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Proposals on virus taxonomy using the examples from the families of *Phenuiviridae*, *Nairoviridae*, and *Peribunyavidae*

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Abstract

In recent years, the taxonomy of the families of *Phenuiviridae*, *Nairoviridae*, and *Peribunyavidae* in *Bunyavirales* was updated frequently, because many novel viruses in these families have been identified and the species demarcation criteria of these families have been changed. As per these criteria and sequence analysis, we found that the taxonomy of 19 species in these families should be revised. We presented six proposals for optimizing virus species taxonomy using the examples from these families. First, the species demarcation criteria for the same family (e.g., *Peribunyavidae*) should be unified. Second, the methods and parameters for the taxonomic calculation in the same order (e.g., *Bunyavirales*) should be unified. Third, virus species taxonomy should be based on phylogenetic relationships, rather than a cutoff value of sequence identities that is a self-contradictory demarcation criterion, although sequence identities aid virus taxonomy greatly. Fourth, virus species taxonomy should be based on the phylogenetic relationship of a key viral gene (e.g., the RdRp gene of *Bunyavirales*), which is important for the taxonomy of virus recombinants or reassortants. Fifth, a virus can be demarcated without a species before its biomedical significance has been revealed. Sixth, names of all viruses and virus species should be constituted exclusively with common characters (English letters and Arab numbers), to minimize difficulty in spelling and communication. These proposals are rational, flexible, and can accommodate all known viruses. They can also bridge the taxonomy history and the future demands due to their flexibility.

Keywords

Bunyavirales; *Nairoviridae*, *Peribunyaviridae*, *Phenuiviridae;* taxonomy; nomenclature; species demarcation

1. Introduction

The family *Bunyaviridae* was upgraded by the International Committee on Taxonomy of Viruses (ICTV) as the order *Bunyavirales* in 2017.[1] Many species in *Bunyavirales*, such as *Hantaan orthohantavirus*, *Lassa mammarenavirus*, *Rift Valley fever phlebovirus*, and *Rice stripe tenuivirus* contain important pathogenic viruses of humans, domestic animals, or crops.[2-4] They have great significance in public health, veterinary medicine, food production, and biodiversity conservation.

Currently, *Bunyavirales* accommodates 12 families: *Arenaviridae*, *Cruliviridae*, *Fimoviridae*, *Hantaviridae*, *Leishbuviridae*, *Mypoviridae*, *Nairoviridae*, *Peribunyaviridae*, *Phasmaviridae*, *Phenuiviridae*, *Tospoviridae*, and *Wepedeviridae*.[5]

In recent years, the taxonomy of the genera and species in the families of *Phenuiviridae*, *Nairoviridae*, and *Peribunyavidae* in *Bunyavirales* was updated frequently, because many novel viruses in these families have been identified and the species demarcation criteria of these families have been changed. [6-11] As per these criteria and sequence analysis, we found that the taxonomy of 19 species in these families should be revised.

We found some problems about the species taxonomy of viruses through this work. We presented the relevant proposals for optimizing virus species taxonomy using the examples from the above three families.

2. Materials and methods

2.1 Abbreviations

To simplify relevant expressions, the Razdan virus strain LEIV-Arm2741 corresponding to the GenBank accession number NC022630 in the species *Razdan bandavirus* was abbreviated as Razdan virus (NC022630), Razdan virus (NC022630, *Razdan bandavirus*), or *Razdan bandavirus* (NC022630), as appropriate. Other viruses in this report were abbreviated in the same way. “As per **Table N** and **Figure M**” in this report meant “as per their sequence identities in the amino acid sequences of the viral RdRp protein shown in **Table N** and phylogenetic relationships shown in **Figure M**”.

2.2 Taxonomy information

The current taxonomy information of the viruses in *Nairoviridae* listed in **Section 3.1–3.2** was from an ICTV report;[6] the current taxonomy information of the viruses in *Peribunyaviridae* listed in **Section 3.3–3.17** was from another ICTV report;[7] and the current taxonomy information of the viruses in *Phenuiviridae* listed in **Section 3.18–3.19** was from the menu of “Taxonomy” in the ICTV website.[8] The species demarcation criteria of some genera and families currently employed by ICTV were from the ICTV reports or proposals, and they were summarized in **Table 1.**

2.3 Sequence alignment and sequence identity calculation

Sequences were downloaded from GenBank and aligned with the software tools Clustal W using the default settings, as the same as the ICTV report for the family *Peribunyaviridae*.[7] Sequence identities were calculated using the software tool Mega (version X) and the aligned sequences.[9]

2.4 Phylogenetic relationship calculation

Phylogenetic relationships were calculated using the software tool Mega (version X) using the neighbor-joining method and the Jones-Taylor-Thornton model, as the same as the ICTV report for the family *Peribunyaviridae*.[7] Bootstrap values were calculated with 1000 replicates.

Table 1. Species demarcation criteria in some genera or families of *Bunyavirales*.

Taxa	**Species demarcation criterion**
Nairoviridae	Viruses with <93% identity in the amino acid sequence of the RdRp protein represent a species.[11]
Pacuvirus, *Peribunyaviridae*	Viruses with <90% identity 0.1 when using the WAG substitution model on concatenated amino acid sequences of all three segments represent a species.[7]
Herbevirus, *Peribunyaviridae*	Viruses with < 90% identity in the amino acid sequence for the approximately 1 kb sequence fragment containing the core polymerase domain (premotif A to motif E) of the third conserved region of the RdRp protein represent a species.[7]
Orthobunyavirus, *Peribunyaviridae*	Viruses with <96% identity in the complete amino acid sequence of the RdRp protein represent a species; the species *Acara orthobunyavirus, Anopheles B orthobunyavirus, Bakau orthobunyavirus*, *Batama orthobunyavirus*, *Bertioga orthobunyavirus*, *Minatitlan orthobunyavirus*, *M'Poko orthobunyavirus*, *Olifantsvlei orthobunyavirus*, *Turlock orthobunyavirus* were established according to previous demarcation criteria.[7]
Phenuiviridae	For *Entovirus, Lentinuvirus, Rubodvirus, Ixovirus, Coguvirus, Bandavirus, and Uukuvirus* in *Phenuiviridae,* viruses with <95% identity in the amino acid sequence of the RdRp represent a species.[12]

3. Results

3.1 *Hughes orthonairovirus* in *Nairoviridae.*

Hughes orthonairovirus contains multiple strains, including Caspiy virus (KP792708), Great Saltee virus (KU925467), Raza virus (KU925479), and Hughes virus (KU925470). These strains should be classified into two species, as per **Table 1** and **Figure 1.** These two species were tentatively marked as *Hughes orthonairovirus* A and B in **Table 1**: one contains Caspiy virus (KP792708) and Great Saltee virus (KU925467); the other contains Raza virus (KU925479), and Hughes virus (KU925470). The identities in the amino acid sequences of the RdRp protein between these two species were 67.4–67.8% (**Table 2**), much lower than the species demarcation criterion (93%) of *Nairoviridae* (**Table 1**).

3.2 *Abu Hammd orthonairovirus* and *Tunis orthonairovirus* in *Nairoviridae*.

Abū Ḥammād virus (KU925434, *Abū Ḥammād orthonairovirus*) and Tunis virus (NC040770, *Tunis orthonairovirus*) should be classified into the same species, as per **Table 1** and **Figure 1.** The identities in the amino acid sequences of the RdRp protein between these viruses were 93.2% (**Table 2**), higher than the species demarcation criterion (93%) of *Nairoviridae* (**Table1**).

3.3 *Alajuela orthobunyavirus* and *Gamboa orthobunyavirus* in *Peribunyaviridae.*

Alajuela virus (KM272186, *Alajuela_orthobunyavirus*) should be classified into *Gamboa orthobunyavirus* with *Gamboa orthobunyavirus* (KM272174) and *Gamboa orthobunyavirus* (KX900438), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 99.8% (**Table 3**), higher than the species demarcation criterion (96%) of *Peribunyaviridae* (**Table1**).

If strictly according to the species demarcation criterion, *Gamboa orthobunyavirus* (KX900438) and *Gamboa orthobunyavirus* (KM272183) should be classified into two species. The identities in the amino acid sequences of the RdRp protein between these viruses were 93.1–95.5% (**Table 3**), lower than the species demarcation criterion (96%) of *Peribunyaviridae* (**Table1**).

3.4 *Bunyamwera orthobunyavirus* in *Peribunyaviridae.*

Bunyamwera orthobunyavirus contains multiple strains, including Northway virus (MH484312), Santa Rosa virus (MH484324), Lokern virus (MG828823), Shokwe virus (MH484330), Ngari virus (KC608152), and Bunyamwera virus (X14383). These strains should be classified into four species, as per **Table 3** and **Figure 2**, tentatively marked as *Bunyamwera orthobunyavirus* A–D in **Table 3**. *Bunyamwera orthobunyavirus* A contains Northway virus (MH484312); *Bunyamwera orthobunyavirus* B contains Lokern virus (MG828823) and Santa Rosa virus(MH484324); *Bunyamwera orthobunyavirus* C contains Shokwe virus (MH484330); *Bunyamwera orthobunyavirus* D contains Ngari virus (KC608152) and Bunyamwera virus (X14383); The identities in the amino acid sequences of RdRp protein between four species were 82.0–91.2% (**Table 3**), much lower than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table 1**).

3.5 *Bunyamwera orthobunyavirus* and *Main Drain orthobunyavirus* in *Peribunyaviridae.*

Main Drain orthobunyavirus (MH484306) should be classified into the species corresponding to *Bunyamwera orthobunyavirus* (MH484324) and *Bunyamwera orthobunyavirus* (MG828823), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 98.8–99.1% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.6 *Tete orthobunyavirus* and *Matruh orthobunyavirus* in *Peribunyaviridae***.**

Bahig virus (KP792654, *Tete orthobunyavirus*) and Matruh virus (KP792693, *Matruh orthobunyavirus*) should be classified into the same species, as per **Table 3** and **Figure 2.** The identities in the amino acid sequences of the RdRp protein between these viruses were 99.1% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.7 *Aino orthobunyavirus* and *Shuni orthobunyavirus* in *Peribunyaviridae*

Aino virus (HE795087, *Aino orthobunyavirus*) should be classified into *Shuni orthobunyavirus* with Kaikalur virus (MH484297, *Shuni orthonairovirus*), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 98.6% (**Table 3**), higher than the species demarcation criterion (96%) of *Peribunyaviridae (***Table1**).

If strictly according to the species demarcation criterion, *Shuni orthonairovirus (*KF153118) should be classified into a novel species distinct from the species covering Aino virus (HE795087) and *Shuni orthonairovirus (*MH484297). The identities in the amino acid sequences of the RdRp protein between these viruses were 93.1-95.5% (**Table 3**), lower than the species demarcation criterion (96%) of *Peribunyaviridae (***Table1**).

3.8 *Bakau orthobunyavirus* in *Peribunyaviridae*

Bakau orthobunyavirus contains multiple strains, including Nola virus (MK896512), Telok Forest virus (MK896453), Bakau virus (MK896635), and Ketapang virus (MK896548). These strains should be classified into four species, as per **Table 3** and **Figure 2**. These four species were tentatively marked as *Bakau orthobunyavirus* A–D in **Table 3**. *Bakau* *orthobunyavirus* A contains Nola virus (MK896512); *Bakau orthobunyavirus* B contains Telok Forest virus (MK896453); *Bakau orthobunyavirus* C contains Bakau virus (MK896635); *Bakau orthobunyavirus* D contains Ketapang virus (MK896548); The identities in the amino acid sequences of RdRp protein between four species were 76.9– 92.4% (**Table 3**), much lower than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table 1**).

3.9 *Maguari orthobunyavirus* and *Cache Valley orthobunyavirus* in *Peribunyaviridae*

Playas virus (KX100123, *Maguari orthobunyavirus*) should be classified into the species corresponding to Cache Valley virus (KX100135, *Cache Valley orthobunyavirus*) and Tlacotalpan virus (KX100120, *Cache Valley orthobunyavirus*), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 99.2–99.8% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.10 *Patois orthobunyavirus* and *Abras orthobunyavirus* in *Peribunyaviridae.*

Babahoya virus (MH017276, *Patois orthobunyavirus*) should be classified into *Abras orthobunyavirus* with Abras virus (MH017275, *Abras orthobunyavirus*), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 99.2% (**Table 3**), higher than the species demarcation criterion (96%) of *Peribunyaviridae (***Table1**).

If strictly according to the species demarcation criterion, Babahoya virus (MH017276, *Patois orthobunyavirus*) and Patois virus (MH017277, *Patois orthobunyavirus*) should be classified into two species. The identities in the amino acid sequences of the RdRp protein between these viruses were 85.0% (**Table 3**), lower than the species demarcation criterion (96%) of *Peribunyaviridae (***Table1**).

3.11 *Oriboca orthobunyavirus* and *Marituba orthobunyavirus* in *Peribunyaviridae***.**

Oriboca virus (KF254773, *Oriboca orthobunyavirus*) should be classified into the species corresponding to Murutucú virus (MG029284, *Marituba orthobunyavirus*) and Restan virus (KM280932, *Marituba orthobunyavirus*), as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were

97.2–99.6% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.12 *Bushbush orthobunyavirus* in *Peribunyaviridae*.

Bushbush orthobunyavirus contains multiple strains, including Bushbush virus (MK896599), Benfica virus (MK896617) and Juan Díaz virus (MK896554). These strains should be classified into three species, as per **Table 3** and **Figure 2**. These three species were tentatively marked as *Bushbush orthobunyavirus* A–C in **Table 3**. *Bushbush orthobunyavirus* A contains Bushbush virus (MK896599); *Bushbush orthobunyavirus* B contains Benfica virus (MK896617); *Bushbush orthobunyavirus* C contains Juan Díaz virus (MK896554). The identities in the amino acid sequences of RdRp protein between three species were 76.1– 92.1% (**Table 3**), much lower than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table 1**).

3.13 *Acara orthobunyavirus* and *Bushbush orthobunyavirus* in *Peribunyaviridae*.

Moriche Virus (MK896521, *Acara orthobunyavirus*) and Bushbush virus (MK896599, *Bushbush orthobunyavirus*) should be classified into the same species, as per **Table 3** and **Figure 2.** The identities in the amino acid sequences of the RdRp protein between these viruses were 98.2% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.14 *Acara orthobunyavirus* and *Benevides orthobunyavirus* in *Peribunyaviridae*.

Acará virus (MK896653, *Acara orthobunyavirus*) and Benevides virus (MK896620, *Benevides orthobunyavirus*) should be classified into the same species, as per **Table 3** and **Figure 2.** The identities in the amino acid sequences of the RdRp protein between these viruses were 99.5% (**Table 3**), higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.15 *Marituba orthobunyavirus* in *Peribunyaviridae*.

Marituba orthobunyavirus contains multiple strains, including Murutucú virus (MG029284), Restan virus (KM280932), Marituba virus (KF254770), Gumbo Limbo virus (KM280930) and Nepuyo virus (MG029287). These strains should be classified into four species, as per **Table 3** and **Figure 2**. These four species were tentatively marked as *Marituba* *orthobunyavirus* A–D in **Table 3**. *Marituba orthobunyavirus* A contains Murutucú virus (MG029284) and Restan virus (KM280932); *Marituba orthobunyavirus* B contains Marituba virus (KF254770); *Marituba orthobunyavirus* C contains Gumbo Limbo virus (KM280930); *Marituba orthobunyavirus* D contains Nepuyo virus (MG029287). The identities in the amino acid sequences of RdRp protein between four species were 78.4– 91.3% (**Table 3**), much lower than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table 1**).

3.16 *Bimiti orthobunyavirus* and *Guama orthobunyaviru* in *Peribunyaviridae*.

The two species corresponding to bimiti virus (KP792657, *Bimiti orthobunyavirus*) and Guamá virus (KP792666, *Guama orthobunyaviru*) should be classified into the same species, as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of the RdRp protein between these viruses were 98.0% (**Table 3**), which is higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table1**).

3.17 *Catu orthobunyavirus* and *Moju orthobunyavirus* in *Peribunyaviridae*.

The two species corresponding to Catu virus (KP792660, *Catu orthobunyavirus*) and Moju virus (KP792675, *Moju orthobunyavirus*) should be classified into the same species, as per **Table 3** and **Figure 2**. The identities in the amino acid sequences of RdRp protein between four species were 96.2% (**Table 3**), which are much higher than the species demarcation criterion (96%) of *Perbunyaviridae* (**Table 1**).

3.18 *Razdan bandavirus* and *Bhanja bandavirus* in *Phenuiviridae*.

*Razdan bandavirus (*NC022630) should be classified into *Bhanja bandavirus,* as per the sequence identity (97.9%) between *Razdan bandavirus (*NC022630) and *Bhanja bandavirus* (X961622), which was higher than the species demarcation criterion (95%) of *Bandavirus* **(Table 1).** Moreover, the phylogenetic relationships of this family also demonstrated that *Razdan bandavirus (*NC022630) was in the same branch with viruses in *Bhanja bandavirus* (X961622) (**Figure 3**).

3.19 *Frijoles phlebovirus* in *Phenuiviridae.*

*Frijoles phlebovirus (*MK330765) and *Frijoles phlebovirus (*KX611391) should be classified into two species, as per their identity in the viral RdRp gene amino acid sequence (77.0%) which was higher than the species demarcation criterion (95%) of *Phlebovirus*

(**Table 1**). Moreover, the phylogenetic relationships of this family also demonstrated that *Frijoles phlebovirus* (KX611391) was closer to the species *Mona Grita phlebovirus* than to *Frijoles phlebovirus* (MK330765) (**Figure 3**).

3. Discussion

The taxonomic errors shown in **Sections 3.1–3.19** also existed in the taxonomy report of *Negarnaviricota*.[5] Besides these errors, there were some writing errors in the ICTV report on *Nairoviridae*. For instance, Taggert virus (KU925491) was incorrectly assigned to *Sakhalin orthonairovirus*, Bandia virus (KU925446) incorrectly to *Qalyub orthonairovirus*, Zirqa virus (KU925500) incorrectly to *Hughes orthonairovirus*, and Sapphire II virus (KU925485) incorrectly to *Dera Ghazi Khan orthonairovirus***.**[6] Additionally, *Toscana phlebovirus* (NC006319) and *Leticia phlebovirus* (HM566167) were incorrectly assigned to the species of *Naples phlebovirus* in the GenBank (**Figure 3**), possibly by the relevant sequence submitters.

All the above suggestions on species taxonomy revision were based on sequence alignment using Clustal X and phylogenetic relationships calculated using the neighbor-joining method and the Jones-Taylor-Thornton model. We found that these suggestions keep valid if the relevant sequences were aligned with the software tools Clustal W, Muscle, or MAFFT, or the relevant phylogenetic relationships were calculated with the maximum likelihood or the minimum evolution method, or the amino acid substitution were set in the Poisson or Dayhoff model.

Table 1 demonstrated that the species demarcation criteria for viruses in *Bunyavirales* were miscellaneous and distinct among families and genera. Moreover, for the genus *Orthobunyavirus* in *Peribunyaviridae*, the new species demarcation criterion and the old species demarcation criterion were employed together. Additionally, the methods and parameters for the current calculation of sequence identities and phylogenetic relationships were different for different families in *Bunyavirales*,[6,7] which adds difficulty in the taxonomy of new viruses in *Bunyavirales*.

The current demarcation of many viruses in *Bunyavirales* is based on sequence identities. This strategy is rigescent with limited flexibility. For instance, if the demarcation criterion is <96.0% sequence identify, two strains with 95.9% should be classified into two species, and two strains with 96.1% should be classified into the same species, which is usually not rational. Moreover, this demarcation strategy is self-contradictory. For instance, if the demarcation criterion is <96.0% sequence identify, the identity between virus A and virus B is 96.2%, the identity between virus B and virus C is 96.5%, and the identity between virus A and virus C is 94.3%, then as per the demarcation criterion, it is self-contradictory to classify these three viruses into one or two species.

The current names of some viruses and species in *Bunyavirales* contain non-English letters (e.g., Abū Ḥammād virus, Shāyáng spider virus 1). This adds much difficulty with limited benefits for correctly writing these names.

With the above considerations, we presented six proposals for virus taxonomy. First, the species demarcation criteria for the same family (e.g., *Peribunyaviridae*) should be unified. Second, the methods and parameters for the Taxonomic calculation (i.e., calculation of sequence identities or phylogenetic relationships) in the same order (e.g., *Bunyavirales*) should be unified. Third, virus species taxonomy should be based on the phylogenetic relationship, rather than a rigescent cutoff value of sequence identities that is a self-contradictory criterion, although sequence identities have aided virus taxonomy greatly and can continue to aid virus taxonomy in a flexible way. Fourth, virus species taxonomy should be based on the phylogenetic relationship of a key viral gene (e.g., *Citrus cogusvirus* was classified into *Phenuiviridae* based on its RdRp gene sequence, although this species clustered with the genus *Ophiovirus* in *Aspiviridae*, as per its M genomic segment sequence).[10] This is important for the taxonomy of virus recombinants or reassortants. Fifth, a virus can be demarcated without a species before its biomedical significance has been revealed, and those viruses can be demarcated with a genus. This rule can reduce greatly the difficulty in virus taxonomy. Sixth, names of all viruses and species should be constituted exclusively with common characters (English letters and Arab numbers), to minimize difficulty in spelling and communication. These proposals are rational, flexible, and can accommodate all known viruses. They can also bridge the taxonomy history and the future demands due to their flexibility.

Table 2. Identities between two certain nairoviruses in their RdRp gene amino acid sequences.

The first nairovirus	**The second nairovirus**	**Identity**
Caspiy virus (KP792708, *Hughes orthobunyaviru* A)	Great Saltee virus (KU925467, *Hughes orthobunyavirus* A)	94.6%
Caspiy virus (KP792708, *Hughes orthobunyaviru* A)	Raza virus (KU925479, *Hughes orthobunyavirus* B)	67.4%
Caspiy virus (KP792708, *Hughes orthobunyaviru* A)	Hughes virus (KU925470, *Hughes orthobunyavirus* B)	67.5%
Great Saltee virus (KU925467, *Hughes orthobunyaviru* A)	Raza virus (KU925479, *Hughes orthobunyavirus* B)	67.8%
Great Saltee virus (KU925467, *Hughes orthobunyaviru* A)	Hughes virus (KU925470, *Hughes orthobunyavirus* B)	68.1%
Raza virus (KU925479, *Hughes orthobunyaviru* B)	Hughes virus (KU925470, *Hughes orthobunyavirus* B)	95.3%
Abu Hammad virus (KU925434, *Abu Hammd orthonairovirus*)	Tunis virus (NC040770, *Tunis orthonairovirus*)	93.2%

Table 3. Identities between two certain peribunyaviruses in their RdRp gene amino acid sequences.

The first peribunyavirus	**The second peribunyavirus**	**Identity**
Alajuela virus (KM272186, *Alajuela_orthobunyavirus*)	Gamboa virus (KM272174, *Gamboa orthobunyavirus*)	99.8%
Alajuela virus (KM272186, *Alajuela_orthobunyavirus*)	Pueblo Viejo virus (KX900438, *Gamboa orthobunyavirus*)	95.5%
Alajuela virus (KM272186, *Alajuela_orthobunyavirus*)	Calchaqu ívirus (KM272183, *Gamboa orthobunyavirus*)	93.6%
Pueblo Viejo virus (KX900438, *Gamboa orthobunyavirus*)	Calchaqu ívirus (KM272183, *Gamboa orthobunyavirus*)	93.1%
Pueblo Viejo virus (KX900438, *Gamboa orthobunyavirus*)	Gamboa virus (KM272174, *Gamboa orthobunyavirus*)	95.5%
Northway virus (MH484312, *Bunyamwera orthobunyavirus* A)	Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	87.0%
Northway virus (MH484312, *Bunyamwera orthobunyavirus* A)	Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	87.0%

Northway virus (MH484312, *Bunyamwera orthobunyavirus* A)	Shokwe virus (MH484330, *Bunyamwera orthobunyavirus* C)	82.0%
Northway virus (MH484312, *Bunyamwera orthobunyavirus* A)	Ngari virus (KC608152, *Bunyamwera orthobunyavirus* D)	82.2%
Northway virus (MH484312, *Bunyamwera orthobunyavirus* A)	Bunyamwera virus (X14383, *Bunyamwera orthobunyavirus* D)	82.1%
Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	98.7%
Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	Shokwe virus (MH484330, *Bunyamwera orthobunyavirus* C)	81.2%
Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	Ngari virus (KC608152, *Bunyamwera orthobunyavirus* D)	81.2%
Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	Bunyamwera virus (X14383, *Bunyamwera orthobunyavirus* D)	81.3%
Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	Shokwe virus (MH484330, *Bunyamwera orthobunyavirus* C)	81.1%
Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	Ngari virus (KC608152, *Bunyamwera orthobunyavirus* D)	81.1%
Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	Bunyamwera virus (X14383, *Bunyamwera orthobunyavirus* D)	81.2%
Shokwe virus (MH484330, *Bunyamwera orthobunyavirus* C)	Ngari virus (KC608152, *Bunyamwera orthobunyavirus* D)	91.0%
Shokwe virus (MH484330, *Bunyamwera orthobunyavirus* C)	Bunyamwera virus (X14383, *Bunyamwera orthobunyavirus* D)	91.2%
Ngari virus (KC608152, *Bunyamwera orthobunyavirus* D)	Bunyamwera virus (X14383, *Bunyamwera orthobunyavirus* D)	99.4%
Main Drain virus (MH484306, *Main Drain orthobunyavirus*)	Santa Rosa virus (MH484324, *Bunyamwera orthobunyavirus* B)	98.8%
Main Drain virus (MH484306, *Main Drain orthobunyavirus*)	Lokern virus (MG828823, *Bunyamwera orthobunyavirus* B)	99.1%
Bahig virus (KP792654, *Tete orthobunyavirus*)	Matruh virus (KP792693, *Matruh orthobunyavirus*)	99.1%
Aino virus (HE795087, *Aino orthobunyavirus*)	Kaikalur virus (MH484297, *Shuni orthonairovirus*)	98.6%
Aino virus (HE795087, *Aino orthobunyavirus*)	Shuni virus (KF153118, *Shuni orthonairovirus*)	95.2%
Kaikalur virus (MH484297, *Shuni orthonairovirus*)	Shuni virus (KF153118, *Shuni orthonairovirus*)	95.5%

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Nola virus (MK896512, *Bakau_orthobunyavirus* A)	Telok Forest virus (MK896453, Bakau_orthobunyavirus B)	78.8%
Nola virus (MK896512, *Bakau_orthobunyavirus* A)	Bakau virus (MK896635, Bakau_orthobunyavirus C)	76.9%
Nola virus (MK896512, *Bakau_orthobunyavirus* A)	Ketapang virus (MK896548, Bakau_orthobunyavirus D)	77.1%
Telok Forest virus (MK896453, Bakau_orthobunyavirus B)	Bakau virus (MK896635, Bakau_orthobunyavirus C)	78.1%
Telok Forest virus (MK896453, Bakau_orthobunyavirus B)	Ketapang virus (MK896548, Bakau_orthobunyavirus D)	78.1%
Bakau virus (MK896635, Bakau_orthobunyavirus C)	Ketapang virus (MK896548, Bakau_orthobunyavirus D)	92.4%
Playas virus (KX100123, *Maguari orthobunyavirus*)	Cache Valley virus (KX100135, *Cache Valley orthobunyavirus*)	99.8%
Playas virus (KX100123, *Maguari orthobunyavirus*)	Tlacotalpan virus (KX100120, *Cache Valley orthobunyavirus*)	99.2%
Cache Valley virus (KX100135, *Cache Valley orthobunyavirus*)	Tlacotalpan virus (KX100120, *Cache Valley orthobunyavirus*)	99.2%
Patois virus (MH017277, *Patois orthobunyavirus*)	Babahoya virus (MH017276, *Patois orthobunyavirus*)	85.0%
Abras virus (MH017275, *Abras orthobunyavirus*)	Babahoya virus (MH017276, *Patois orthobunyavirus*)	99.2%
Oriboca virus (KF254773, *Oriboca orthobunyavirus*)	Murutucú virus (MG029284, *Marituba orthobunyavirus*)	99.6%
Oriboca virus (KF254773, *Oriboca orthobunyavirus*)	Restan virus (KM280932, *Marituba orthobunyavirus*)	97.2%
Bushbush virus (MK896599, *Bushbush orthobunyavirus* A)	Benfica virus (MK896617, *Bushbush orthobunyavirus* B)	76.6%
Bushbush virus (MK896599, *Bushbush orthobunyavirus* A)	Juan Díaz virus (MK896554, *Bushbush orthobunyavirus* C)	92.1%
Benfica virus (MK896617, *Bushbush orthobunyavirus* B)	Juan Díaz virus (MK896554, *Bushbush orthobunyavirus* C)	76.1%
Moriche virus (MK896521, *Acara orthobunyavirus*)	Bushbush virus (MK896599, *Bushbush orthobunyavirus*)	98.2%
Acará virus (MK896653, *Acara orthobunyavirus*)	Benevides virus (MK896620, *Benevides orthobunyavirus*)	99.5%
Murutucú virus (MG029284, *Marituba orthobunyavirus* A)	Restan virus (KM280932, *Marituba orthobunyavirus* A)	97.2%

Murutucú virus (MG029284, *Marituba orthobunyavirus* A)	Marituba virus (KF254770, *Marituba orthobunyavirus* B)	91.2%
Murutucú virus (MG029284, *Marituba orthobunyavirus* A)	Gumbo Limbo virus (KM280930, *Marituba orthobunyavirus* C)	78.4%
Murutucú virus (MG029284, *Marituba orthobunyavirus* A)	Nepuyo virus (MG029287, *Marituba orthobunyavirus* D)	79.2%
Restan virus (KM280932, *Marituba orthobunyavirus* A)	Marituba virus (KF254770, *Marituba orthobunyavirus* B)	91.3%
Restan virus (KM280932, *Marituba orthobunyavirus* A)	Gumbo Limbo virus (KM280930, *Marituba orthobunyavirus* C)	78.4%
Restan virus (KM280932, *Marituba orthobunyavirus* A)	Nepuyo virus (MG029287, *Marituba orthobunyavirus* D)	79.2%
Marituba virus (KF254770, *Marituba orthobunyavirus* B)	Gumbo Limbo virus (KM280930, *Marituba orthobunyavirus* C)	78.9%
Marituba virus (KF254770, *Marituba orthobunyavirus* B)	Nepuyo virus (MG029287, *Marituba orthobunyavirus* D)	79.6%
Gumbo Limbo virus (KM280930, *Marituba orthobunyavirus* C)	Nepuyo virus (MG029287, *Marituba orthobunyavirus* D)	89.2%
bimiti virus (KP792657, *Bimiti orthobunyavirus*)	Guamá virus (KP792666, *Guama orthobunyaviru*)	98.0%
Catu orthobunyavirus (KP792660)	*Moju orthobunyavirus* (KP792675)	96.2%

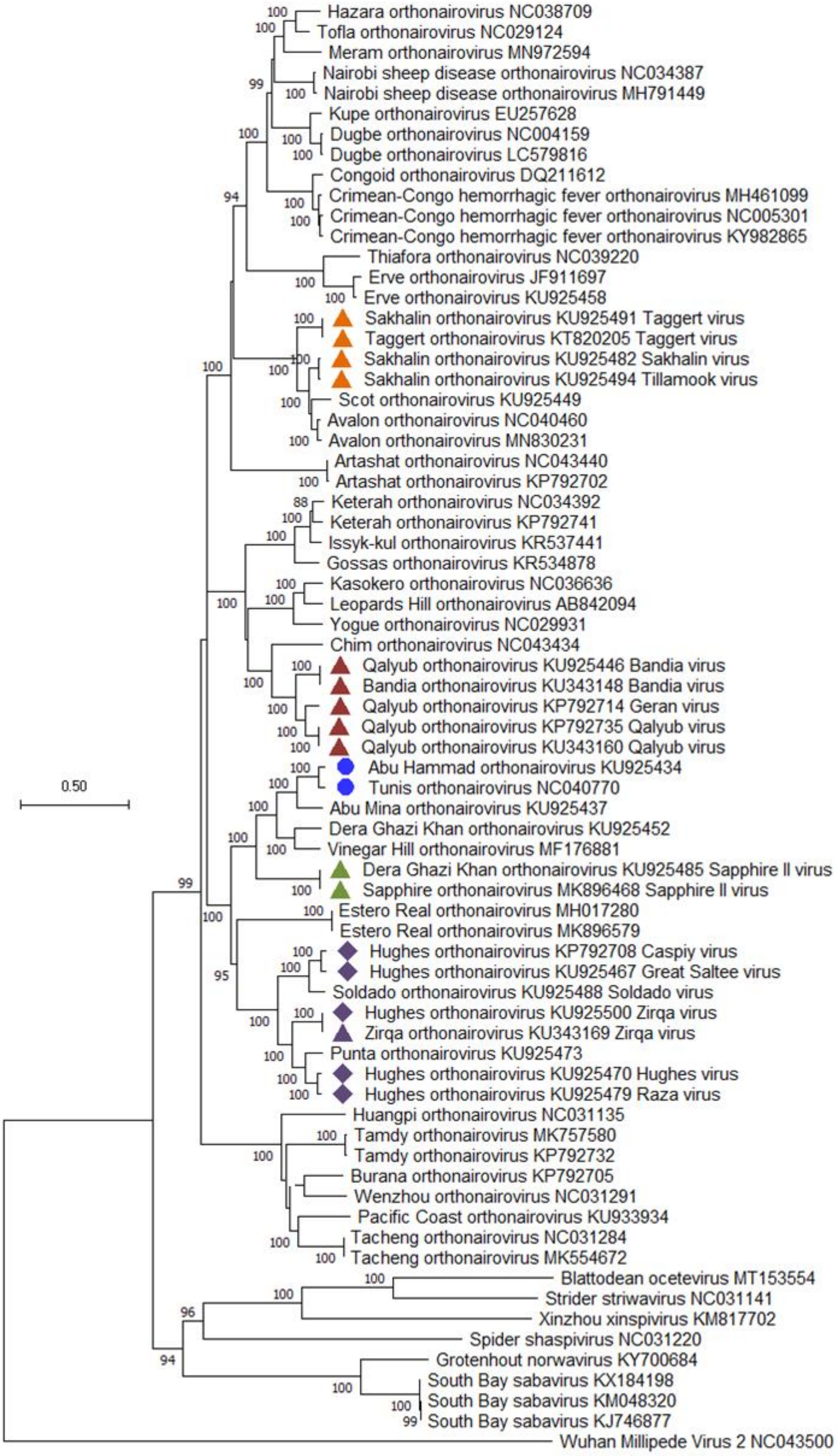

Figure 1. The current taxonomy of *Nairoviridae*, as per the ICTV online report. Those species or viruses with incorrect taxonomy were marked.

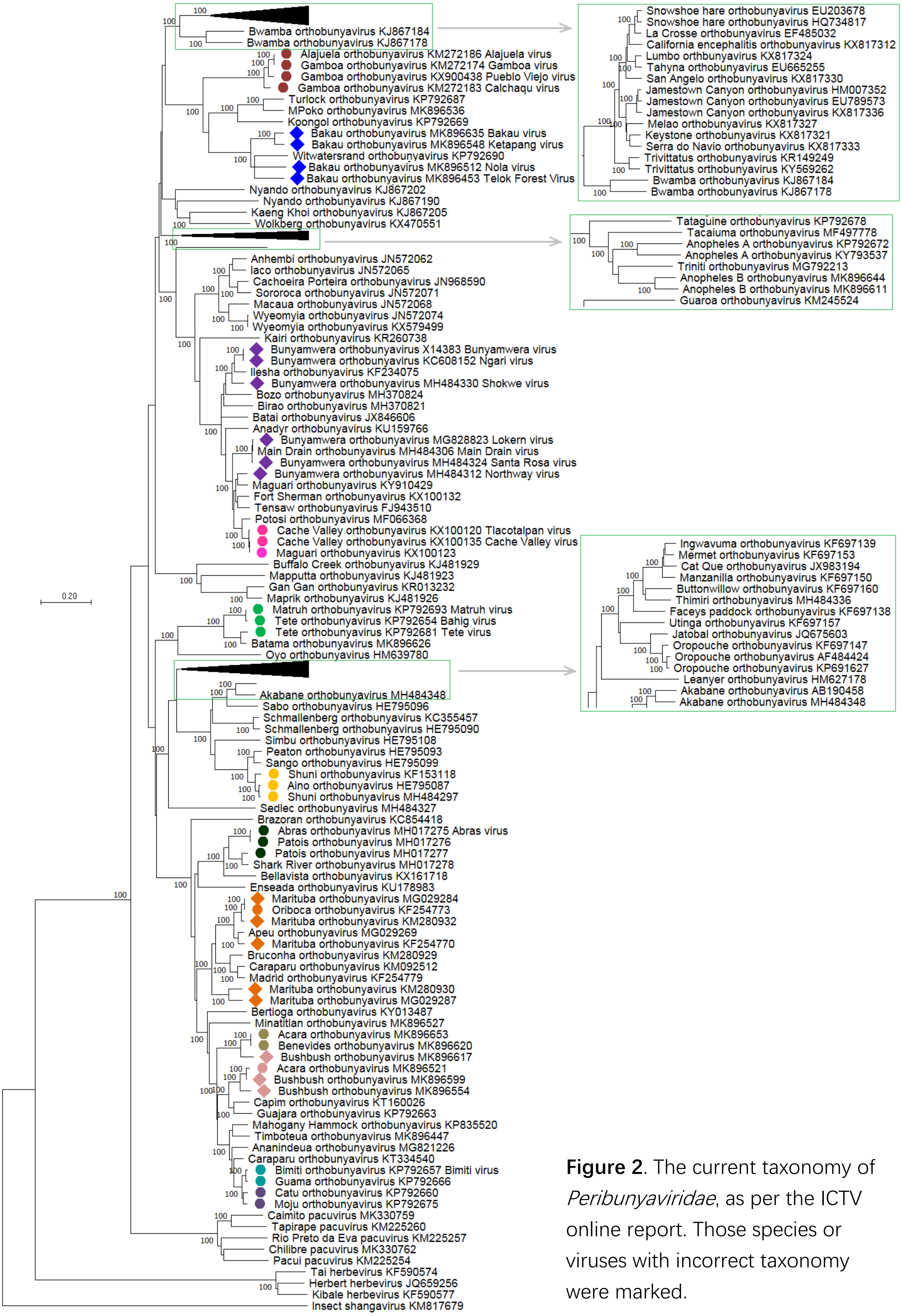

Figure 2. The current taxonomy of *Peribunyaviridae*, as per the ICTV online report. Those species or viruses with incorrect taxonomy were marked.

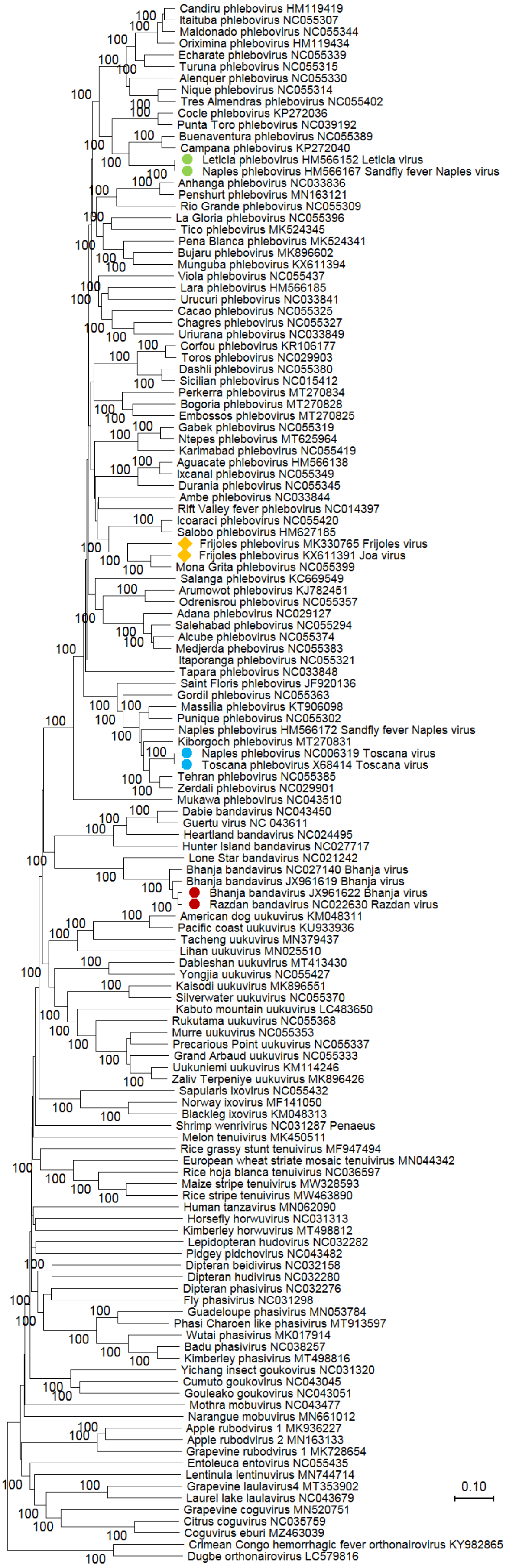

Figure 3. The current taxonomy of *Phenuiviridae*, as per the ICTV online report.[7] Those species or viruses with incorrect taxonomy were marked. Of them, one *Leticia phlebovirus* strain and one *Toscana phlebovirus* strain could be incorrectly assigned to *Naples phlebovirus* by the relevant sequence submitters.

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