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Perspective Piece

Bunyavirus Taxonomy: Limitations and Misconceptions Associated with the Current ICTV Criteria Used for Species Demarcation

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Abstract. The International Committee on Taxonomy of Viruses (ICTV) has implemented numerous changes to the taxonomic classification of bunyaviruses over the years. Whereas most changes have been justified and necessary because of the need to accommodate newly discovered and unclassified viruses, other changes are a cause of concern, especially the decision to demote scores of formerly recognized species to essentially strains of newly designated species. This practice was first described in the seventh taxonomy report of the ICTV and has continued in all subsequent reports. In some instances, viruses that share less than 75% nucleotide sequence identity across their genomes, produce vastly different clinical presentations, possess distinct vector and host associations, have different biosafety recommendations, and occur in nonoverlapping geographic regions are classified as strains of the same species. Complicating the matter is the fact that virus strains have been completely eliminated from ICTV reports; thus, critically important information on virus identities and their associated biological and epidemiological features cannot be readily related to the ICTV classification. Here, we summarize the current status of bunyavirus taxonomy and discuss the adverse consequences associated with the reclassification and resulting omission of numerous viruses of public health importance from ICTV reports. As members of the American Committee on Arthropod-borne Viruses, we encourage the ICTV Bunyavirus Study Group to reconsider their stance on bunyavirus taxonomy, to revise the criteria currently used for species demarcation, and to list additional strains of public and veterinary importance.

BRIEF HISTORY OF BUNYAVIRUS TAXONOMY

The now defunct family *Bunyaviridae* was established by the International Committee on Taxonomy of Viruses (ICTV) in 1975 to accommodate a large group of serologically related enveloped viruses with tripartite, single-stranded, negative-sense RNA genomes.[1] The family was listed for the first time in the second taxonomy report of the ICTV and retained until the ninth report.[1,2] The family *Bunyaviridae* initially contained a single genus, but as additional viruses were discovered, it was expanded to five genera (*Orthobunyavirus*, *Hantavirus*, *Nairovirus*, *Phlebovirus*, and *Tospovirus*). Bunyaviruses were further classified into serogroups (previously above the species level but below genus) based on their antigenic characteristics, as determined by neutralization, hemagglutination inhibition (HI), and complement fixation (CF) tests.[3,4] Although these groupings are not formal taxonomic designations, they have been used as a guide to support these designations.

The taxonomic classification of bunyaviruses underwent a major overhaul in 2016. These changes are currently being incorporated into the 10th report of the ICTV, which will be released in 2018. A preliminary report was made available online in 2017 and can be accessed at https://talk.ictvonline.org/ictv-reports/ictv_online_report. Of particular note is the decision to elevate the family *Bunyaviridae* to the level of an order, designated *Bunyavirales*, which contains at least 11 families and 15 genera of bunyaviruses.[5] The family name *Bunyaviridae* has been retired. These changes were implemented, understandably, in response to the plethora of novel and highly divergent viruses or viral genome sequences discovered in recent years because of advances in genome sequencing technologies and because many viruses previously classified in the family *Bunyaviridae* had not been assigned to a genus.

A total of 257 bunyaviruses were listed in the sixth taxonomy report of the ICTV.[6] The number decreased to 94 in the seventh report because numerous species were reclassified as strains or some other subspecies designation.[7] In most instances, the type species of each serogroup retained its original rank of species, whereas all other species in the serogroup were demoted to strains or some other subspecies designation. Strains were then completely omitted beginning with the ninth report of the ICTV, and this practice is maintained in the 10th report.[2,5] The loss of virus names from ICTV taxonomy reports is a cause for alarm, leaving current and future arbovirologists with a diminished understanding of these viruses and an inability to relate the past literature to

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the current taxonomy. Herein, we explore the ramifications of those taxonomic changes made by the ICTV using the Bunyamwera (BUN) group (genus *Orthobunyavirus*) as a case study, although these issues can be broadly applied.

GENETIC RELATEDNESS AMONG VIRUSES IN THE BUN GROUP

The prototype member of the BUN group is Bunyamwera virus (BUNV), now formally known as a member of the species *Bunyamwera orthobunyavirus*. Many other viruses also belong to this species, including Batai virus (BATV), Cache Valley virus (CVV), Ngari virus (NRIV), Potosi virus (POTV), and Tensaw virus (TENV) (Table 1). Of these, only BUNV is now recognized by ICTV as a species; all other viruses in this group that were previously classified as species in this group are now considered viruses, strains, or some other subspecies designation, based on their omission by the ICTV. This decision is perplexing, given the amount of genetic diversity among these viruses, their associated biological and epidemiological features, and their importance to public and/or veterinary health. We believe that there is sufficient genomic sequence divergence, as well as supporting serological and other phenotypic data, to uphold previous species-level designations. To illustrate this point, pairwise nucleotide sequence alignments were performed by Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) using the available complete small (S), medium (M), and large (L) genome sequences of all BUN group viruses (Tables 2–6) listed in the eighth ICTV taxonomy report (the last report to contain names of viruses below the rank of species), although at least four novel BUN group viruses (Abbey Lake, Anadyr, Cholul, and Córdoba viruses) have been identified since its publication.[8–12]

TABLE 1
Viruses classified in the species BUNV in the eighth report of the ICTV

Virus*	Abbreviation	Source of original isolation (host, country, and date)†
Bunyamwera virus	BUNV	*Aedes* spp. mosquitoes, Uganda, 1943
Batai virus	BATV	*Culex gelidus*, Malaysia, 1955
Birao virus	BIRV	*Anopheles pharoensis*, Central African Republic, 1969
Bozo virus	BOZOV	*Aedes opok*, Central African Republic, 1975
Cache Valley virus	CVV	*C. inornata*, United States, 1956
Fort Sherman virus	FSV	*Homo sapiens*, Panama, 1985
Germiston virus	GERV	*Culex* spp. mosquitoes, South Africa, 1958
Ilesha virus	ILEV	*H. sapiens*, Nigeria, 1957
Lokern virus	LOKV	*Culex tarsalis*, United States, 1962
Maguari virus	MAGV	Mixed mosquito pool, Brazil, 1957
Mboke virus	MBOV	*Aedes (Finlaya) ingrami*, Cameroon, 1970
Ngari virus	NRIV	*Aedes simpsoni*, Senegal, 1979
Northway virus	NORV	*Aedes* spp. mosquitoes, United States, 1972
Playas virus	PLAV	*Aedes taeniorhynchus*, Ecuador, 1975
Potosi virus	POTV	*Aedes albopictus*, United States, 1994
Santa Rosa virus	SARV	*Aedes angustivittatus*, Mexico, 1972
Shokwe virus	SHOV	*Aedes cumminsil*, South Africa, 1962
Tensaw virus	TENV	*Anopheles crucians*, United States, 1968
Tlacotalpan virus	TLAV	*Mansonia titillans*, Mexico, 1961
Xingu virus	XINV	*H. sapiens*, Brazil, unknown

ICTV = International Committee on Taxonomy of Viruses.

* Iaco and Tucunduba viruses are listed as BUNVs in the eighth report of the ICTV but are not included here because recent data suggest that they should be reclassified as Wyeomyia group viruses.[34]

† Information on original virus isolation was obtained from the Arbovirus catalog (https://wwwn.cdc.gov/arbocat) with the exceptions of POTV and XINV, which are not listed in the catalog.[35,36]

The S genome segments of BUN group viruses exhibit 65.9–98.2% nucleotide identity with a mean value of 80.0% (Tables 2 and 3). The values obtained in the NRIV/BUNV and CVV/POTV sequence alignments were not included when calculating the range and mean because NRIV and POTV are reassortants that acquired their S segments from BUNV and CVV, respectively.[13–15] The M and L genome segments of BUN group viruses are less conserved than the S segment, with mean nucleotide identities of 65.4% and 74.7%, respectively, excluding reassortants (Tables 2, 4, and 5). To determine the level of nucleotide identity across the entire genome, all three genome segments were concatenated and aligned to reveal nucleotide identities ranging from 68.3% to 77.1% with a mean of 72.2% (Tables 2–6). Outside the order *Bunyavirales*, viruses with this high level of nucleotide divergence are usually considered to be distinct species, as discussed later.

To further assess the genetic relatedness of BUN group viruses, alignments were performed using the deduced amino acid sequences of the nucleocapsid (N) protein, polyprotein precursor, and RNA-dependent RNA polymerase (RdRp) encoded by the S, M, and L genome segments, respectively (Tables 2–6). The N proteins possess 66.1–99.6% amino acid identity with a mean of 88.8%. The M polyprotein and RdRp are less conserved, with mean amino acid identities of 65.7% and 84.0%, respectively. The findings from the N protein sequence alignments are of particular interest because the ninth ICTV taxonomy report states that species demarcation in the genus *Orthobunyavirus* is "primarily defined by serological criteria" and where known "amino acid sequences of the N proteins differ by more than 10%."[2] Our analysis revealed that the N proteins of BUN group viruses differ by more than 10% in more than one-third of the pairwise alignments and some even differ by more than 30% (Table 3). Thus, the ICTV is not adhering to its previous criteria for species demarcation, yet no explanation if offered in the 10th report.

INCONSISTENCIES IN THE CRITERIA USED FOR SPECIES DEMARCATION

Another major concern with the ICTV classification of bunyaviruses is the inconsistent criteria used for the designation of

TABLE 2
Genetic relatedness among Bunyamwera group viruses

	% Nucleotide identity		% Amino acid identity	
Segment	Range	Mean	Range	Mean
Small (S)	65.9–98.2	80.0	66.1–99.6	88.8
Medium (M)	55.4–76.4	65.4	50.1–85.8	65.7
Large (L)	72.3–81.4	74.7	80.7–91.8	84.0
Concatenated*	68.3–77.1	72.2	71.9–87.9	78.5

Percent nucleotide and amino acid identities obtained with Ngari virus were excluded on some occasions (see underlined values in Tables 3–6) because the virus is a reassortant.[13,14]

* Complete S, M, and L genome sequences were concatenated as were amino acid sequences of the nucleocapsid protein, M segment–encoded polyprotein, and RNA-dependent RNA polymerase.

TABLE 3
Genetic relatedness of the S genome segment of viruses in the Bunyamwera group

	% Nucleotide identity (complete S genome segment; upper right) and amino acid identity (nucleocapsid protein; lower left)													
Virus	BUNV	BATV	BIRV	BOZOV	CVV	GERV	ILEV	MAGV	MBOV	NRIV	NORV	POTV	SHOV	TENV
Bunyamwera virus	–	78.9	88.1	86.8	80.7	70.0	83.8	81.1	83.4	95.9	80.1	81.3	87.3	79.6
Batai virus	92.3	–	78.6	74.9	80.6	72.7	75.6	80.5	75.0	85.3	80.4	81.4	78.9	80.2
Birao virus	93.1	89.7	–	80.1	79.5	70.4	80.3	80.2	80.3	88.2	78.3	79.7	84.3	78.6
Bozo virus	87.1	82.8	81.6	–	78.5	65.9	78.4	76.6	77.8	87.3	76.0	77.9	81.8	75.0
Cache Valley virus	90.6	94.0	88.8	81.6	–	70.2	77.8	83.3	76.7	85.3	85.9	88.4	81.4	83.6
Germiston virus	75.1	76.8	73.8	66.1	75.1	–	68.2	70.0	67.1	75.2	71.5	71.2	69.4	71.2
Ilesha virus	94.4	90.1	91.8	84.1	90.6	75.1	–	78.7	98.2	89.9	78.4	78.4	82.6	79.4
Maguari virus	91.4	93.6	89.7	81.6	96.1	74.2	89.3	–	77.5	87.3	84.6	83.1	81.7	83.0
Mboke virus	94.0	90.1	91.8	83.7	90.1	75.1	99.6	88.8	–	89.6	77.9	78.1	81.9	78.1
Ngari virus	100.0	92.3	93.1	87.1	90.6	75.1	94.4	91.4	94.0	–	85.9	87.6	90.3	85.0
Northway virus	92.7	94.9	90.1	82.8	96.1	76.0	90.6	95.3	90.1	92.7	–	86.3	80.0	86.0
Potosi virus	91.4	94.0	88.8	82.4	99.1	74.7	90.6	96.1	90.1	91.4	95.3	–	82.3	83.9
Shokwe virus	97.4	91.8	91.8	85.8	91.8	76.0	93.1	91.8	92.7	97.4	93.6	92.7	–	81.0
Tensaw virus	93.1	94.4	89.7	82.8	96.1	75.1	90.1	96.6	89.7	93.1	97.0	95.3	92.7	–

S = small. Lokern and Santa Rosa viruses are not included because their S genome segments have not been fully sequenced. Fort Sherman, Playas, Tlacotalpan, and Xingu viruses are not included because they are antigenic variants of CVV.[36,37] Iaco and Tucunduba viruses are not included because they have been reclassified as Wyeomyia group viruses.[34] Underlined values were obtained when the S genomic sequence of a reassortant was aligned to the corresponding sequence of its donor virus (these values were excluded when calculating means and ranges). Abbreviations are defined in Table 1. Genbank accession numbers used for the analysis are as follows: BUNV (NC_001927.1 and NP_047213.1), BATV (KU746869.1 and APU88427.1), BIRV (AM711131.1 and CAM97976.1), BOZOV (AM711132.1 and CAM97977.1), CVV (KX100133.1 and ARI46659.1), GERV (M19420.1 and AAA87603.1), ILEV (KF234073.1 and AGU99594.1), MAGV (KY910431.1 and ATJ04179.1), MBOV (AY593727.1 and AAT01933.1), NRIV (KM507341.1 and AIZ49766.1), NORV (X73470.1 and CAA51855.1), POTV (MF066370.1 and ATJ04184.1), SHOV (EU564831.1 and ACE07184.1), and TENV (FJ943505.1 and ACV95620.1).

species in various genera. In the ninth taxonomy report of the ICTV, species in the genus *Orthobunyavirus* were defined using serologic data (neutralization and HI tests) and N protein sequence information.[2] By contrast, in the genus *Nairovirus* (now defunct), sequence information was not used and "species were defined by serological relationships and are distinguishable by 4-fold differences in two-way neutralization tests." Species in the genus *Phlebovirus* were defined solely by "serological reactivity," but remarkably no serologic tests or values were provided. In the genus *Tospovirus*, species were defined on the basis of "serological relationships of the N protein and on the criterion that their N protein sequence should show less than 90% amino acid identity." A more stringent cutoff value was applied to the genus *Hantavirus* (< 93% amino acid identity) and both N protein and M polyprotein sequences were used. Inexplicably, the criteria used for bunyavirus species designations are not discussed in the 10th report of the ICTV. It would seem prudent to use the same or similar criteria for species demarcation across all bunyavirus genera.

A further limitation of the current taxonomic approach is that most species designations are based on the outcome of a single (or a few) serologic test(s) or sequence analysis of a single genomic segment. Because of the segmented nature of the bunyavirus genome and the ability of genomic segments to reassort during coinfections, different serologic tests and sequence alignments may produce different results. Complement fixation antigenic determinants are associated with the S segment–encoded N protein, whereas HI and neutralization tests react with the M segment–encoded surface glycoproteins.[15–18] Therefore, a reassortant with the S segment of one virus and the M segment of another distinct virus would be classified as one virus based on CF serology but as a different virus based on the results of a HI or neutralization test. There are no serologic assays for the detection of L segment–encoded antigens. Sequence comparisons are often limited to the N protein, but this approach cannot differentiate between reassortants and their S segment donors. A more robust approach, one that includes the analysis of S, M, and L sequence data, should be used for species designations.

TABLE 4
Genetic relatedness of the M genome segment of viruses in Bunyamwera group

	% Nucleotide identity (complete M genome segment; upper right) and amino acid identity (polyprotein precursor; lower left)									
Virus	BUNV	BATV	CVV	GERV	ILEV	MAGV	NRIV	NORV	POTV	TENV
Bunyamwera virus	–	63.4	62.9	62.6	65.0	63.7	64.0	63.3	58.5	64.2
Batai virus	63.6	–	69.9	59.4	68.0	71.3	89.0	70.4	59.2	70.0
Cache Valley virus	64.1	75.1	–	58.4	67.5	75.6	70.4	74.1	59.8	73.0
Germiston virus	60.2	54.8	55.2	–	60.6	59.5	60.1	59.3	55.4	59.4
Ilesha virus	63.3	69.0	69.7	54.9	–	68.1	68.8	67.9	60.6	68.0
Maguari virus	63.1	75.4	85.1	54.9	69.1	–	71.6	76.4	59.8	74.2
Ngari virus	63.7	94.4	75.1	54.6	68.9	75.7	–	71.3	59.5	70.3
Northway virus	64.2	76.0	84.1	55.5	68.8	85.8	76.0	–	60.4	73.1
Potosi virus	53.7	54.6	55.8	50.1	55.0	55.8	54.9	55.6	–	60.4
Tensaw virus	63.6	73.6	79.9	54.5	68.1	80.6	73.4	79.1	56.1	–

M = medium. Birao, Bozo, Lokern, Mboke, Santa Rosa, and Shokwe viruses are not included because their M genome segments have not been fully sequenced. Fort Sherman, Playas, Tlacotalpan, and Xingu viruses are not included because they are antigenic variants of CVV.[36,37] Iaco and Tucunduba viruses are not included because they have been reclassified as Wyeomyia group viruses.[34] Underlined values were obtained when the M genomic sequence of a reassortant was aligned to the corresponding sequence of its donor virus (these values were excluded when calculating means and ranges). Abbreviations are defined in Table 1. Genbank accession numbers used for the analysis are as follows: BUNV (M11852.1 and AAA42777.1), BATV (KU746870.1 and APU88429.1), CVV (KX100134.1 and ARI46661.1), GERV (M21951.1 and AAA42778.1), ILEV (KF234074.1 and AGU99596.1), MAGV (KY910430.1 and ATJ04178.1), NRIV (KM514677.1 and AIZ49776.1), NORV (EU004188.1 and ABV68911.1), POTV (MF066369.1 and ATJ04183.1), and TENV (FJ943506.1 and ACV95623.1).

TABLE 5

Genetic relatedness of the L genome segment of viruses in the Bunyamwera group

Virus	% Nucleotide identity (complete L genome segment; upper right) and amino acid identity (RNA-dependent RNA polymerase; lower left)							
	BUNV	BATV	CVV	ILEV	MAGV	NRIV	POTV	TENV
Bunyamwera virus	–	73.5	73.4	81.4	73.1	95.9	73.2	73.0
Batai virus	81.6	–	73.8	73.5	74.6	73.9	73.8	73.7
Cache Valley virus	82.2	83.0	–	73.2	77.0	74.0	82.0	77.0
Ilesha virus	91.6	81.2	81.2	–	73.3	81.3	72.5	72.3
Maguari virus	82.5	83.3	88.8	81.6	–	73.7	76.5	77.1
Ngari virus	98.9	81.9	82.3	91.8	82.6	–	73.7	72.8
Potosi virus	81.9	82.6	93.5	80.7	88.7	82.2	–	75.7
Tensaw virus	81.5	83.0	87.7	81.0	89.5	81.4	87.0	–

L = large. Birao, Bozo, Germiston, Lokern, Mboke, Northway, Santa Rosa, and Shokwe viruses are not included because their L genome segments have not been fully sequenced. Fort Sherman, Playas, Tlacotalpan, and Xingu viruses are not included because they have been classified as antigenic variants of CVV.[36,37] Iaco and Tucunduba viruses are not included because they have been reclassified as Wyeomyia group viruses.[34] Underlined values were obtained when the L genomic sequence of a reassortant was aligned to the corresponding sequence of its donor virus (these values were excluded when calculating means and ranges). Abbreviations are defined in Table 1. Genbank accession numbers used for the analysis are as follows: BUNV (X14383.1 and CAA32553.1), BATV (KU746871.1 and APU88430.1), CVV (KX100135.1 and ARI46662.1), ILEV (KF234075.1 and AGU99597.1), MAGV (KY910429.1 and ATJ04177.1), NRIV (KM507334.1 and AIZ49759.1), POTV (MF066368.1 and ATJ04182.1), and TENV (FJ943509.1 and ACV95628.1).

THE LOSS OF SPECIES IDENTITY MAY RESULT IN CONFUSION AND MISINTERPRETATION OF SCIENTIFIC DATA

Viruses in the BUN group often produce different disease manifestations and have distinct geographic distributions. For example, CVV is a common cause of pregnancy loss and congenital defects in sheep in North America,[19] whereas the sympatric TENV, which is transmitted by some of the same mosquito vectors, does not cause these syndromes.[20] Ngari virus has been associated with large outbreaks of hemorrhagic disease in humans in Africa.[13] Batai virus is an occasional cause of febrile illness in humans in Europe, Asia, and Africa.[21] Other BUN group viruses, such as POTV, are not recognized pathogens of humans or vertebrate animals in nature. The principal transmission vectors and vertebrate hosts of most BUN group viruses have not been fully identified, but available evidence suggests that these viruses often have distinct vector and host associations. Cache Valley virus has been isolated from mosquitoes of many species but most frequently from *Anopheles quadrimaculatus*, *Culiseta inornata*, and *Coquillettidia perturbans*, with white-tailed deer implicated as important vertebrate hosts.[20,22] Many BUN group viruses have geographic distributions that do not overlap with those of white-tailed deer or of any of the aforementioned mosquito species. The classification of viruses with fundamentally distinct phenotypic and ecologic characteristics as a single species, with no information provided on important viruses or strains, markedly reduces the value of the taxonomic system for the virology and public health communities and could result in the misinterpretation of data, as discussed below.

Bunyamwera virus was originally considered to have a geographic distribution restricted to Africa and to cause a nonspecific febrile illness in humans.[23,24] However, the loss of species identity has created the disconcerting situation in which other members (strains) of the species BUNV are now a cause of pregnancy loss and congenital defects in sheep in North America, hemorrhagic disease in humans in Africa, and febrile illness in humans in Eurasia. When these viruses are designated only by their species membership and no longer listed by the ICTV, the result will be confusion among public health virologists, epidemiologists, vector control personnel, and persons involved in regulation of virus shipments, biosafety, and risk assessment. This confusion will result in the publication of data that can easily be misinterpreted. Two reports of BUNV in Argentina can serve as an example.[25,26] After close inspection of these reports, it is apparent that CVV, or one of its antigenic variants, was isolated from equids and mosquitoes. One study describes the isolation of BUNV (strain CVV) from two horses that died of encephalitis and from an aborted equine fetus.[26] The article gives the impression that BUNV, an African virus, has been introduced into the Americas and is now associated with serious equine disease. We do not fault the authors as they followed the nomenclature guidelines established by the ICTV.

In this regard, two of us recently published an article describing two new members of the California encephalitis virus (CEV) group (genus *Orthobunyavirus*).[27] The two viruses, designated Infirmatus (INFV) and Achiote (ACHOV), were isolated from mosquitoes collected in Florida and Panama, respectively. California encephalitis virus is the prototype virus of the serogroup and has been designated by the ICTV as the species name. Accordingly, the other 13 named CEV group viruses were downgraded to strains or synonyms of the species CEV and were deleted from the ninth and 10th ICTV reports on virus taxonomy. On submission of the aforementioned manuscript, two of the reviewers suggested that INFV and ACHOV were not novel viruses and that they were instead strains of CEV. In response, the authors argued that omission of the names INFV and ACHOV would diminish the value of the article and would give the impression that CEV, a virus known only from the western United States and Canada,[28] now occurs in Florida and Panama. The journal editor subsequently accepted the justification and allowed the article to be published with the original names (INFV and ACHOV).[27] But this is another example of how the loss of species identity in recent ICTV reports is now translating into a loss of species identity in the scientific literature.

TABLE 6

Genetic relatedness of concatenated S, M, and L genome sequences of viruses in the Bunyamwera group

Virus	% Nucleotide identity (concatenated S, M, and L genome segments; upper right) and amino acid identity (concatenated N protein, M segment polyprotein, and RNA-dependent RNA polymerase sequences; lower left)							
	BUNV	BATV	CVV	ILEV	MAGV	NRIV	POTV	TENV
Bunyamwera virus	–	70.2	70.0	75.7	70.3	84.1	68.3	70.1
Batai virus	75.7	–	72.8	71.8	73.8	79.6	69.1	72.9
Cache Valley virus	76.1	80.8	–	71.5	77.1	73.1	74.3	75.9
Ilesha virus	81.5	77.3	77.6	–	72.0	76.9	68.6	71.4
Maguari virus	76.0	81.1	87.9	77.5	–	73.5	71.0	76.6
Ngari virus	86.1	87.1	80.2	83.6	80.6	–	69.2	72.3
Potosi virus	72.1	73.0	79.9	71.9	77.0	72.7	–	70.6
Tensaw virus	75.7	80.3	85.3	76.9	86.7	79.2	76.2	–

L = large; M = medium; S = small. Birao, Bozo, Germiston, Lokern, Mboke, Northway, Santa Rosa, and Shokwe viruses are not included because their genomes have not been fully sequenced. Fort Sherman, Playas, Tlacotalpan, and Xingu viruses are not included because they have been classified as antigenic variants of CVV.[36,37] Iaco and Tucunduba viruses are not included because they have been reclassified as Wyeomyia group viruses.[34] Underlined values were obtained when the genomic sequence of a reassortant was aligned to the genome sequence of one of its donor viruses (these values were excluded when calculating means and ranges). Abbreviations are defined in Table 1. Genbank accession numbers used for the analysis are listed in the footnotes of Tables 3–5.

THE LOSS OF SPECIES IDENTITY COULD IMPACT BIOSAFETY REGULATIONS

Ngari, Germiston, and Xingu viruses are listed as biosafety level (BSL) 3 viruses in the Biosafety in Microbial and Biomedical Laboratories, whereas all other BUN group viruses are listed as BSL2 viruses (accessed at: https://www.cdc.gov/biosafety/publications/bmbl5/bmbl.pdf). These biosafety guidelines are not used only in the United States; many other countries, especially Latin America, also follow US recommendations and may be concerned about specific "viruses" with familiar common names in their geographic region. With the new nomenclature as approved by ICTV, which lumps viruses into common species containing both BSL2 and BSL3 agents, clinical and public health laboratories, biosafety offices, and regulatory agencies could potentially be confused by the lack of common and familiar names because most individuals working in those places will not understand or have any background on the new ICTV classification and its omission of virus names. This could lead to unnecessary concerns about public health risks, restrictions on laboratory work, or other consequences.

IN A PARALLEL UNIVERSE WHERE FLAVIVIRUSES ARE BUNYAVIRUSES

To further highlight the problems with the recent bunyavirus classification and taxonomy, we have applied the logic (or lack thereof) used on bunyaviruses to another group containing arboviruses. For this exercise, we focused on the Japanese encephalitis (JE) complex (genus *Flavivirus* and family *Flaviviridae*), which consists of eight species: JE, Cacipacore, Koutango, Murray Valley encephalitis, St. Louis encephalitis, Usutu, West Nile, and Yaounde viruses.[29] Pairwise alignments were performed using the nucleotide sequences of all five JE complex viruses that have had their genomes fully sequenced. The genomes of these viruses have 64.1–73.0% nucleotide identity with a mean of 68.1% (data not shown), which is not dissimilar to that obtained for BUN group viruses (68.3–77.1% and 72.2%). Thus, a case could be made that, for consistency with the species criteria for bunyaviruses, every species in the JE group, with the exception of the type species (Japanese encephalitis virus [JEV]), should be reclassified as a strain or some other subspecies designation of the species JEV. This would create the situation in which JEV has a worldwide distribution, is associated with avian mortality, uses rodent reservoir hosts, and where the current JEV vaccine could be considered ineffective because it protects against only a single strain of the virus. This hypothetical scenario also would have diminished the seriousness of the introduction of West Nile virus into the United States in 1999. The event would not have been considered an incursion of a new virus species into the United States because St. Louis encephalitis virus has been recognized in the United States since the 1930s.[30] This situation would potentially cause confusion among public health officials, health-care providers, veterinarians, regulatory authorities, and diagnostic personnel, as well as the media and general public.

FINAL REMARKS

We are aware that virus taxonomy is both challenging and contentious, and commend the ICTV for their efforts to accommodate into the most recent taxonomic treatment the exponential growth in the number and diversity of viruses in the order *Bunyavirales*. The taxonomic classification of viruses has become particularly challenging in recent years because of the plethora of new virus genome sequences continually being discovered using metagenomics. Because phenotypic characterizations cannot possibly keep pace with viral genome sequence discovery, virus classification and taxonomy are now primarily based on sequence data and phylogenetic relationships; ecologic and phenotypic characteristics are typically no longer considered. However, many new viruses have never been cultured and are known only from partial sequence data; consequently, little to nothing is known about their ecology, phenotypic characteristics, or even their natural hosts.[31,32] One unfavorable outcome of this change in classification is that numerous individual bunyaviruses have been omitted from recent ICTV reports. What are the implications of the associated virus deletions from the ICTV publications? Some of us remember when BUNV, BATV, CVV, NRIV, POTV, and TENV were considered distinct virus species based on their different geographical distributions, vector and host associations, and pathogenicities. But will future arbovirologists know that, or even know that these other viruses exist? Likewise, will future public health officials, health-care providers, veterinarians, regulatory authorities, and diagnostic personnel know of these other viruses? We urge the ICTV to find a way to retain virus names in their official publications and databases and to work toward uniformity in their criteria for species designations across virus families and genera. Excessive lumping as exhibited in the 10th report, especially when virus names are not retained, as with the current bunyavirus taxonomy, could have serious implications for virology, public health, diagnostics, and biosecurity. The issue will be further compounded by the discovery of additional bunyaviruses and bunyavirus genome sequences. In this regard, it has been estimated that 99.99% of the eukaryotic virosphere is currently undiscovered or unclassified.[33]

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