus New York virus	SNV
38	*Thailand orthohantavirus*	Thailand virus 741 Anjozorobe virus Jurong virus	THAIV
39	*Thottapalayam orthohantavirus*	Thottapalayam virus	TPMV
40	*Tula orthohantavirus*	Tula virus Adler virus	TULV
41	*Yakeshi orthohantavirus*	Yakeshi virus Yakeshi-Si-210	YKSV

Tentative members of the genus

(*Viruses of which at least one genomic segment has been sequenced and* which are identified as members of possible new species by DEmARC).

(a) Altai virus
(b) Camp Ripley virus
(c) Isla Vista virus
(d) Jemez Springs virus
(e) Kilimanjaro virus
(f) Muleshoe virus
(g) Qian Hu Shan virus
(h) Rio Segundo virus
(i) Seewis virus
(j) Shenyang virus
(k) Serang virus
(l) Uluguru virus
(m) Ussuri virus
(n) Xinyi virus
(o) Xuan Son virus
(p) Yuanjiang virus