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:	***2016.030a-vM***	(to be completed by ICTV officers)

Short title: Create a new order, *Bunyavirales*, to accommodate nine families (eight new, one renamed) comprising thirteen genera
(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:

This proposal is built on the content and acceptance of co-submitted negative-strand RNA virus TaxoProps 2016.020M, 2016.021M, 2016.022M, 2016.023M, 2016.024M, 2016.025M, 2016.026M, 2016.027M, 2016.028M, and 2016.029M and plant virus TaxoProps 2016.016P, 2016.017P, and 2016.018P. A summary of all these proposals is included in the appendix of this proposal (Table 2) in the form of a table showing the proposed entire new taxonomy of bunyaviruses.

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:

The ICTV *Bunyaviridae* Study Group and the authors of all 2016 bunyavirus-related taxonomic proposals have seen and discussed this proposal, and agreed to its submission to the ICTV Executive Committee based on majority votes of support by individual Study Group members or the absence of dissenting votes.

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2016.030aM***	(assigned by ICTV officers)

To create 8 new families containing the genera listed below within the Order: *Bunyavirales*

If there is no Order, write "**unassigned**" here.
If the Order has yet to be created (in Module 6) please write **"(new)"** after the proposed name.

Code	***2016.030bM***	(assigned by ICTV officers)

To name the new families:

1. *Feraviridae*
2. *Fimoviridae*
3. *Hantaviridae*
4. *Jonviridae*
5. *Nairoviridae*
6. *Phasmaviridae*
7. *Phenuiviridae*
8. *Tospoviridae*

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)

To assign the following subfamilies (if any) to the new family:
You may list several subfamilies here. For each subfamily, please state whether it is new or existing.

- If the subfamily is new, it must be created in Module 4
- If the subfamily already exists, please complete Module 7 to 'MOVE' it from its existing family

N/A

Code	***2016.030cM***	(assigned by ICTV officers)

To assign the following genera to the new families:
You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'MOVE' it from that family

1. *Feraviridae*: *Orthoferavirus*
2. *Fimoviridae*: *Emaravirus*
3. *Hantaviridae*: *Orthohantavirus*
4. *Jonviridae*: *Orthojonvirus*
5. *Nairoviridae*: *Orthonairovirus*
6. *Phasmaviridae*: *Orthophasmavirus*

7. *Phenuiviridae*: *Goukovirus*, *Phasivirus*, *Phlebovirus*, *Tenuivirus*
8. *Tospoviridae*: *Orthotospovirus*

The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):**

0

Reasons to justify the creation of the new family:

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

See Module 6.

Origin of the new family names:

In the case of families that include only single genera, the family names are typically derived from genus names (e.g., *Orthottospovirus*→*Tospoviridae*). An exception is *Fimoviridae*, which is a contraction of the name of a member virus (fig mosaic virus). In the case of the families that includes more than a single genus, the family name is a sigil of included genus names (e.g.*Phlebovirus* + *Tenuivirus* →*Phenuiviridae*).

MODULE 6: **NEW ORDER**

creating and naming a new order

Code	***2016.030dM***	(assigned by ICTV officers)

To create a new Order containing the families listed below

Code	***2016.030eM***	(assigned by ICTV officers)

To name the new Order: *Bunyavirales*

---

assigning families and genera to a new order

Code	***2016.030fM***	(assigned by ICTV officers)

To assign the following families to the new Order:

You may list several families here. For each family, please state whether it is new or existing.

- If the family is new, it must be created in Module 5
- If the family already exists, please state whether it is unassigned or is to be removed from another order and, if the latter, complete Module 7 to 'MOVE' it from that order

1. Tospoviridae
2. Hantaviridae
3. Phasmaviridae
4. Phenuiviridae
5. Nairoviridae
Fimoviridae
***6. Peribunyaviridae* (former name *Bunyaviridae*)**
7. Jonviridae
8. Feraviridae

Code		(assigned by ICTV officers)

To assign the following unassigned genera to the new Order (i.e. within the order but not assigned to any family):

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, you should 'MOVE' it from its current position by completing Module 7

0

Reasons to justify the creation of a new Order:

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

The ICTV *Bunyaviridae* Study Group acknowledges that that the current family *Bunyaviridae* requires urgent revision. Prior to the submitted 2016 TaxoProps, the family *Bunyaviridae* included five established genera (*Hantavirus*, *Nairovirus*, *Orthobunyavirus*, *Phlebovirus*, and *Tospovirus*) for trisegmented negative-strand RNA viruses (Plyusnin *et al*.). Approximately half of the currently known ≈530 bunyaviruses (i.e., presumed members of the family) have not been assigned to these five genera or cannot be assigned to any of these five genera based on established classification criteria. In addition, novel viruses were recently discovered that clearly cluster with classical trisegmented bunyaviruses in phylogenetic analyses of all their proteins, yet are bisegmented (e.g., South Bay virus, Wǔhàn millipede virus 2) (Li *et al*., Tokarz *et al*.). Finally, numerous plant viruses with more than three genomic segments, currently members of the unassigned free-floating genera *Emaravirus* and *Tenuivirus*, have long been referred to as clearly "bunyavirus-like" based on clear clustering of encoded proteins with bunyavirus proteins (Elebaino *et al*., van Poelwijk *et al*.).

In 2016, the ICTV *Bunyaviridae* Study Group pledged to take initial steps to remedy this taxonomic confusion. It was agreed to establish the basis for a thorough overhaul of the "bunyavirus-like supergroup" through a series of TaxoProps in 2016, starting with straightforward proposals leading to classification of currently unassigned viruses to existing genera; followed by proposals to establish novel genera to assign typical bunyaviruses that cannot be assigned to the existing five genera (Junglen); followed by acceptance of emaraviruses and tenuiviruses as official members of the bunyavirus supergroup; and finally taxonomic reorganization of the family to adequately reflect the relationships of the various now included and classified bunyaviruses while at the same time establishing taxonomic "room" for further revisions in 2017.

The current TaxoProp format does not contain go-no-go decision points (e.g., "if this part of the proposal gets accepted move on to module x, otherwise move on to module y"). To prevent a total stand-still of *Bunyaviridae* reorganization efforts in case of a rejection by the ICTV Executive Committee of a single TaxoProp, the ICTV *Bunyaviridae* Study Group decided to approach the above-described reorganization steps through a series of multiple proposal as the acceptance of any of the submitted proposals would be considered progress. Consequently, the following TaxoProps were submitted in 2016 in direct collaboration with the ICTV *Emaravirus* and *Tenuivirus* Study Groups and numerous other collaborators: negative-strand RNA virus TaxoProps 2016.020M, 2016.021M, 2016.022M, 2016.023M, 2016.024M, 2016.025M, 2016.026M, 2016.027M, 2016.028M, and 2016.029M and plant virus TaxoProps 2016.016P, 2016.017P and 2016.018P.

This TaxoProp is contingent on the acceptance of these TaxoProps and is a logical extension of them. It proposes the *de-facto* elevation of the currently existing family *Bunyaviridae* to an order (→"*Bunyavirales*") to better reflect the evolutionary relationships of the various bunyaviruses in a larger taxonomic framework.

This TaxoProp is based on the realization of the ICTV *Bunyaviridae*, *Emaravirus*, and *Tenuivirus* Study Groups and other collaborators that the evolutionary relationships of even those bunyaviruses that are currently classified cannot be adequately represented in a hierarchy with family as the highest taxonomic rank. For instance, a recent analysis of the current genus *Hantavirus* (proposed to be renamed *Orthohantavirus*, TP 2016.023M) indicates that certain current hantavirus species form clear taxonomic sub-groups that can be differentiated from other subgroups, while current species already contain numerous distinct virus members that probably should be assigned to separate species in the future. Because the ICTV does not offer ranks such as subgenus or subspecies, an elevation of the genus (*Ortho*)*hantavirus* to family (→*Hantaviridae*) is a first step to create the necessary room to create subfamilies and additional genera in the future to address this problem. Likewise, recent analyses of the genus *Nairovirus* (proposed to be renamed *Orthonairovirus*, TP 2016.026M) identified numerous viruses that are clearly more closely related to (ortho)nairoviruses than to any other bunyavirus, yet cluster in different groups from the currently recognized monophyletic genus (*Ortho*)*nairovirus* (Kuhn *et al*., Walker *et al*.). Again, an (*Ortho*)*nairovirus*→*Nairoviridae* elevation will create the necessary room for further modification and inclusion of those viruses into novel (ortho)nairovirus-like genera in the future.

However, because the evolutionary relationship of, for instance, nairoviruses (*sensu stricto* or *sensu lato* including nairo-like viruses) and hantaviruses is not up for debate, it follows logically that both families *Hantaviridae* and *Nairoviridae* ought to be grouped in a higher taxon, which based on the ICTV-approved ranking system would be that of order (→"*Bunyavirales*").

More importantly, the establishment of such an order is further substantiated by phylogentic analyses. For instance, DEmARC analysis and Bayesian MCMC phylogeny using concatenated sequences of the bunyavirus-typical S, M, and L segments (Figures 1-3, Table 1) confirm that, for instance, emaraviruses (currently unassigned genus *Emaravirus*) are more closely related to orthobunyaviruses than to phleboviruses, whereas tenuiviruses (currently unassigned genus *Tenuivirus*) are more closely related to phleboviruses than to nairoviruses. These relationships have also been unveiled in other phylogenetic analyses (see L segment phylogeny in Junglen). Both analyses further clarify that maintaining a family *Bunyaviridae* simply including numerous genera would not represent our knowledge of bunyaviral evolutionary relationships.

Origin of the new Order name:

Sigil derived from Bunyamwera virus (an orthobunyavirus).

MODULE 7A: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030gM***	(assigned by ICTV officers)

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

Genus *Emaravirus*

The present taxonomic position of these taxon/taxa:

Genus:	***N/A***	Fill in all that apply.
Subfamily:	unassigned	
Family:	unassigned	
Order:	unassigned	

Code	***2016.030hM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***N/A***	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	unassigned	
Family:	***Fimoviridae* (NEW)**	
Order:	***Bunyavirales* (NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6 and:

The genus *Emaravirus* is recognized by the ICTV, but has not yet been assigned to a family. This genus includes six species, i.e. *Fig mosaic virus* (for fig mosaic virus, FMV) (Elbeaino et al., 2009a, 2009b, 2012); *Rose rosette virus* (for rose rosette virus, RRV) (Laney *et al.*, 2011); *Raspberry leaf blotch virus* (for raspberry leaf blotch virus, RLBV) (McGavin *et al.*, 2012); *Pigeonpea sterility mosaic virus* (for pigeonpea sterility mosaic virus 1, PPSMV-1) (Elbeaino *et al.*, 2014; Kumar *et al.*, 2003), *High Plains wheat mosaic virus* (for High Plains wheat mosaic virus, HPWMoV) (Tatineni *et al.*, 2014; Skare *et al.*, 2006); and *European mountain ash ringspot-associated virus* (for European mountain ash ringspot-associated virus, EMARaV) as the type species of the genus (Mielke-Ehret & Mühlbach, 2007). Other tentative emaraviruses (TaxoProps submitted by the ICTV *Emaravirus* Study Group in parallel to this proposal) are: redbud yellow ringspot-associated virus (RYRSaV) (Laney *et* *al*., 2010), pigeonpea sterility mosaic virus 2 (PPSMV-2) (Elbeaino *et al*., 2015) and actinidia chlorotic ringspot-associated virus (AcCRaV) (Zheng *et al*., 2016).

Emaraviruses are clearly related to bunyaviruses by having :

i) multipartite negative single-stranded RNAs (four to eight segments);
ii) sharing high sequence identity with bunyaviral orthologous proteins at equivalent genome positions in the first three RNAs (corresponding to bunyaviral L, M, and S RNAs) (Figure 4), i.e. RNA-dependent RNA polymerase (RdRp, RNA-1), putative glycoprotein precursor (GP, RNA-2) and putative nucleocapsid (NP, RNA-3);
iii) five conserved motifs (A–E) in the amino acid sequence of their RdRps similar to those in bunyaviral L segments (Figure 5);
iv) enveloped virion;
v) stretches of nucleotides at both 5' and 3' termini of all RNA segments almost complementary to each other and conserved in all genomic RNAs of emaraviruses that are similar, but not identical, to those of classified bunyaviruses (Figure 7); and
vi) common evolutionary history of several emaravirus-encoded proteins with bunyavirus orthologs: phylogenetic analyses based on amino acid sequences of RNA-1, 2-, 3-encoded proteins consistently allocate the emaraviruses together with bunyaviruses. Particularly, in trees constructed using RdRp and NP sequences, emaraviruses consistently cluster with (ortho)tospoviruses (Figure 6).

Emaraviruses differ from classified bunyaviruses by having a higher number of genomic RNA segments [four segments (EMARaV) to eight segments (HPWMoV)]. The function of proteins encoded by some of these segments remains unknown

MODULE 7F: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030iM***	(assigned by ICTV officers)

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

Genus *Phlebovirus*

The present taxonomic position of these taxon/taxa:

Genera:	***N/A***	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	***Bunyaviridae***	
Order:	**unassigned**	

Code	***2016.030jM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genera:	***N/A***	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	**unassigned**	
Family:	***Phenuiviridae* (NEW)**	
Order:	***Bunyavirales* (NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6.

MODULE 7G: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.029kM***	(assigned by ICTV officers)

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

Genus *Tenuivirus*

The present taxonomic position of these taxon/taxa:

Genus:	***N/A***	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	**unassigned**	
Order:	**unassigned**	

Code	***2016.029lM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***N/A***	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	**unassigned**	
Family:	***Phenuiviridae*** **(NEW)**	
Order:	***Bunyavirales*** **(NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6 and:

The genus *Tenuivirus* is recognized by the ICTV, but has not yet been assigned to a family. However, tenuiviruses are discernibly related to bunyaviruses, and specifically to those from the genus *Phlebovirus*. Tenuiviruses are similar to bunyaviruses because:

vii) they have an overall similar genome organization and employ a similar gene expression strategy;

viii) tenuivirus and phlebovirus genomic segments share highly conserved octanucleotide at 5' (5'-ACACAAAG) and 3' (CUUUGUGU-3') termini;

ix) they encode functionally related proteins at equivalent genome positions;

x) the tenuivirus RNA-dependent RNA polymerases (RdRp) and 94 KDa proteins are homologous to the RdRps and glycoproteins of bunyaviruses;

xi) phylogenetic analyses of the viral RdRp consistently places tenuiviruses in the bunyavirus supergroup, most closely related to, but distinct from, phleboviruses;

and

xii) their infection cycle includes arthropod transmission and the ability to replicate in the arthropod vector.

The differences between tenuiviruses and “standard” bunyaviruses are:

i) tenuiviruses are more complex in terms of the extent of genome segmentation and generally encode more proteins than phleboviruses. However, differences in number of genome segments are not uncommon traits among genera of viruses belonging to the same family (e.g., *Reoviridae*, *Closteroviridae*, *Secoviridae*, *Potyviridae*, *Rhabdoviridae*), or even between members of the same genus (e.g., *Emaravirus*);

ii) bunyaviruses, but not tenuiviruses, produce enveloped virions. The deep evolutionary history and host adaptation processes that have led to the divergences are unclear at present. Although enveloped tenuivirions have not been found yet, tenuiviruses do encode a glycoprotein closely related to those of phleboviruses (a similar situation can be found in the *Rhabdoviridae* among members of the genus *Dichorhavirus*).

Therefore, the two above-listed differences may not be taxonomically relevant and should not be used to preclude the assignment of *Tenuivirus* as a bunyaviral genus.

MODULE 7H: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030mM***	(assigned by ICTV officers)

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

genus *Orthohantavirus* (former name *Hantavirus;* see 2016.023M)

The present taxonomic position of these taxon/taxa:

Genus:	**N/A**	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	***Bunyaviridae***	
Order:	**unassigned**	

Code	***2016.030nM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	**N/A**	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	**unassigned**	
Family:	***Hantaviridae* (NEW)**	
Order:	***Bunyavirales* (NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6.

MODULE 7I: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030oM***	(assigned by ICTV officers)

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

genus *Orthonairovirus* (former name *Nairovirus;* see 2016.026M)

The present taxonomic position of these taxon/taxa:

Genus:	**N/A**	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	***Bunyaviridae***	
Order:	**unassigned**	

Code	***2016.030pM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	**N/A**	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	**unassigned**	
Family:	***Nairoviridae*** **(NEW)**	
Order:	***Bunyavirales*** **(NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6.

MODULE 7J: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030qM***	(assigned by ICTV officers)

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

genus *Orthotospovirus* (former name *Tospovirus;* see 2016.030vM)

The present taxonomic position of these taxon/taxa:

Genus:	***N/A***	Fill in all that apply.
Subfamily:	**unassigned**	
Family:	***Bunyaviridae***	
Order:	**unassigned**	

Code	***2016.030rM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***N/A***	Fill in all that apply. • If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it. If no genus is specified, enter "**unassigned**" in the genus box.
Subfamily:	**unassigned**	
Family:	***Tospoviridae* (NEW)**	
Order:	***Bunyavirales* (NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6.

MODULE 7L: **MOVE**

Use this module whenever an existing taxon needs to be moved and re-assigned (e.g. when a species is moved from one genus to another).

moving an existing taxon

Code	***2016.030sM***	(assigned by ICTV officers)

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

Peribunyaviridae **(former name *Bunyaviridae*; see 2016.030uM)**

The present taxonomic position of these taxon/taxa:

Genera:	**N/A**	Fill in all that apply.
Subfamily:	**N/A**	
Family:	**N/A**	
Order:	**unassigned**	

Code	***2016.030tM***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genera:	**N/A**	Fill in all that apply. • If the higher taxon has yet to be created write “**(new)**” after its proposed name and complete relevant module to create it. If no genus is specified, enter “**unassigned**” in the genus box.
Subfamily:	**N/A**	
Family:	***Peribunyaviridae*** **(RENAMED)**	
Order:	***Bunyavirales*** **(NEW)**	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 11

See Module 6.

MODULE 9A: **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.
.

Renaming one or more taxa

Code	***2016.030uM***	(assigned by ICTV officers)
To rename the following taxon (or taxa):		

Current name	**Proposed name**
Bunyaviridae	***Peribunyaviridae***

Reasons to justify the renaming: Explain why the taxon (or taxa) should be renamed
The family *Bunyaviridae* was effectively upgraded to an order *Bunyavirales* through this proposal. This leaves the need for a family for the two remaining genera *Orthobunyavirus* and *Herbevirus*, for which we propose the name *Peribunyaviridae*. Procedurally, this needs to be accomplished by renaming the at this point still existing family *Bunyaviridae*. The prefix "*Peri*-" was added to differentiate the members of this new family (→"peribunyaviruses") from those of the entire order (→"bunyaviruses") and those of the genus *Orthobunyavirus* (→"orthobunyaviruses"), i.e. to prevent ambiguities.

MODULE 9B: **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	***2016.030vM***	

To rename the following taxon (or taxa):

Current genus name	**Proposed genus name**
Tospovirus	***Orthotospovirus***
Current species name	**Proposed species name**
Groundnut bud necrosis tospovirus	*Groundnut bud necrosis orthotospovirus*
Groundnut ringspot tospovirus	*Groundnut ringspot orthotospovirus*
Groundnut yellow spot tospovirus	*Groundnut yellow spot orthotospovirus*
Impatiens necrotic spot tospovirus	*Impatiens necrotic spot orthotospovirus*
Iris yellow spot tospovirus	*Iris yellow spot orthotospovirus*
Polygonum ringspot tospovirus	*Polygonum ringspot orthotospovirus*
Tomato chlorotic spot tospovirus	*Tomato chlorotic spot orthotospovirus*
Tomato spotted wilt tospovirus	*Tomato spotted wilt orthotospovirus*
Watermelon bud necrosis tospovirus	*Watermelon bud necrosis orthotospovirus*
Watermelon silver mottle tospovirus	*Watermelon silver mottle orthotospovirus*
Zucchini lethal chlorosis tospovirus	*Zucchini lethal chlorosis orthotospovirus*

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

References (order):

Elbeaino T, Digiaro M, Martelli GP (2009) Complete nucleotide sequence of four RNA segments of fig mosaic virus. Arch Virol 154:1719-1727

Junglen S (2016) Evolutionary origin of pathogenic arthropod-borne viruses – a case study in the family *Bunyaviridae*. Arch Virol 154:1719-1727

Kuhn JH, Seregin SV, Morzunov SP, Petrova ID, Vyshemirskii OI, Lvov DK, Tyunnikov GI, Gutorov VV, Netesov SV, Petrov VS (2004) Genetic analysis of the M RNA segment of Crimean-Congo hemorrhagic fever virus strains involved in the recent outbreaks in Russia. Archives of Virology (Wien/Vienna) 149:2199-2213

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Plyusnin A, Beaty BJ, Elliott RM, Goldbach R, Kormelink R, Lundkvist A, Schmaljohn CS, Tesh RB (2011) Family *Bunyaviridae*. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus Taxonomy - Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, London, United Kingdom, pp 725-741

Tokarz R, Williams SH, Sameroff S, Sanchez Leon M, Jain K, Lipkin WI (2014) Virome analysis of *Amblyomma americanum*, *Dermacentor variabilis*, and *Ixodes scapularis* ticks reveals novel highly divergent vertebrate and invertebrate viruses. J Virol 88:11480-11492

van Poelwijk F, Prins M, Goldbach R (1997) Completion of the impatiens necrotic spot virus genome sequence and genetic comparison of the L proteins within the family Bunyaviridae. J Gen Virol 78 (Pt 3):543-546

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

References (emaraviruses):

Elbeaino T., Digiaro M., Alabdullah A.K., De Stradis A., Minafra A., Mielke N., Castellano M.A., Martelli G.P., 2009a. A multipartite negative-sense single-stranded RNA virus is the putative agent of fig mosaic disease. *Journal of General Virology*, 90 (5), 1281-1288.

Elbeaino T., Digiaro M., Martelli G.P., 2009b. Complete nucleotides sequence of four viral RNAs segments of fig mosaic virus. *Archives of Virology*, 154 (11). 1719-1727.

Elbeaino T., Digiaro M., Martelli G.P., 2012. RNA-5 and -6, two additional negative-sense RNA segments associated with Fig mosaic virus. *Journal of Plant Pathology*, 94 (2), 421-425.

Elbeaino T., Digiaro M., Uppala M., Sudini H., 2014. Deep sequencing of Pigeonpea sterility mosaic virus discloses five RNA segments related to emaraviruses. *Virus Research*, 188: 27–31.

Elbeaino T., Digiaro M., Uppala M., Sudini H., 2015. Deep-sequencing of dsRNAs recovered from mosaic-diseased pigeonpea (*Cajanus cajan* L.) revealed the presence of a novel emaravirus: Pigeonpea sterility mosaic virus 2 (PPSMV2). *Archives of Virology*, 160:2019–2029.

Kumar P.L., Jones A.T., Reddy D., 2003. A novel mite-transmitted virus with a divided RNA genome closely associated with pigeonpea sterility mosaic disease. *Phytopathology*, 93, 71-81.

Laney A.G., Gergerich R., Keller K., Martin R., Tzanetakis I., 2010. Rose rosette and redbud yellow ringspot are caused by two new emaraviruses. *Phytopathology*, 100, S67.

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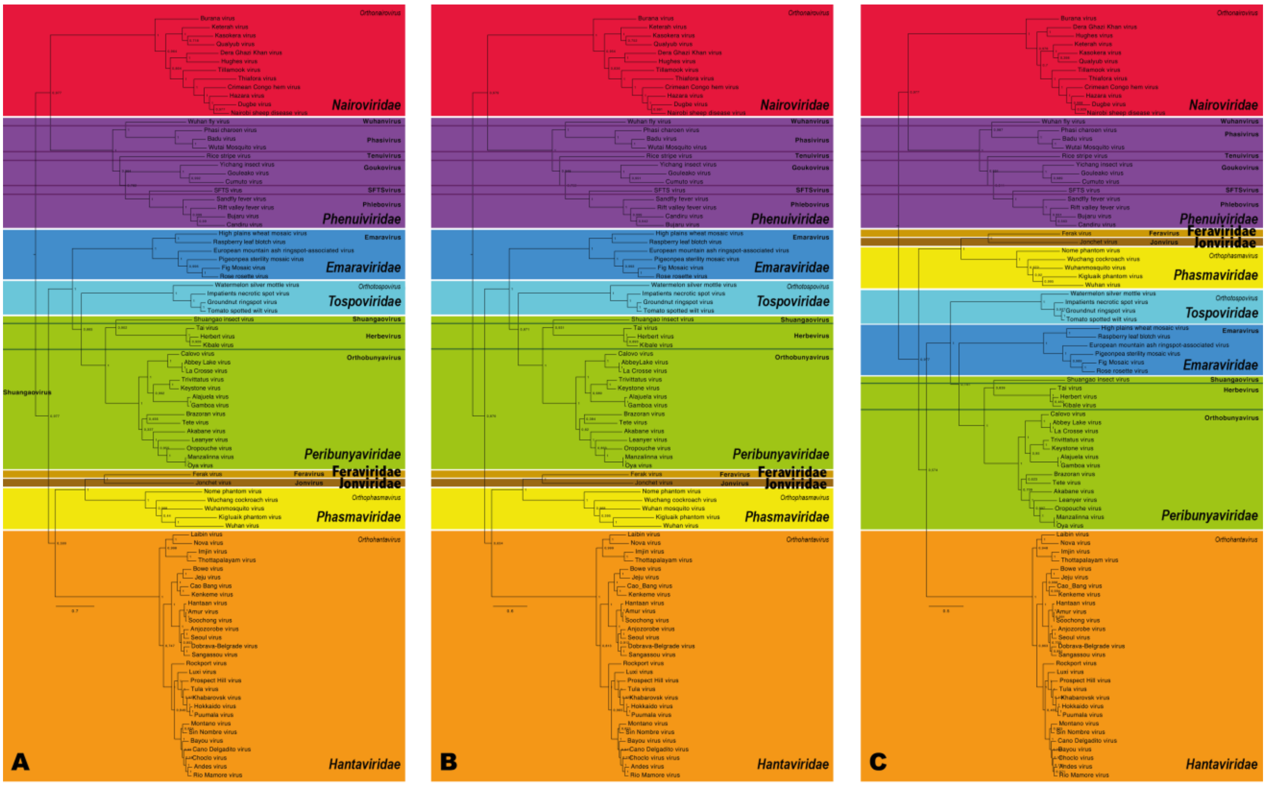
Tatineni S, McMechan AJ, Wosula EN, Wegulo SN, Graybosch RA, French R, Hein GL. (2014). An eriophyid mite-transmitted plant virus contains eight genomic RNA segments with unusual heterogeneity in the nucleocapsid protein. *Journal of Virology*, 88: 11834-11845.

Zheng Y, Navarro B, Wang G, Wang Y, Yang Z, Xu W, Zhu C, Wang L, Di Serio F, Hong N. (2016). Actinidia chlorotic ringspot-associated virus: a novel emaravirus infecting kiwifruit plants. *Molecular Plant Pathology*: DOI: 10.1111/mpp.12421.



No correction
10400 sites

Heuristic correction
7254 sites

Global correction
1587 sites

Figure 1: Influence of the multiple alignment on the phylogenetic relationship of the order *Bunyavirales*. The dataset used consists of full length products of coding regions of the S, M, and L segments (nucleocapsid protein, glycoprotein precursor, and RNA-dependent RNA polymerase, respectively) Phylogenetic relationships were inferred with maximum likelihood on (A) uncorrected alignment, (B) heuristically corrected alignment using Trimal (v1.2rev59) based on local variation blocks, and (C) trimmed to 5% gapped regions based on the global alignment. The nine families cluster separately with high bootstrap support with each of the alignments in a comparable way. The heuristically corrected alignment was chosen as the best method to correct the alignment.

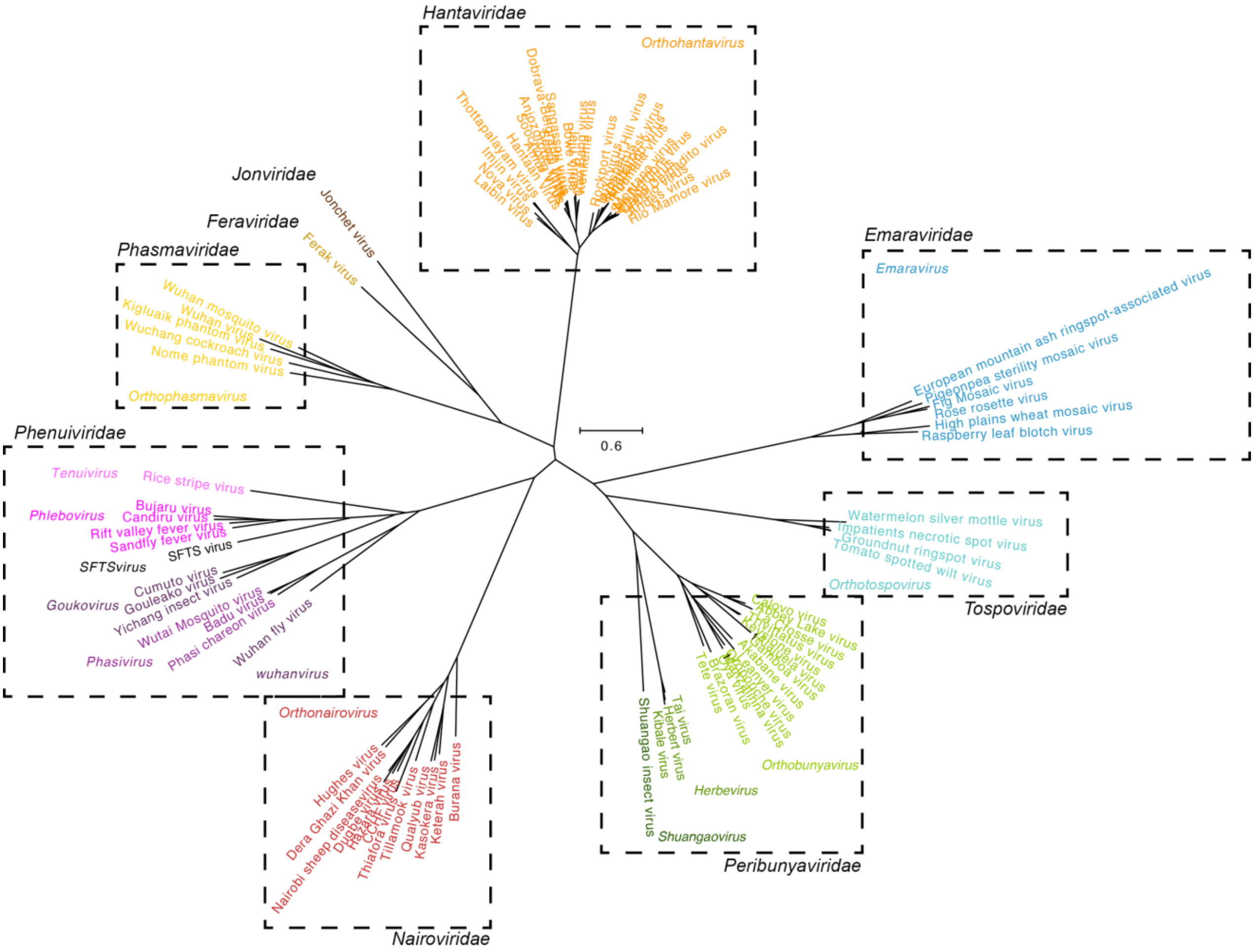


Figure 2. The figure shows a Bayesian MCMC tree estimated using a Bayesian Markov Chain Monte Carlo method implemented in BEAST/πBUSS, using the WAG amino acid model of amino acid substitutions with 100 million generations. Maximum clade credibility trees were determined using TreeAnnotator with a burn-in of 10% of the sampled trees. The dataset used consists of full length products of coding regions of the S, M, and L segments (nucleocapsid protein, glycoprotein precursor, and RNA-dependent RNA polymerase, respectively) and concatenated in one multiple alignment. The dashed boxes show the proposed family delineation as calculated with DEmARC version 1.0. The DEmARC method is an approach for partitioning the genetic diversity of a virus family /genus within a hierarchically organized framework. The developed approach can provide quantitative support for both the delineated classification levels and the inferred taxa by objectively devising the number and values of thresholds on family genetic divergence at each level in a rational and family/genus-wide manner. Genetic divergence is quantified by pairwise evolutionary distances (PEDs) estimated by maximum likelihood inference on a multiple alignment of proteins.

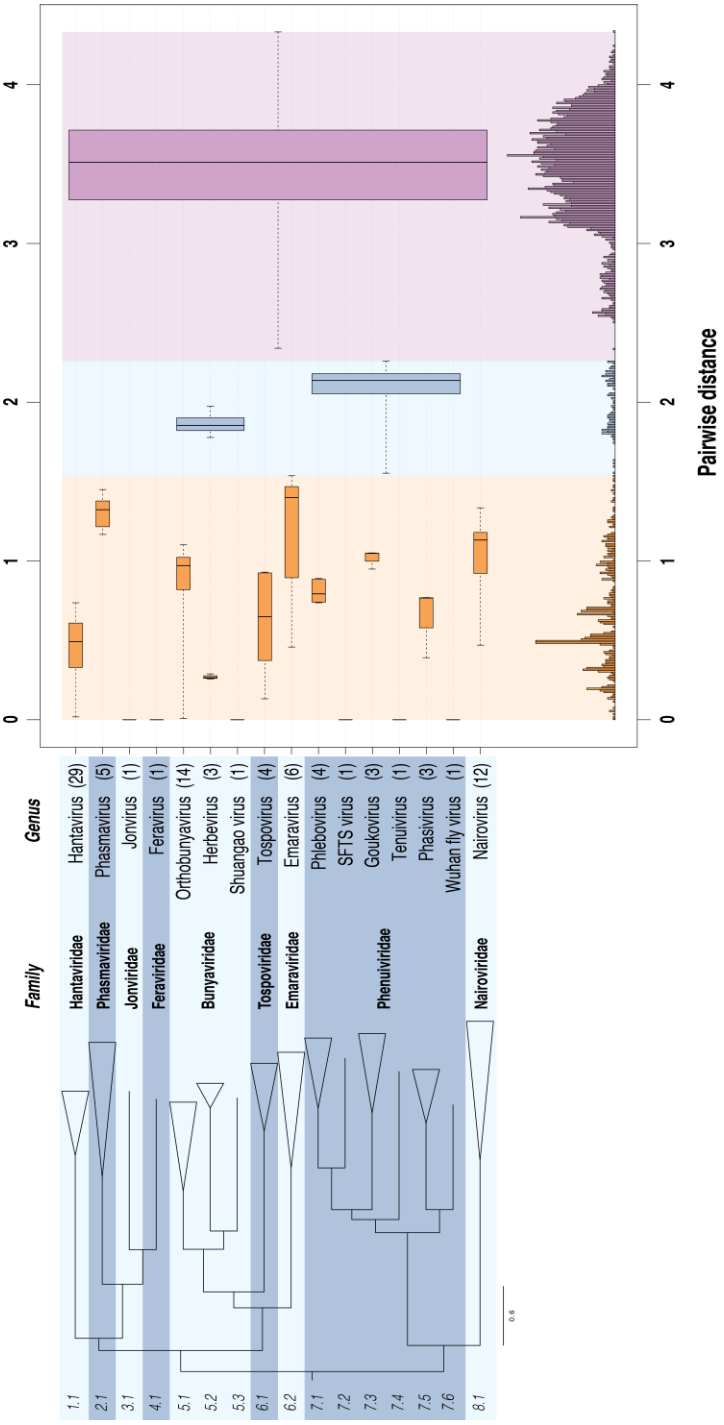


Figure 3: Intra-order genetic divergence in three-level hierarchical clustering of bunyaviruses by DEmARC (version 1.0). Levels are defined by the three strongest PED thresholds. The number of viruses in the identified clusters are shown in brackets. All identified clusters correspond to monophyletic groups in the tree of **Figure 2**. Box-and-whisker graphs were used to plot distributions of distances between viruses from the same genus (orange), and between viruses from different species but the same genus (blue), and between viruses from different genera but the same family (blue). The boxes span from the first to the third quartile and include the median (bold line), and the whiskers (dashed lines) extend to the extreme values. The corresponding part of the PED distribution is shown below. The left panel shows a Bayesian MCMC tree estimated using a Bayesian Markov Chain Monte Carlo method implemented in BEAST/πBUSS, using the WAG amino acid model of amino acid substitutions with 100 million generations. Maximum clade credibility trees were determined using TreeAnnotator with a burn-in of 10% of the sampled trees. The dataset used consists of full length products of

products of coding regions of the S, M, and L segments (nucleocapsid protein, glycoprotein precursor, and RNA-dependent RNA polymerase, respectively), concatenated in one multiple alignment and heuristicely corrected with Trimal v1.2.

Figure 4: Coding strategies and genome segments of prototypic bunyaviruses and emaraviruses (modified from 9th ICTV Report). Arrows represent the virion-complementary sense RNA, from which the proteins shown are translated. Gn and Gc are the two putative glycoproteins cleaved from the precursor molecule. NP is the nucleocapsid protein. Figure not drawn to scale. BUNV, Bunyamwera virus; HTNV, Hantaan virus; DUGV, Dugbe virus; UUKV, Uukuniemi virus.

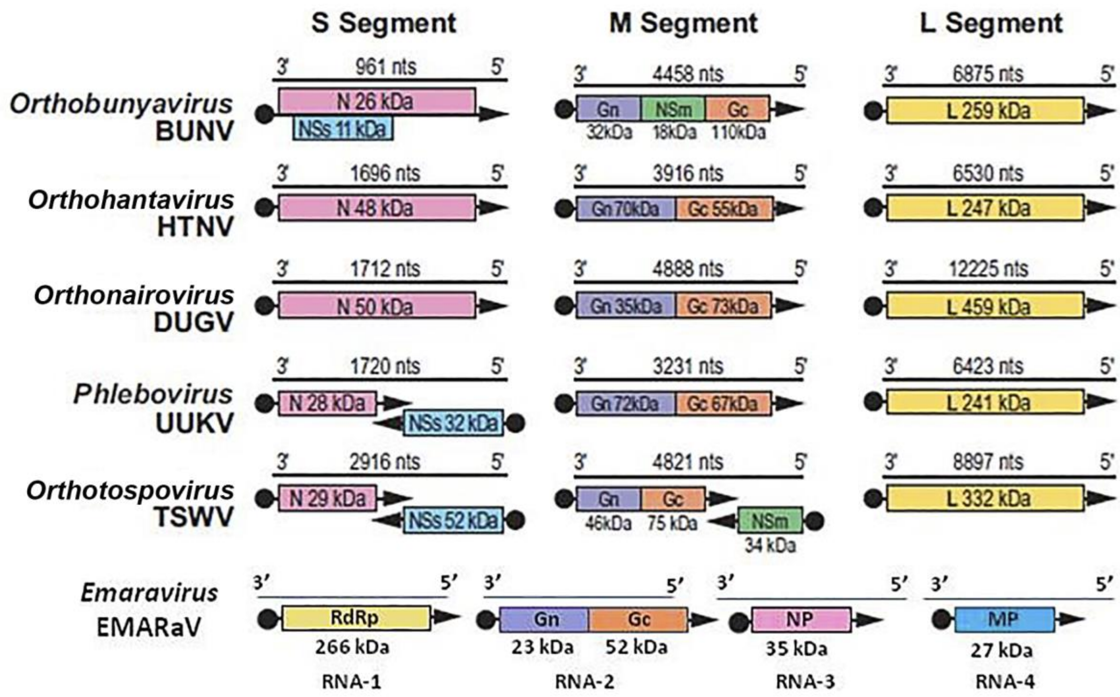
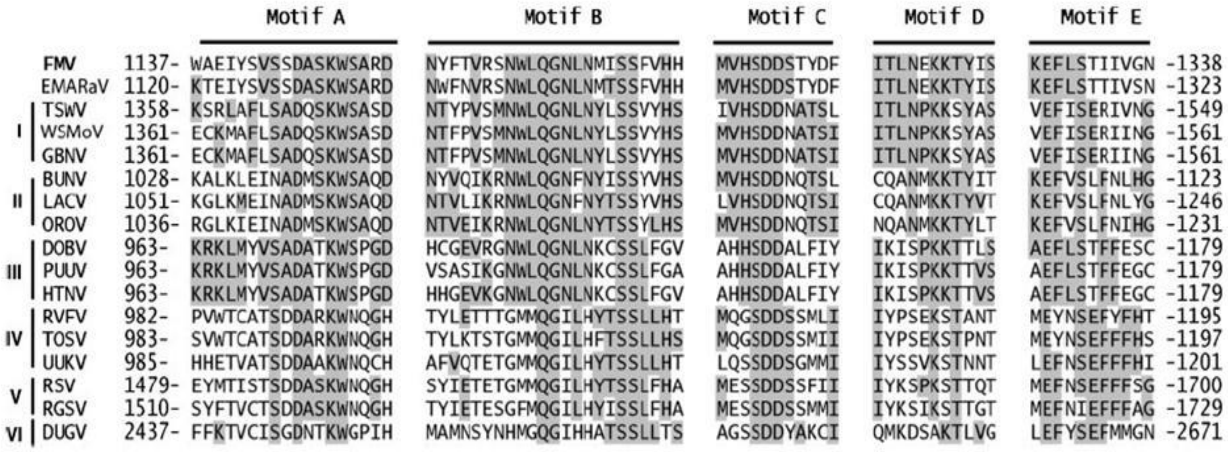


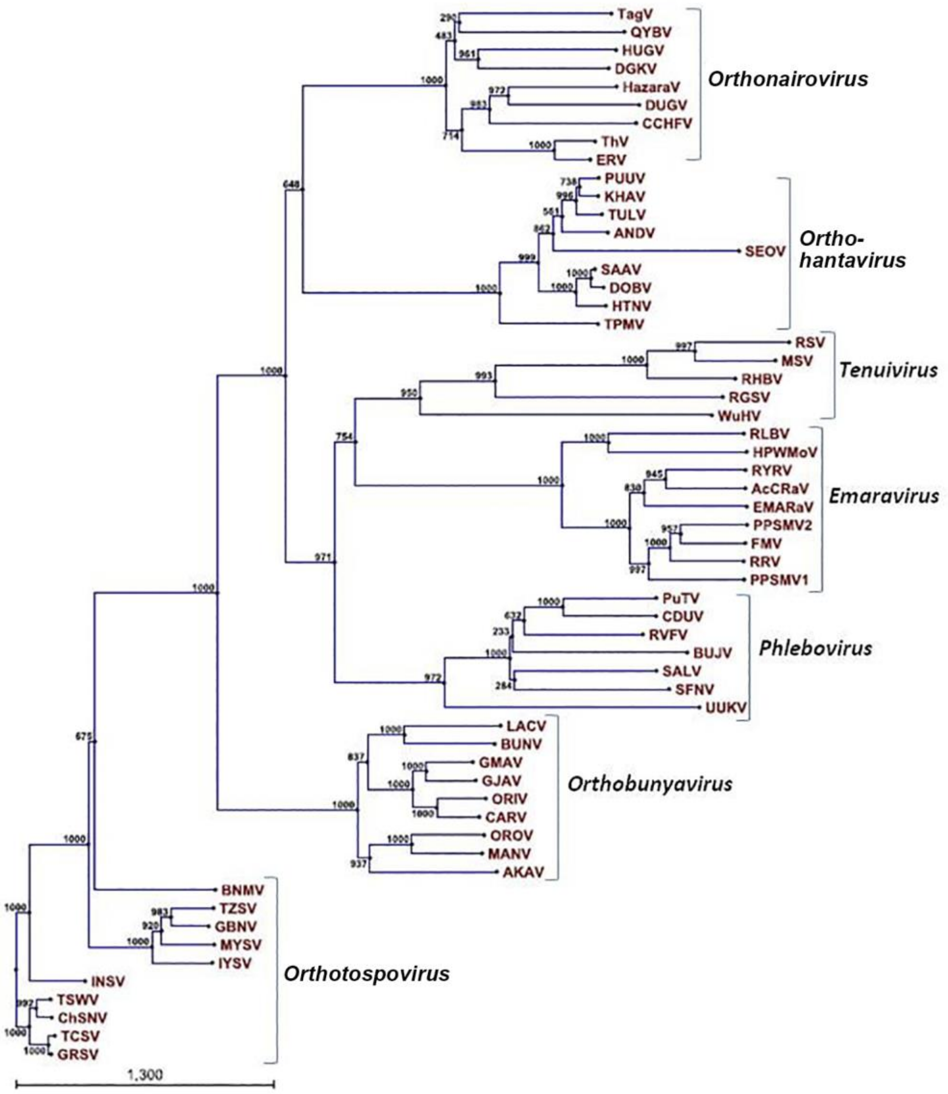
Figure 5: Amino acid alignment between conserved RdRp motifs A–E of bunyaviruses, two members of the unassigned genus *Tenuivirus*, and two recognized members of the genus *Emaravirus*, i.e. FMV (AM941711) and EMARaV (AY653040). I, Genus *(Ortho)tospovirus*: TSWV, tomato spotted wilt virus (GenBank accession no. D10066); WSMoV, watermelon silver mottle virus (NC003832); GBNV, groundnut bud necrosis virus (AF025538). II, Genus *Orthobunyavirus*: LACV, La Crosse virus (GenBank accession no. U12396); BUNV, Bunyamwera virus (X14383); OROV, Oropouche virus (AF484424). III, Current genus (*Ortho*)*hantavirus*: DOBV, Dobrava-Belgrade virus (GenBank accession no. AJ410619); HTNV, Hantaan virus (X55901); PUUV, Puumala virus (Z66548). IV, Genus *Phlebovirus*: RVFV, Rift Valley fever virus (GenBank accession no. X56464); TOSV, Toscana virus (X68414); UUKV, Uukuniemi virus (D10759). V, Genus *Tenuivirus*: RSV, rice stripe virus (GenBank accession no. AY186787); RGSV, rice grassy stunt virus (AF509470). VI, Current genus (*Ortho*)*nairovirus*: DUGV, Dugbe virus (GenBank accession no. U15018).



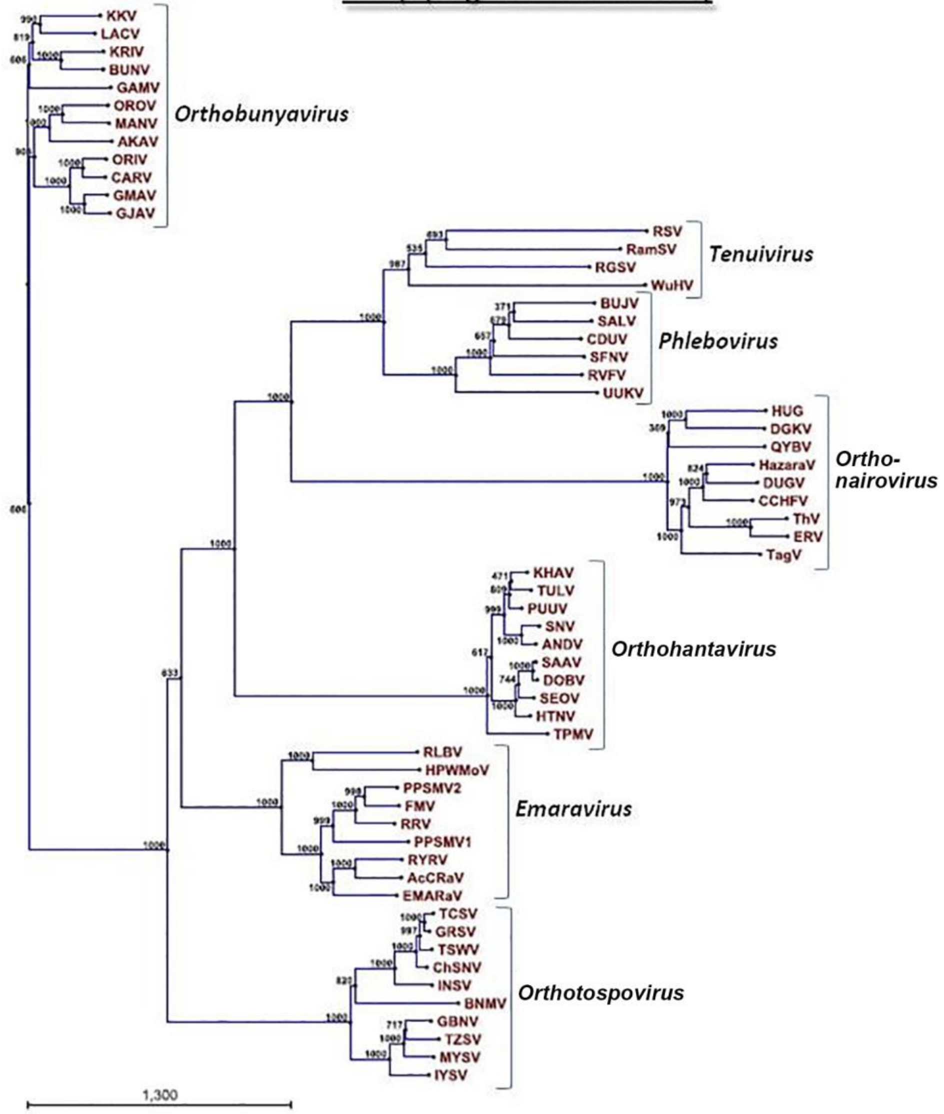
			Motif A	Motif B	Motif C	Motif D	Motif E	
	FMV	1137-	WAEIYSVSSDASKWSARD	NYFTVRSNWLQGNLNMISSFVHH	MVHSDDSTYDF	ITLNEKKTYIS	KEFLSTIIVGN	-1338
	EMARaV	1120-	KTEIYSVSSDASKWSARD	NWFNVRSNWLQGNLNMTSSFVHH	MVHSDDSTYDF	ITLNEKKTYIS	KEFLSTTIVSN	-1323
I	TSWV	1358-	KSRLAFLSADQSKWSASD	NTYPVSMNWLQGNLNYLSSVYHS	IVHSDDNATSL	ITLNPKKSYAS	VEFISERIVNG	-1549
I	WSMoV	1361-	ECKMAFLSADQSKWSASD	NTFPVSMNWLQGNLNYLSSVYHS	MVHSDDNATSI	ITLNPKKSYAS	VEFISERIING	-1561
I	GBNV	1361-	ECKMAFLSADQSKWSASD	NTFPVSMNWLQGNLNYLSSVYHS	MVHSDDNATSI	ITLNPKKSYAS	VEFISERIING	-1561
II	BUNV	1028-	KALKLEINADMSKWSAQD	NYVQIKRNWLQGNFNYISSYVHS	MVHSDDNQTSL	CQANMKKTYIT	KEFVSLFNLHG	-1123
II	LACV	1051-	KGLKMEINADMSKWSAQD	NTVLIKRNWLQGNFNYTSSYVHS	LVHSDDNQTSI	CQANMKKTYVT	KEFVSLFNLYG	-1246
II	OROV	1036-	RGLKIEINADMSKWSAQD	NTVEIKRNWLQGNLNYTSSYLHS	MVHSDDNQTSI	NQANMKKTYLT	KEFVSLFNIHG	-1231
III	DOBV	963-	KRKLMYVSADATKWSPGD	HCGEVRGNWLQGNLNKCSSLFGV	AHHSDDALFIY	IKISPKKTTLS	AEFLSTFFESC	-1179
III	PUUV	963-	KRKLMYVSADATKWSPGD	VSASIKGNWLQGNLNKCSSLFGA	AHHSDDALFIY	IKISPKKTTVS	AEFLSTFFEGC	-1179
III	HTNV	963-	KRKLMYVSADATKWSPGD	HHGEVKGNWLQGNLNKCSSLFGV	AHHSDDALFIY	IKISPKKTTVS	AEFLSTFFEGC	-1179
IV	RVFV	982-	PVWTCATSDDARKWNQGH	TYLETTTGMMQGILHYTSSLLHT	MQGSDDSSMLI	IYPSEKSTANT	MEYNSEFYFHT	-1195
IV	TOSV	983-	SVWTCATSDDARKWNQGH	TYLKTSTGMMQGILHFTSSLLHS	MQGSDDSSMII	IYPSEKSTPNT	MEYNSEFFFHS	-1197
IV	UUKV	985-	HHETVATSDDAAKWNQCH	AFVQTETGMMQGILHYTSSLLHT	LQSSDDSGMMI	IYSSVKSTNNT	LEFNSEFFFHI	-1201
V	RSV	1479-	EYMTISTSDDASKWNQGH	SYIETETGMMQGILHYTSSLFHA	MESSDDSSFII	IYKSPKSTTQT	MEFNSEFFFSG	-1700
V	RGSV	1510-	SYFTVCTSDDASKWNQGH	TYIETESGFMQGILHYISSLFHA	MESSDDSSMMI	IYKSIKSTTGT	MEFNIEFFFAG	-1729
VI	DUGV	2437-	FFKTVCISGDNTKWGPIH	MAMNSYNHMGQGIHHATSSLLTS	AGSSDDYAKCI	QMKDSAKTLVG	LEFYSEFMMGN	-2671

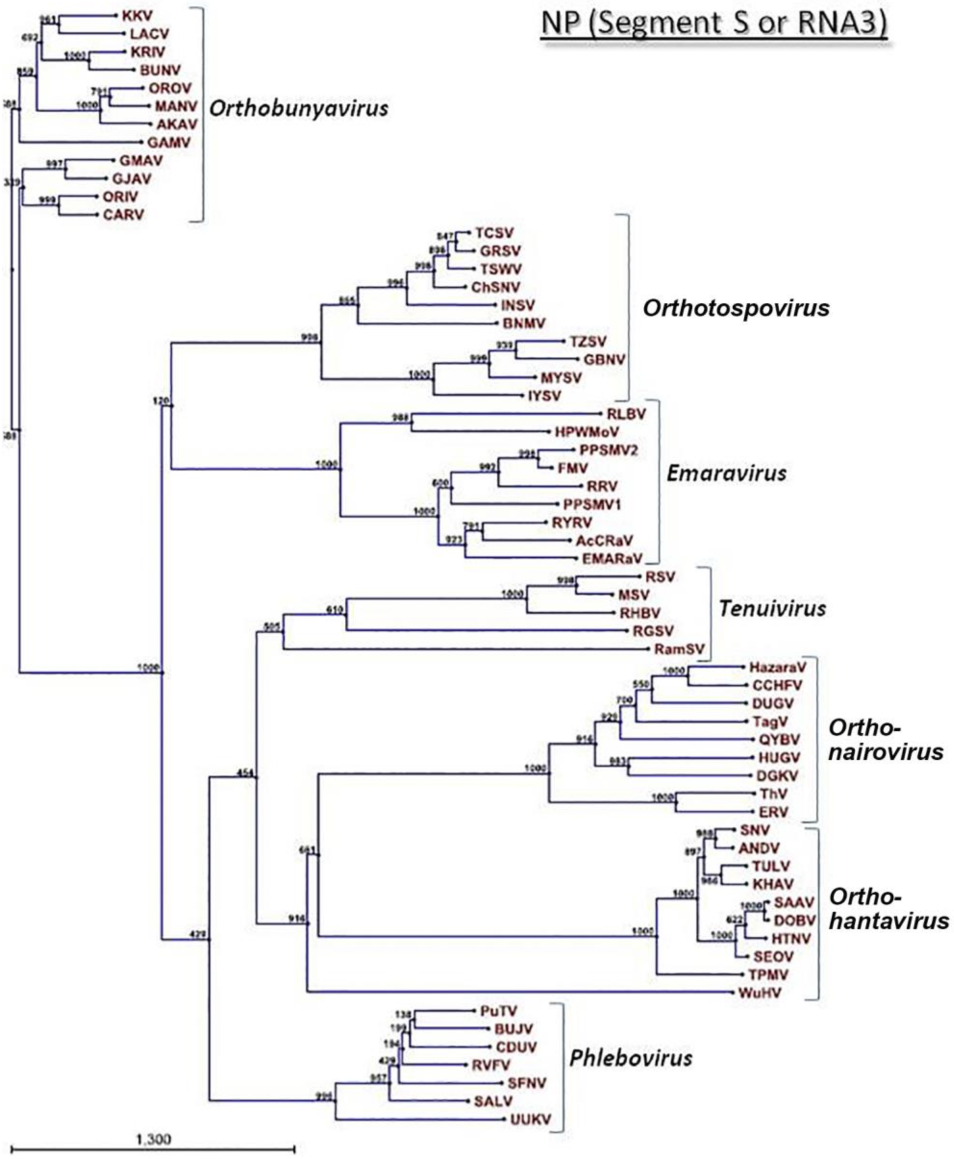
Figure 6. Phylogenetic trees constructed with amino acid sequences of L-, M-, and S-segment-encoded proteins of bunyaviruses and tenuiviruses and proteins encoded by RNA-1 (RdRp), RNA-2 (GP), and RNA-3 (NP) of emaraviruses. Some unassigned bunyaviruses were also included. Predicted amino acid sequences were aligned by MUSCLE using MEGA6, and their relationship was determined using the Neighbor Joining method, with 1,000 bootstrap replicates. For abbreviations of all viruses see 9th ICTV Report.

GP (Segment M or RNA2)



RdRp (Segment L or RNA1)




NP (Segment S or RNA3)
KKV
LACV
KRIV
BUNV
OROV
MANV
AKAV
GAMV
GMAV
GJAV
ORIV
CARV
Orthobunyavirus
TCSV
GRSV
TSWV
ChSNV
INSV
BNMV
TZSV
GBNV
MYSV
IYSV
Orthotospovirus
RLBV
HPWMoV
PPSMV2
FMV
RRV
PPSMV1
RYRV
AcCRaV
EMARaV
Emaravirus
RSV
MSV
RHBV
RGSV
RamSV
Tenuivirus
HazaraV
CCHFV
DUGV
TagV
QYBV
HUGV
DGKV
ThV
ERV
Ortho-nairovirus
SNV
ANDV
TULV
KHAV
SAAV
DOBV
HTNV
SEOV
TPMV
WuHV
Ortho-hantavirus
PuTV
BUJV
CDUV
RVFV
SFNV
SALV
UUKV
Phlebovirus
1,300

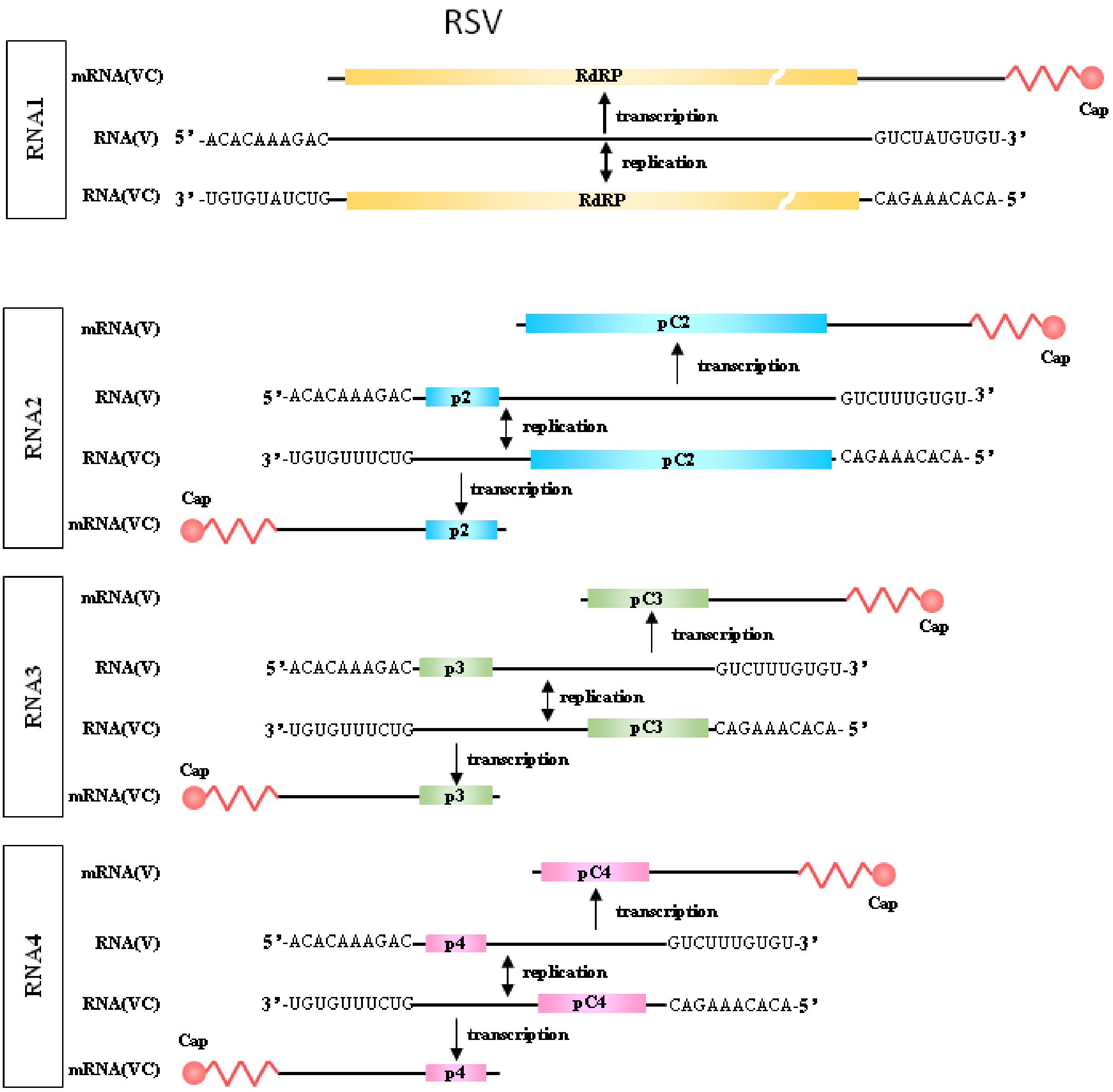
]

Figure 7. The conserved nucleotide stretches present at the 5′ and 3′ termini of the RNAs of emaraviruses and members of different bunyaviral.

Genus	5′ terminus (5′ to 3′)	3′ terminus (5′ to 3′)
Emaravirus	**AGU AGU GUU CUC C---**	**--- G GAG UUC ACU ACU**
Orthobunyavirus	**AGU AGU GU**g **CU--------**	**---------AG U**a**C ACU ACU**
Hantavirus (proposed *Orthohantavirus*)	**AGU AGU** a**U**g **CU-------**	**---------AG U**cu **ACU ACU**
Tospovirus (proposed *Orthotospovirus*)	**AG**a gca a**U---------------**	**-----------------**au ugc u**CU**

Figure 8

A comparison of the genomic organization and gene expression strategy of the tenuivirus rice stripe virus (RSV) and the phlebovirus Rift Valley fever virus (RVFV). The genome of RSV is composed of four (RNA 1–RNA 4) and that of RVFV is composed of three (L, M, S) single stranded RNAs. RSV RNA 1 and RVFV L and M RNAs each contain a single ORF in the virus genome-complementary sense RNA (vcRNA). RSV RNAs 2–4 and RVFV S RNA encode proteins in ambisense orientation, each containing two non-overlapping ORFs: one in the 5′ half of the vRNA and the other in the 5′ half of the vcRNA, respectively. Viral vRNAs and vcRNAs serve as templates for both transcription and replication. Whereas replication gives rise to a full-length copy of the vRNA or vcRNA, transcription involves a non-viral snatched capped leader RNA about 10–20 nt in length (shown in red) as a primer and terminates at specific sites that contain transcription termination signals. The conserved 5' (5'-ACACAAAG) and 3' (CUUUGUGU-3') termini in the genomic RNA segments are shown.


RSV

RNA1
mRNA(VC)
RdRP
Cap
transcription
RNA(V)
5' -ACACAAAGAC
GUCUAUGUGU-3'
replication
RNA(VC)
3' -UGUGUAUCUG
RdRP
CAGAAACACA-5'
RNA2
mRNA(V)
pC2
Cap
transcription
RNA(V)
5'-ACACAAAGAC
p2
GUCUUUGUGU-3'
replication
RNA(VC)
3'-UGUGUUUCUG
pC2
CAGAAACACA-5'
transcription
Cap
mRNA(VC)
p2
RNA3
mRNA(V)
pC3
Cap
transcription
RNA(V)
5'-ACACAAAGAC
p3
GUCUUUGUGU-3'
replication
RNA(VC)
3'-UGUGUUUCUG
pC3
CAGAAACACA-5'
transcription
Cap
mRNA(VC)
p3
RNA4
mRNA(V)
pC4
Cap
transcription
RNA(V)
5'-ACACAAAGAC
p4
GUCUUUGUGU-3'
replication
RNA(VC)
3'-UGUGUUUCUG
pC4
CAGAAACACA-5'
transcription
Cap
mRNA(VC)
p4

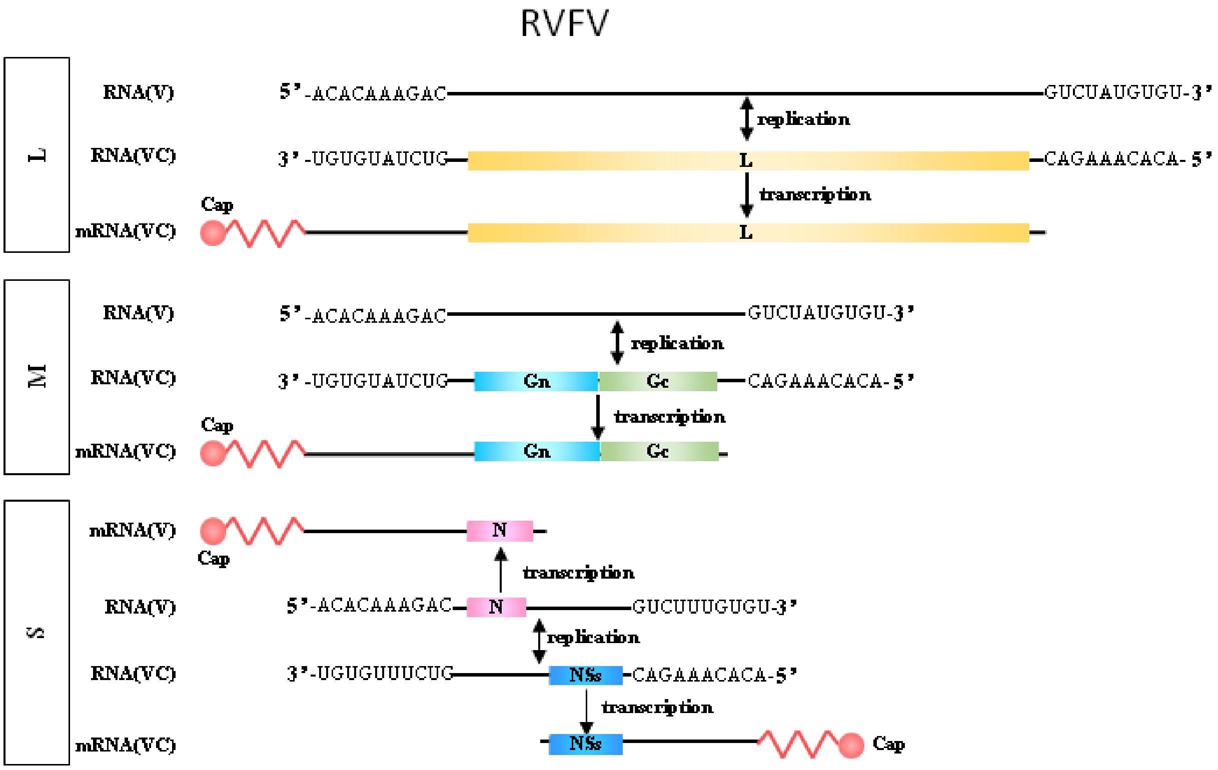

RVFV
L
RNA(V)
5'-ACACAAAGAC
GUCUAUGUGU-3'
replication
RNA(VC)
3'-UGUGUAUCUG
L
CAGAAACACA-5'
transcription
Cap
mRNA(VC)
L
M
RNA(V)
5'-ACACAAAGAC
GUCUAUGUGU-3'
replication
RNA(VC)
3'-UGUGUAUCUG
Gn
Gc
CAGAAACACA-5'
transcription
Cap
mRNA(VC)
Gn
Gc
S
mRNA(V)
N
Cap
transcription
RNA(V)
5'-ACACAAAGAC
N
GUCUUUGUGU-3'
replication
RNA(VC)
3'-UGUGUUUCUG
NSs
CAGAAACACA-5'
transcription
mRNA(VC)
NSs
Cap

Figure 9

Phylogenetic relationships between tenuiviruses and selected bunyaviruses. A Neighbor-Joining tree was constructed using MEGA7 based on a multiple amino acid sequence alignment of the RdRp core domain (Bunya RdRp super family; cl20265). The optimal tree with the sum of branch length = 3.47043919 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1,000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the p-distance method and are depicted in the units of the number of amino acid differences per site. The analysis involved 12 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 407 positions in the final dataset.

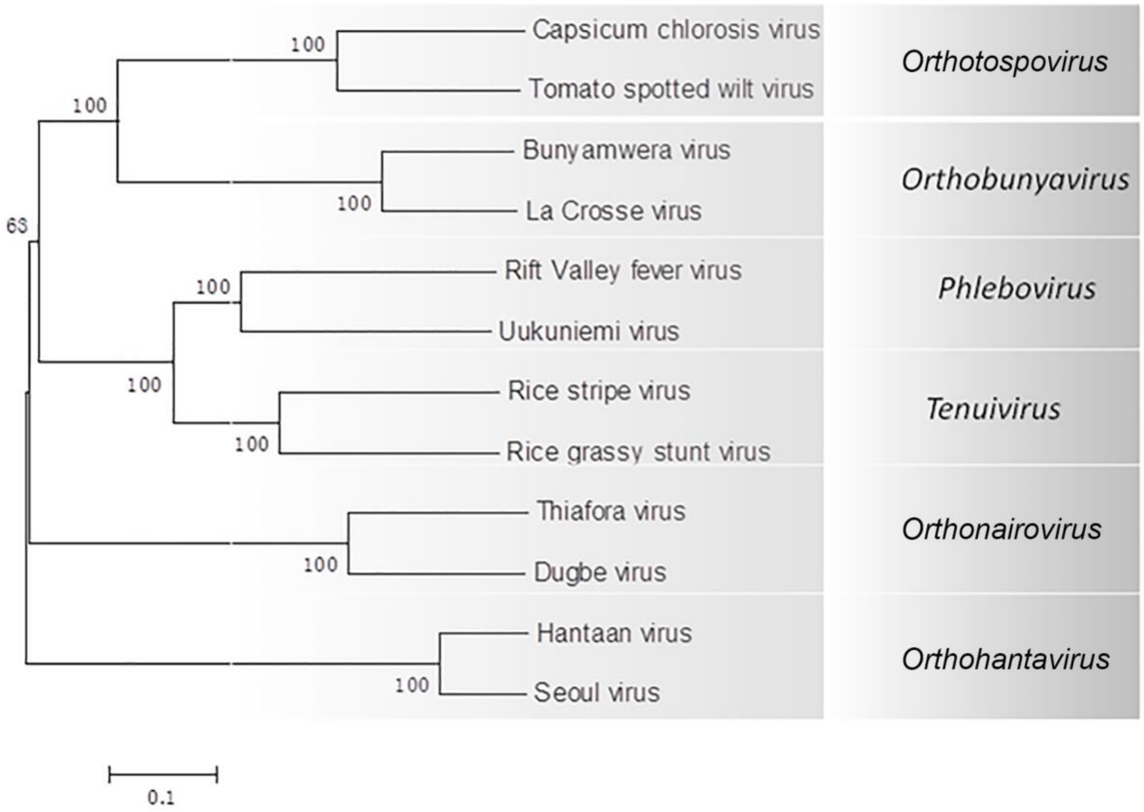


Table 1: A concatenated dataset consisting of full length coding regions of the S, M, and L segments (nucleocapsid protein, glycoprotein precursor, and RNA-dependent RNA polymerase, respectively) was used for DEmARC analysis. The dataset was aligned with MAFFT v7.123. Sequences used with their respective NCBI GenBank accession numbers can be found below.

Virus	Accession Numbers
(Ortho)hantaviruses	
Andes virus	NC003466, NC003467, NC003468
Amur virus	JX473004, JX473003, JX473002
Anjozorobe virus	KC490916 KC490921 KC490923
Bayou virus	GQ200820, GQ244521, GQ244526
Bowé virus	KC631782, KC631783, KC631784
Caño Delgadito virus	DQ285566, DQ284451, GQ200821
Cao Bang virus	EF543524, EF543526, EF543525
Choclo virus	DQ285046, DQ285047, EF397003
Dobrava-Belgrade virus	GU904031, GU904037, GU904044
Luxi virus	HM756286, HM756287, HQ404253
Hantaan virus	KT935057, KT935023, KT934989
Hokkaido virus	AB675463, AB676848, AB712372
Imjin virus	KJ420559, KJ420541, KJ420567
Jeju virus	HQ834695, HQ834696, HQ834697
Kenkeme virus	KJ857341, KJ857337, KJ857320
Khabarovsk virus	KJ857345, KJ857329, KJ857312
Laibin virus	KM102247, KM102248, KM102249
Montano virus	AB620100, AB620101, AB620102
Nova virus	KT004445, KT004446, KT004447
Puumala virus	KJ994776, KJ994777, KJ994778
Rio Mamoré virus	FJ532244 FJ608550 FJ809772
Rockport virus	HM015223, HM015219, HM015221
Sangassou virus	JQ082300, JQ082301, JQ082302
Seoul virus	KP645198, KP645197, KP645196
Sin Nombre virus	L37904, L37903, L37902
Soochong virus	AY675349, AY675353, DQ056292
Thottapalayam virus	NC010704, NC010708, NC010707
Tula virus	NC005227, NC005228, NC005226
Emaraviruses	
European mountain ash ringspot-associated virus virus	DQ831831, AY563041, AY563040
Fig mosaic virus	NC029563, NC029565, NC029562
High plains wheat mosaic virus	NC029550, NC029549, NC029570
Pigeonpea sterility mosaic virus	NC029574, NC029556, NC029575
Raspberry leaf blotch virus	NC029559, NC029558, NC029567
Rose rosette virus	NC015300, NC015299, NC015298
Orthoferaviruses	
Ferak virus	KP710267, KP710264, KP710246
Orthojonviruses	
Jonchet virus	KP710243, KP710240, KP710232
Goukoviruses	
Gouléako virus	HQ541736, HQ541737, HQ541738
Cumuto virus	KF543246, KF543245, KF543244
Yíchāng insect virus	KM817763, KM817730, KM817703
Herbeviruses	
Herbert virus	KF590584, KF590585, KF590586
Taï virus	KF590572, KF590573, KF590574
Kibale virus	KF590575, KF590576, KF590577
Shuangao insect virus 1	KM817742, KM817716, KM817681
(Ortho)nairoviruses	
Hazare virus	KP406725, KP406724, KP406723
Keterah virus	KR537449, KR537448, KR537447
Nairobi sheep disease virus	KM464724, KM464725, KM464726
Crimean-Congo hemorrhagic fever virus	JN572088, JN572083, JN572090
Dera Ghazi Khan virus	KU925454, KU925453, KU925452
Dugbe virus	NC004157, NC004158, NC004159
Hughes virus	KU925472, KU925471, KU925470

Qualyub virus	KU925478, KU925477, KU925476
Tillamook virus	KU925496, KU925495, KU925494
Thiafora virus	KR537452, KR537451, KR537450
Phasiviruses	
Phasi chareon virus	KR003785, KR003784, KR003786
Badu virus	KT693189, KT693188, KT693187
Wutai Mosquito virus	KM817761, KM817728, KM817700
Orthophasmaviruses	
Kigluaik phantom virus	KJ434184, KJ434183, KJ434182
Nome Phantom virus	KJ434187, KJ434186, KJ434185
Wuhan mosquito virus 2	KM817759, KM817727, KM817698
Wuchang cockroach virus 1	KM817748, KM817721, KM817688
Tenuiviruses	
Rice stripe virus	NC003753, NC003754, NC003755
(Ortho)tospoviruses	
Groundnut ringspot virus	KT972594, KT972592, KT972590
Impatiens necrotic spot virus	NC003624, DQ425095, NC003625
Tomato spotted wilt virus	JF960235, JF960236, JF960237
Watermelon silver mottle virus	JX177645, JX177646, JX177647
Phleboviruses	
Rift Valley fever virus	KX096943, KX096942, KX096941
Munguba/Bujaru virus	HM566166, HM566165, HM566164
Candiru virus	NC015375, NC015373, NC015374
Sandfly fever Sicilian virus	KM042104, KM042103, KM042102
SFTS virus	KC292273, KC292300, KC292327
Orthobunyaviruses	
Akabane virus	KR260714, KR260715, KR260716
Alajuela virus	KM272188, KM272187, KM272186
Leanyer virus	HM627177, HM627176, HM627178
Trivittatus virus	KR149247, KR149248, KR149249
Abbey Lake virus	KJ710424, KJ710423, KJ710425
Čalovo virus	KC608157, KC608156, KC608155
La Crosse virus	GU591164, GU591165, GU591166
Gamboa virus	KT950262, KT950270, KT950266
Brazoran virus	NC022037, NC022038, NC022039
Oropouche virus	KP691608, KP691607, KP691606
Oya virus	JX983192, JX983193, JX983194
Tete virus	KP792679, KP792680, KP792681
Keystone virus	KT630293, KT630289, KT630291

The multiple alignments used in this taxonomy proposal can be downloaded at:

http://www.regatools.be/bunyaalignment1.fasta for the uncorrected alignment;
http://www.regatools.be/bunyaalignment2.fasta for the heuristical corrected alignment by Trimal v1.2; and
http://www.regatools.be/bunyaalignment3.fasta for the alignment block-trimmed to 5% gaps (Trimal v1.2).

Table 2. Taxonomic summary of the proposed order *Bunyavirales* (taxa only).

Order	Family	Genus	Species
Bunyavirales (NEW, TP 2016.030M)	*Feraviridae* (NEW, TP 2016.030M)	*Orthoferavirus* (NEW, TP 2016.021M)	*Ferak orthoferavirus* (NEW, TP 2016.021M)
	Fimoviridae (NEW, TP 2016.030M)	*Emaravirus* (MOVED from unassigned, TP 2016.030M)	*Actinidia chlorotic ringspot-associated emaravirus* (NEW, TP 2016.016P)
			European mountain ash ringspot-associated emaravirus (RENAMED *European mountain ash ringspot-associated virus*, TP 2016.020M)
			Fig mosaic emaravirus (RENAMED *Fig mosaic virus*, TP 2016.020M)
			High Plains wheat mosaic emaravirus (RENAMED *High Plains wheat mosaic virus*, TP 2016.020M)
			Pigeonpea sterility mosaic emaravirus 1 (RENAMED *Pigeonpea sterility mosaic virus*, TP 2016.020M)
			Pigeonpea sterility mosaic emaravirus 2 (NEW, TP 2016.017P)
			Raspberry leaf blotch emaravirus (RENAMED *Raspberry leaf blotch virus*, TP 2016.020M)
			Redbud yellow ringspot-associated emaravirus (NEW, TP 2016.018P)
			Rose rosette emaravirus (RENAMED *Rose rosette virus*, TP 2016.020M)
	Hantaviridae (NEW, TP 2016.030M)	*Orthohantavirus* (RENAMED *Hantavirus*, TP 2016.023M)	*Amga orthohantavirus* (NEW, TP 2016.023M)
			Andes orthohantavirus (RENAMED *Andes hantavirus*, TP 2016.023M)
			Asama orthohantavirus (NEW, TP 2016.023M)
			Asikkala orthohantavirus (NEW, TP 2016.023M)
			Bayou orthohantavirus (RENAMED *Bayou hantavirus*, TP 2016.023M)

			Black Creek Canal orthohantavirus (RENAMED *Black Creek Canal hantavirus*, TP 2016.023M)
			Bowe orthohantavirus (NEW, TP 2016.023M)
			Bruges orthohantavirus (NEW, TP 2016.023M)
			Cano Delgadito orthohantavirus (RENAMED Caño Delgadito *hantavirus*, TP 2016.023M)
			Cao Bang orthohantavirus (NEW, TP 2016.023M)
			Choclo orthohantavirus (NEW, TP 2016.023M)
			Dabieshan orthohantavirus (NEW, TP 2016.023M)
			Dobrava-Belgrade orthohantavirus (RENAMED *Dobrava-Belgrade hantavirus*, TP 2016.023M)
			El Moro Canyon orthohantavirus (RENAMED *El Moro hantavirus*, TP 2016.023M)
			Fugong orthohantavirus (NEW, TP 2016.023M)
			Fusong orthohantavirus (NEW, TP 2016.023M)
			Hantaan orthohantavirus (RENAMED *Hantaan hantavirus*, TP 2016.023M)
			Imjin orthohantavirus (NEW, TP 2016.023M)
			Jeju orthohantavirus (NEW, TP 2016.023M)
			Kenkeme orthohantavirus (NEW, TP 2016.023M)
			Khabarovsk orthohantavirus (RENAMED *Khabarovsk hantavirus*, TP 2016.023M)
			Laguna Negra orthohantavirus (RENAMED *Laguna Negra hantavirus*, TP 2016.023M)
			Laibin orthohantavirus (NEW, TP 2016.023M)
			Longquan orthohantavirus (NEW, TP 2016.023M

			Luxi orthohantavirus (NEW, TP 2016.023M)
			Maporal orthohantavirus (NEW, TP 2016.023M)
			Montano orthohantavirus (NEW, TP 2016.023M)
			Necocli orthohantavirus (NEW, TP 2016.023M)
			Nova orthohantavirus (NEW, TP 2016.023M)
			Oxbow orthohantavirus (NEW, TP 2016.023M)
			Prospect Hill orthohantavirus (RENAMED *Prospect Hill hantavirus*, TP 2016.023M)
			Puumala orthohantavirus (RENAMED *Puumala hantavirus*, TP 2016.023M)
			Quezon orthohantavirus (NEW, TP 2016.023M)
			Rockport orthohantavirus (NEW, TP 2016.023M)
			Sangassou orthohantavirus (RENAMED *Sangassou hantavirus*, TP 2016.023M)
			Seoul orthohantavirus (RENAMED *Seoul hantavirus*, TP 2016.023M)
			Sin Nombre orthohantavirus (RENAMED *Sin Nombre hantavirus*, TP 2016.023M)
			Thailand orthohantavirus (RENAMED *Thailand hantavirus*, TP 2016.023M)
			Thottapalayam orthohantavirus (RENAMED *Thottapalayam hantavirus*, TP 2016.023M)
			Tula orthohantavirus (RENAMED *Tula hantavirus*, TP 2016.023M)
			Yakeshi orthohantavirus (NEW, TP 2016.023)
			(DELETED: *Isla Vista hantavirus, Muleshoe hantavirus, New York hantavirus, Rio Mamore hantavirus, Rio Segundo hantavirus Saaremaa hantavirus, Topografov hantavirus*, TP 2016.023M)
	Jonviridae (NEW, TP 2016.030M)	*Orthojonvirus* (NEW, TP 2016.025M)	*Jonchet orthojonvirus* (NEW, TP 2016.025M)

	Nairoviridae (NEW, TP 2016.030M)	*Orthonairovirus* (RENAMED *Nairovirus*, TP 2016.026M)	*Burana orthonairovirus* (NEW, TP 2016.026M)
			Crimean-Congo hemorrhagic fever orthonairovirus (RENAMED *Crimean-Congo hemorrhagic fever nairovirus*, TP 2016.026M)
			Dera Ghazi Khan orthonairovirus (RENAMED *Dera Ghazi Khan nairovirus*, TP 2016.026M)
			Dugbe orthonairovirus (RENAMED *Dugbe nairovirus*, TP 2016.026M)
			Hazara orthonairovirus (NEW, TP 2016.026M)
			Hughes orthonairovirus (RENAMED *Hughes nairovirus*, TP 2016.026M)
			Keterah orthonairovirus (NEW, TP 2016.026M)
			Kasokero orthonairovirus (NEW, TP 2016.026M)
			Nairobi sheep disease virus orthonairovirus (NEW, TP 2016.026M)
			Qalyub orthonairovirus (RENAMED *Qalyub nairovirus*, TP 2016.026M)
			Sakhalin orthonairovirus (RENAMED *Sakhalin nairovirus*, TP 2016.026M)
			Thiafora orthonairovirus (RENAMED *Thiafora nairovirus*, TP 2016.026M)
	Peribunyaviridae (RENAMED *Bunyaviridae*, TP 2016.030M)	*Herbevirus* (NEW, TP 2016.024M)	*Herbert herbevirus* (NEW, TP 2016.024M)
			Kibale herbevirus (NEW, TP 2016.024M)
			Shuangao insect herbevirus 1 (NEW, TP 2016.024M)
			Tai herbevirus (NEW, TP 2016.024M)
		Orthobunyavirus	*Acara orthobunyavirus*
			Akabane orthobunyavirus

			Alajuela orthobunyavirus
			Anopheles A orthobunyavirus
			Anopheles B orthobunyavirus
			Bakau orthobunyavirus
			Batama orthobunyavirus
			Benevides orthobunyavirus
			Bertioga orthobunyavirus
			Bimiti orthobunyavirus
			Botambi orthobunyavirus
			Bunyamwera orthobunyavirus
			Bushbush orthobunyavirus
			Bwamba orthobunyavirus
			California encephalitis orthobunyavirus
			Capim orthobunyavirus
			Caraparu orthobunyavirus
			Catu orthobunyavirus
			Estero Real orthobunyavirus
			Gamboa orthobunyavirus
			Guajara orthobunyavirus
			Guama orthobunyavirus
			Guaroa orthobunyavirus
			Kaeng Khoi orthobunyavirus
			Kairi orthobunyavirus
			Koongol orthobunyavirus

			Madrid orthobunyavirus
			Main Drain orthobunyavirus
			Manzanilla orthobunyavirus
			Minatitlan orthobunyavirus
			Marituba orthobunyavirus
			MPoko orthobunyavirus
			Nyando orthobunyavirus
			Olifantsvlei orthobunyavirus
			Oriboca orthobunyavirus
			Oropouche orthobunyavirus
			Patois orthobunyavirus
			Sathuperi orthobunyavirus
			Shamonda orthobunyavirus
			Shuni orthobunyavirus
			Simbu orthobunyavirus
			Tacaiuma orthobunyavirus
			Tete orthobunyavirus
			Thimiri orthobunyavirus
			Timboteua orthobunyavirus
			Turlock orthobunyavirus
			Wyeomyia orthobunyavirus
			Zegla orthobunyavirus
	Phasmaviridae (NEW, TP 2016.030M)	*Orthophasmavirus* (NEW, TP 2016.028M)	*Kigluaik phantom orthophasmavirus* (NEW, TP 2016.028M)
			Nome phantom orthophasmavirus

			(NEW, TP 2016.028M)
			Shuangao insect orthophasmavirus 2 (NEW, TP 2016.028M)
			Wuchang cockroach orthophasmavirus 1 (NEW, TP 2016.028M)
			Wuhan mosquito orthophasmavirus 1 (NEW, TP 2016.028M)
			Wuhan mosquito orthophasmavirus 2 (NEW, TP 2016.028M)
	Phenuiviridae (NEW, TP 2016.030M)	*Goukovirus* (NEW, TP 2016.022M)	*Cumuto goukovirus* (NEW, TP 2016.022M)
			Gouleako goukovirus (NEW, TP 2016.022M)
			Yichang insect goukovirus (NEW, TP 2016.022M)
		Phasivirus (NEW, TP 2016.027M)	*Badu phasivirus* (NEW, TP 2016.027M)
			Phasi Charoen-like phasivirus (NEW, TP 2016.027M)
			Wuhan fly phasivirus (NEW, TP 2016.027M)
			Wutai mosquito phasivirus (NEW, TP 2016.027M)
		Phlebovirus	*Bujaru phlebovirus*
			Candiru phlebovirus
			Chilibre phlebovirus
			Frijoles phlebovirus
			Punta Toro phlebovirus
			Rift Valley fever phlebovirus
			Salehabad phlebovirus
			Sandfly fever Naples phlebovirus
			SFTS phlebovirus

			Uukuniemi phlebovirus
		Tenuivirus (MOVED from unassigned, TP 2016.030M)	*Echinochloa hoja blanca tenuivirus* (RENAMED *Echinochloa hoja blanca virus*, TP 2016.029M)
			Iranian wheat stripe tenuivirus (RENAMED *Iranian wheat stripe virus*, TP 2016.029M)
			Maize stripe tenuivirus (RENAMED *Maize stripe virus*, TP 2016.029M)
			Rice grassy stunt tenuivirus (RENAMED *Rice grassy stunt virus*, TP 2016.029M)
			Rice hoja blanca tenuivirus (RENAMED *Rice hoja blanca virus*, TP 2016.029M)
			Rice stripe tenuivirus (RENAMED *Rice stripe virus*, TP 2016.029M)
			Urochloa hoja blanca tenuivirus (RENAMED *Urochloa hoja blanca virus*, TP 2016.029M)
	Tospoviridae (NEW, TP 2016.030M)	*Orthotospovirus* (RENAMED *tospovirus*, TP 2016.030M)	*Groundnut bud necrosis orthotospovirus* (RENAMED *Groundnut bud necrosis tospovirus*, TP 2016.030M)
			Groundnut ringspot orthotospovirus (RENAMED *Groundnut ringspot tospovirus*, TP 2016.030M)
			Groundnut yellow spot orthotospovirus (RENAMED *Groundnut yellow spot tospovirus*, TP 2016.030M)
			Impatiens necrotic spot orthotospovirus (RENAMED *Impatiens necrotic spot tospovirus*, TP 2016.030M)
			Iris yellow spot orthotospovirus (RENAMED *Iris yellow spot tospovirus*, TP 2016.030M)
			Polygonum ringspot orthotospovirus (RENAMED *Polygonum ringspot tospovirus*, TP 2016.030M)
			Tomato chlorotic spot orthotospovirus (RENAMED *Tomato chlorotic spot tospovirus*, TP 2016.030M)
			Tomato spotted wilt orthotospovirus (RENAMED *Tomato spotted wilt tospovirus*, TP 2016.030M)
			Watermelon bud necrosis orthotospovirus (RENAMED *Watermelon bud necrosis tospovirus*, TP 2016.030M)
			Watermelon silver mottle orthotospovirus (RENAMED *Watermelon silver mottle tospovirus*, TP 2016.030M)
			Zucchini lethal chlorosis orthotospovirus (RENAMED *Zucchini lethal chlorosis tospovirus*, TP 2016.030M)