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:	***2016.010aM***	(to be completed by ICTV officers)

Short title: 7 new species in the genus *Vesiculovirus*, family *Rhabdoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**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 *Rhabdoviridae* SG

ICTV Study Group comments (if any) and response of the proposer:

9 members have advised support for the proposal; 3 members have not responded.

Date first submitted to ICTV:	Jun 2016
Date of this revision (if different to above):	

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.010aM***	(assigned by ICTV officers)

To create 7 new species within:

Genus:	***Vesiculovirus***
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Malpais Spring vesiculovirus	Malpais Spring virus (MSPV; strain 85-488NM)	KC412247
Perinet vesiculovirus	Perinet virus (PERV; strain DakArMg802)	HM566195
Jurona vesiculovirus	Jurona virus (JURV; strain BeAr 40578)	KM204996
Yug Bogdanovac vesiculovirus	Yug Bogdanovac virus (YBV; strain YU4-76)	JF911700
Radi vesiculovirus	Radi virus 2 (RADV; strain ISS Phl-166)	KM205024
Morreton vesiculovirus	Morreton virus (MORV; strain CoAr191048)	KM205007
American bat vesiculovirus	American bat vesiculovirus (ABVV; strain TFFN-2013)	JX569193

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Species demarcation criteria have previously been defined as follows:

"Vesiculovirus species have been defined primarily by serological means coupled with phylogenetic analysis of the genomes. Biological characteristics such as host range and mechanisms of transmission are also used to distinguish viral species within the genus."

To achieve more consistency across taxa, we propose to replace these criteria with the following:

Viruses assigned to different species within the genus Vesiculovirus have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in the N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of

15% in the G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in serological tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.

Like the viruses that have been assigned to existing species, the viruses we propose here to be assigned to new species in the genus *Vesiculovirus* have a genome organisation (3´-N-P-M-G-L-5´), comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L). Additional ORFs (≥ 150 nt) may be present in alternative reading frames in any of these genes (**Figure 1**); however, expression from an alternative ORF has been demonstrated to date only for the VSIV P gene from which carboxy-coterminal C and C´ proteins (55-aa and 65-aa, respectively) are expressed from consecutive initiation codons[1, 2]. The viruses form a monophyletic clade in a maximum likelihood tree inferred from complete L protein sequences of 140 animal rhabdoviruses (**Figure 2**). Species are demarcated according to the criteria specified above, including amino acid sequence divergence in the N, L and G proteins (**Figure 3**).

a. *Malpais Spring vesiculovirus*
   Malpais Spring virus (MSPV) strain 85-488NM was isolated in 1985 from a pool of mosquitoes (*Aedes campestris*) at the White Sands Missile Range in New Mexico, USA[3]. A second isolate of the virus was obtained from mosquitoes of a different species (*Psorophora signipennis*) collected at the same location on the same day[3]. In indirect fluorescent antibody (IFA) tests, MSPV has been shown to cross-react strongly with Chandipura virus (CHNV) and more weakly with several other classified vesiculoviruses including vesicular stomatitis New Jersey virus (VSNJV), vesicular stomatitis Alagoas virus (VSAV), vesicular stomatitis Indiana virus (VSIV), Maraba virus (MARV), Carajas virus (CARV), Cocal virus (COCV), Piry virus (PIRV) and Isfahan virus (ISFV). MSPV was also shown to cross-react strongly in IFA tests with Perinet virus (PERV; see below) and more weakly with Jurona virus (JURV; see below) and Yug Bogdanovac virus (YBV; see below)[3, 4]. In complement-fixation (CF) tests and/or plaque-reduction neutralisation (PRN) tests, MSPV was found to be distinct from each of these vesiculoviruses, as well as Radi virus (RADV; see below) and several unclassified rhabdoviruses[3, 5]. Neutralising antibodies to MSPV have been detected in horses (*Equus caballus*), coyotes (*Canis latrans*), gemsbok (*Oryx gazella*), mule deer (*Odocoileus hemionus*) and pronghorns (*Antilocapra americana*)[3]. The complete MSPV genome (11,019 nt) has been sequenced (**Figure 1**)[5]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and several alternative ORFs ≥ 150 nt in the N gene (Nx; 66-aa, 7.2 kDa), M gene (Mx; 63-aa, 7.4 kDa) and G gene (Gx; 83-aa, 9.3 kDa). The Gx protein is predicted to be a small basic transmembrane protein[5]. Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that MSPV lies in the vesiculovirus clade and is most closely related to CHNV, ISFV and JURV.

b. *Perinet vesiculovirus*
   Perinet virus (PERV) strain DakArMg802 was isolated from mosquitoes (*Culex antennatus*) collected at Perinet, Madagascar, in 1985[6, 7]. The virus is also reported to have been isolated from sandflies (*Phlebotomus berentiensis*) and mosquitoes of several other species. PERV has been reported to cross-react in CF tests with several vesiculoviruses, including COCV, JURV. PIRV, CHNV and ISFV; however, it has been shown to be distinct from VSNJV, VSIV, COCV, JURV, PIRV, CHNV, ISFV and YBV in IFA and PRN tests[8]. Complete coding regions (11,103 nt) of the PERV genome have been sequenced with only the 3´ and 5´ ends incomplete (**Figure 1**)[9]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus

structural proteins (N, P, M, G and L) and several alternative ORFs ≥ 150 nt in the L gene: (Lx; 70-aa, 8.3 kDa), (Ly; 63-aa, 7.3 kDa) and (Lz; 65-aa, 7.7 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that PERV lies in the vesiculovirus clade and is most closely related to PIRV, ISFV and JURV.

c. *Jurona vesiculovirus*
Jurona virus (JURV) strain BeAr40578 was isolated from mosquitoes (*Haemagogus spegazzinii*) collected near Belem in Para State, Brazil, in 1962[6]. JURV has been reported to cross-react in CF and/or IFA tests with several vesiculoviruses, including COCV, VSNJV, VSIV, PIRV, PERV, YBV, CHNV and ISFV; however, it has been shown to be distinct from VSNJV, VSIV, COCV, PERV, PIRV, CHNV, ISFV and YBV in PRN tests[8]. Complete coding regions (11,121 nt) of the JURV genome have been sequenced with only the 3´ and 5´ ends incomplete (**Figure 1**)[9]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and alternative ORFs ≥ 150 nt in the P gene (Px; 66-aa, 8.3 kDa) and L gene (Lx; 66-aa, 7.5 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that JURV lies in the vesiculovirus clade and is most closely related to PERV, PIRV, ISFV, CHNV and MSPV.

d. *Yug Bogdanovac vesiculovirus*
Yug Bogdanovac virus (YBV) strain YU4-76 was isolated from a pool of sandflies (*Phlebotomus perfiliewi*) collected at Merosina, Serbia, in 1976[6, 10]. It has been reported to cross-react weakly in CF tests with several other vesiculoviruses including CHNV, ISFV, PERV and RADV; however, it has been shown to be distinct from VSNJV, VSIV, VSAV, COCV, JURV, PIRV, CHNV, ISFV, PERV, CARV, MARV and in PRN tests[4, 8, 11]. The complete YBV genome (11,202 nt) has been sequenced (**Figure 1**)[10]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and an alternative ORF ≥ 150 nt in the G gene (Gx; 110-aa, 11.6 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that YBV lies in the vesiculovirus clade and is most closely related to RADV.

e. *Radi vesiculovirus*
Radi virus (RADV) strain ISS Phl-166 was isolated from sandflies (*Phlebotomus perfiliewi*) collected at Radi in Toscana, Italy, in 1982[6, 12]. It has been reported to cross-react weakly in IFA and CF tests with YBV[4]. Complete coding regions (11,068 nt) of the RADV genome have been sequenced with only the 3´ and 5´ ends incomplete (**Figure 1**)[9]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and alternative ORFs ≥ 150 nt in the N gene (Nx; 98-aa, 11.0 kDa) and G gene (Gx; 71-aa; 7.9 kDa) (Gy; 90-aa; 10.4 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that RADV lies in the vesiculovirus clade and is most closely related to YBV.

f. *Morreton vesiculovirus*
Morreton virus (MORV) strain CoAr191048 was isolated from sandflies (*Lutzomyia* spp.) collected in Durania, Colombia, in 1986[13] but was then incorrectly identified as VSAV. MORV was shown to cross-react weakly in PRN and CF tests with VSIV, COCV and MARV[13]. Complete coding regions (11,181 nt) of the MORV genome have been sequenced with only the 3´ and 5´ ends incomplete (**Figure 1**)[9]. The genome is typical of

vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and alternative ORFs ≥ 150 nt in the G gene (Gx; 60-aa, 7.0 kDa) and L gene (Lx; 67-aa, 7.7 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that MORV lies in the vesiculovirus clade and is most closely related to VSIV.

g. *American bat vesiculovirus*
American bat vesiculovirus (ABVV) strain TFFN-2013 was detected in pooled liver tissue obtained from 120 big brown bats (*Eptesicus fuscus*) collected in Maryland, USA, in 2008[14]. No data are currently available on antigenic relationships. The complete ABVV genome (10,692 nt) has been sequenced (**Figure 1**)[14]. The genome is typical of vesiculoviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and two alternative ORFs ≥ 150 nt in the P gene: Px (91-aa, 10.6 kDa) and Py (60-aa; 7.0 kDa). Phylogenetic analysis of L protein sequences (**Figure 2**) and amino acid sequence identity in the N, L and G proteins (**Figure 3**) indicate that MORV lies centrally in the vesiculovirus clade and shares similar levels of identity with most other vesiculoviruses.

Each of these viruses meet species demarcation criteria A and B, establishing them as members of distinct species (**Figures 3A and 3C**). All virues also meet demarcation criterion C, except MORV which falls marginally below 15% sequence divergence in the G protein (13.7%) only from VSIV (**Figure 3B**). Each of the viruses can also be distinguished based on criterion D (differences in genome organisation), although the differences pertain exclusively to small alternative ORFs in the major structural protein genes; in most cases, it is not known if these small ORFs are expressed as functional proteins. Although incomplete, classification as distinct species is also supported by the available data on antigenic relationships (criterion E). Ecological data are primarily restricted to the location and source of virus isolation, which is consistent with the observation that of all vesiculoviruses infect mammals and are transmitted by haematophagous insects (primarily sandflies and/or mosquitoes). Demarcation criterion F cannot yet be usefully applied.

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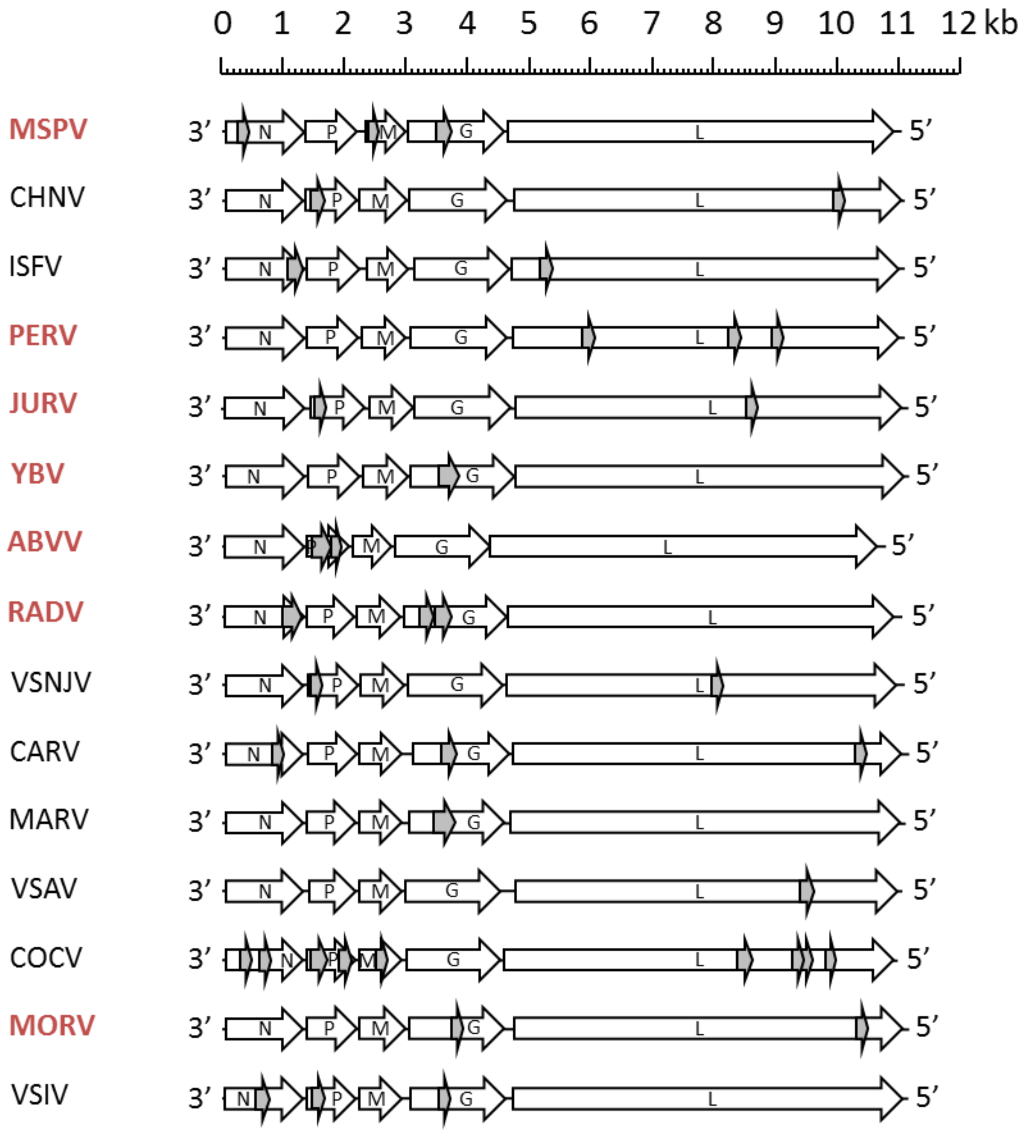
Annex:



. **Figure 1.** Genome organisations of vesiculoviruses. All alternative ORFs ≥ 150 nt (50 aa) are indicated but it is not known which of these may be expressed. In the case of VSIV, two small proteins (C and C´) are expressed from consecutive initiation codons in an alternativeORF (designated here as Px) in the P gene[1, 2].

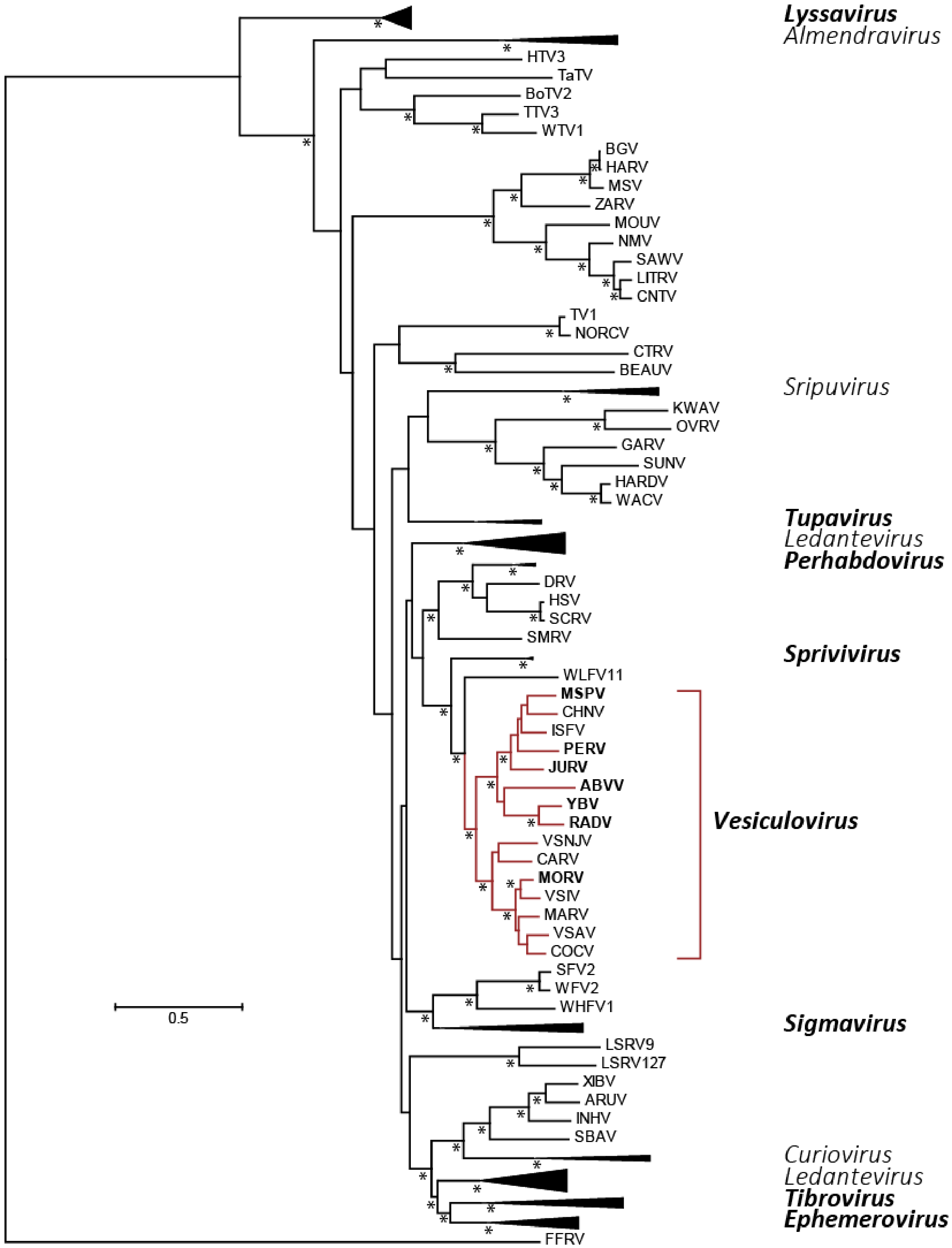


Figure 2. ML phylogenetic tree of 140 animal rhabdovirus L protein sequences. Branches comprising viruses assigned to existing genera (named in bold italics) or proposed new genera (named light italics)[9] have been condensed. The clade representing the genus *Vesiculovirus* is highlighted (red). Horizontal branch lengths are drawn to a scale of amino acid substitutions/site, and all bootstrap support values (BSP) ≥ 80% are shown by the * symbol. The tree is rooted on fecal fox rhabdovirus (FFRV) based on the position observed in a broader analysis that included more distant members of the *Rhabdoviridae* (i.e.,

including members of the genera *Novirhabdovirus*, *Cytorhabdovirus* and *Nucleorhabdovirus*) and in other publications).

	MSPV	CHNV	ISFV	**PERV**	PIRV	**JURV**	**YBV**	**ABVV**	**RADV**	VSNJV	CARV	MARV	VSAV	COCV	**MORV**	VSIV
MSPV	100															
CHNV	58.5															
ISFV	66.1	58.9														
PERV	65.6	54.7	61.1													
PIRV	62.8	56.1	61.8	66.1												
JURV	70.2	61.8	66.6	64.2	62.8											
YBV	53.7	49.6	53.9	52.5	52.5	55.4										
ABVV	48.0	48.0	48.9	49.4	49.4	49.9	49.6									
RADV	56.3	52.0	54.9	56.3	55.1	57.3	75.7	49.2								
VSNJV	55.8	50.4	52.3	55.6	52.3	54.4	53.2	47.0	56.1							
CARV	56.3	50.8	51.1	54.9	50.6	52.5	54.4	47.5	55.1	72.3						
MARV	56.6	50.1	51.3	55.4	53.0	53.7	53.5	46.5	55.6	69.2	73.7					
VSAV	55.4	48.7	52.0	55.6	52.7	54.9	54.9	45.3	55.8	69.2	74.9	82.6				
COCV	55.8	48.4	51.3	54.4	52.3	52.7	53.0	46.1	54.4	69.2	74.2	86.9	85.7			
MORV	54.9	51.1	51.8	55.6	53.7	54.4	53.7	47.0	55.6	68.5	74.9	89.0	83.3	83.8		
VSIV	56.6	51.1	51.8	55.8	54.2	54.2	54.4	46.5	57.0	69.0	75.9	90.2	84.7	84.0	90.5	100

Figure 3A. Amino acid sequence identities (p-distance) of N protein sequences as determined in MEGA 6.0.

	MSPV	CHNV	ISFV	**PERV**	PIRV	**JURV**	**YBV**	**ABVV**	**RADV**	VSNJV	CARV	MARV	VSAV	COCV	**MORV**	VSIV
MSPV	100															
CHNV	49.7															
ISFV	49.7	55.3														
PERV	51.8	54.5	51.6													
PIRV	51.1	54.5	51.8	59.0												
JURV	49.7	54.0	54.9	53.0	52.4											
YBV	44.5	46.6	43.5	48.0	49.5	47.0										
ABVV	29.6	26.7	27.1	27.5	29.0	28.2	27.3									
RADV	41.8	46.2	43.3	46.4	48.4	43.9	69.4	28.0								
VSNJV	39.8	39.1	38.3	40.2	39.3	38.1	36.0	26.5	35.8							
CARV	38.5	42.9	40.4	41.2	42.4	39.8	38.7	28.2	38.3	51.8						
MARV	37.5	42.2	39.8	39.5	40.8	38.7	37.1	27.3	38.9	50.3	57.1					
VSAV	39.1	42.0	38.9	41.4	40.4	38.7	37.5	26.1	37.7	48.2	55.9	65.0				
COCV	38.7	42.2	42.9	38.7	40.0	40.8	36.2	27.3	37.9	47.6	56.1	74.5	67.5			
MORV	39.3	42.4	42.2	40.2	40.0	39.5	38.9	26.9	39.1	49.9	57.8	79.3	65.2	73.7		
VSIV	37.7	40.8	41.6	39.3	40.2	38.9	37.9	26.3	38.1	51.1	57.1	79.3	64.2	72.9	86.3	100

Figure 3B. Amino acid sequence identities (p-distance) of G protein sequences as determined in MEGA 6.0.

	MSPV	CHNV	ISFV	**PERV**	**JURV**	**YBV**	**ABVV**	**RADV**	VSNJV	CARV	MARV	VSAV	COCV	**MORV**	VSIV
MSPV	100														
CHNV	68.2														
ISFV	69.1	69.2													
PERV	67.5	66.8	67.0												
JURV	68.3	66.3	66.7	65.0											
YBV	60.2	60.4	59.6	59.0	59.0										
ABVV	57.9	56.6	56.9	55.8	57.9	55.8									
RADV	61.8	62.3	62.1	60.5	61.1	72.8	56.8								
VSNJV	58.1	58.0	58.1	57.7	57.9	57.0	54.3	57.7							
CARV	60.3	59.6	59.7	59.8	59.5	58.7	54.8	58.5	70.2						
MARV	59.5	58.9	59.5	58.2	58.5	58.3	53.6	57.9	66.1	68.9					
VSAV	60.0	59.2	59.3	58.5	59.0	58.4	55.0	58.4	67.3	70.3	77.7				
COCV	60.3	59.0	59.2	58.8	59.2	58.6	54.2	58.9	65.9	69.4	79.4	78.8			
MORV	59.5	58.8	59.3	59.1	58.1	58.4	54.1	57.8	66.1	69.7	79.1	75.8	77.9		
VSIV	59.9	59.4	59.1	57.9	59.1	57.6	54.3	57.6	66.2	70.3	78.5	75.9	77.1	80.9	100

Figure 3C. Amino acid sequence identities (p-distance) of L protein sequences as determined in MEGA 6.0. Note: The PIRV L protein sequence is not currently available publically.

Table 1. Rhabdoviruses for which genome sequences have been used in this proposal.

Virus	**Abbrev.**	**Strain**	**Rhabdovirus genus**	**Species**	**Genome size (nt)**	**GenBank accession**
fecal fox rhabdovirus	FFRV	S40	not classified		15541+	KF823814
Arboretum virus	ABTV	LO-121	not classified		11492	KC994644
Puerto Almendras virus	PTAMV	LO-39	not classified		11876	KF534749
Rio Chico virus	RCHV	GAM-195	not classified		11286+	KX228197
Balsa virus	BALV	CoB 76	not classified		11287	KX228198
Coot Bay virus	CBV	EVG5-53	not classified		10869	KX228196
Tacheng tick virus 3	TTV3	TC255 (seq)	not classified		partial	KM817640
Wuhan tick virus 1	WTV1	X78-2 (seq)	not classified		10306+	KM817660
Bole tick virus 2	BoTV2	BL076	not classified		11843	KM817629
Huangpi tick virus 3	HTV3	H124-2 (seq)	not classified		13169+	KM817630
Taishun_Tick_virus	TaTV	BL198 (seq)	not classified		11280+	KM817643
Long Island tick rhabdovirus	LITRV	LS1	not classified		11176	KJ396935
Connecticut virus	CNTV	Ar1152-78	not classified		11169+	KM205020
Sawgrass virus	SAWV	64A-1247	not classified		11216	KM205013
New Minto virus	NMV	579	not classified		11156+	KM205009
Zarhedan rhabdovirus	ZARV	ArTeh157764	not classified		11230	KJ830812
Moussa virus	MOUV	D24	unassigned sp.	*Moussa virus*	11526	FJ985749
Muir Springs virus	MSV	76V-23524	not classified		12580	KM204990
Bahia Grande virus	BGV	TB4-1054	not classified		12639	KM205018
Harlingen virus	HARV	PV01-3828	not classified		12626	KM205003
Ikoma virus	IKOV	RV2508	*Lyssavirus*	*Ikoma lyssavirus*	11902	JX193798
West Caucasian bat virus	WCBV	NZ86	*Lyssavirus*	*West Caucasian bat lyssavirus*	12278	EF614258
Shimoni bat virus	SBV	N613	*Lyssavirus*	*Shimoni bat lyssavirus*	12045	GU170201
Lagos bat virus	LBV	0406SEN	*Lyssavirus*	*Lagos bat lyssavirus*	12016	EU293108
Mokola virus	MOKV	RV1035	*Lyssavirus*	*Mokola lyssavirus*	11939	KF155006
rabies virus	RABV	HN10	*Lyssavirus*	*Rabies lyssavirus*	11932	EU643590
Australian bat lyssavirus	ABLV	96-1256	*Lyssavirus*	*Australian bat lyssavirus*	11918	AF081020
Bokeloh bat lyssavirus	BBLV	21961	Lyssavirus	*Bokeloh bat lyssavirus*	11900	JF311903
European bat lyssavirus 2	EBLV2	RV1333	*Lyssavirus*	*European bat lyssavirus 2*	11930	EF157977
Khujand virus	KHUV		*Lyssavirus*	*Khujand lyssavirus*	11903	EF614261
Aravan virus	ARAV		*Lyssavirus*	*Aravan lyssavirus*	11918	EF614259
Duvenhage virus	DUVV	86132SA	*Lyssavirus*	*Duvenhage lyssavirus*	11976	EU293119
European bat lyssavirus 1	EBLV1	RV9	*Lyssavirus*	*European bat lyssavirus 1*	11966	EF157976
Irkut virus	IRKV	J426	*Lyssavirus*	*Irkut lyssavirus*	11980	EF614260
Ozernoe virus	OZEV	OI56	not classified		11980	FJ905105
North Creek virus #	NORCV	954	not classified		partial	KF360973
Riverside virus	RISV	Drava-1	not classified		11713	KU248085
Beaumont virus	BEAUV	6	not classified		partial	KF310911
Culex tritaeniorhynchus rhabdovirus	CTRV	GHK	not classified		11190	LC026102
Merida virus	MERDV	Mex-07	not classified		11798	KU194360
Shayang fly virus 2	SFV2	SYY1-8	not classified		12291+	KM817635
Wuhan fly virus 2	WFV2	SYY1-3	not classified		12247+	KM817646
Wuhan house fly virus 1	WHFV1	SYY2-4	not classified		12651+	KM817648
Drosophila melanogaster sigmavirus	DMelSV	HAP23	*Sigmavirus*	*Drosophila melanogaster sigmavirus*	12390+	GQ375258
Drosophila obscura sigmavirus	DObSV	10A	*Sigmavirus*	*Drosophila obscura sigmavirus*	12676+	NC022580
Pararge aegeria rhabdovirus	PAeRV		not classified		13062	KR822826
Fikirini virus	FKRV	KEN352	not classified		11139+	KC676792
Kolente virus	KOLEV	DakArK7292	not classified		11120	KC984953
Oita virus	OITAV	296-1972	not classified		11355+	KM204998
Kumasi rhabdovirus	KRV	M35	not classified		11072	KJ179955
Wuhan louse fly virus 5	WLFV5	BFJSC-5	not classified		11103+	KM817654
Mount Elgon bat virus	MEBV	BP846	not classified		10941+	KM205026
Kern Canyon virus	KCV	M03790	not classified		11528+	KM204992
Le Dantec virus	LDV	DakHD763	not classified		11450+	KM205006
Yongjia tick virus 2	YTV2	YJ1-2	not classified		10833	KM817662
Nkolbisson virus	NKOV	YM 31-65	not classified		10942+	KM205017
Nishimuro virus	NISV		not classified		10881+	AB609604
Barur virus	BARV	6235	not classified		10853+	KM204983
Fukuoka virus	FUKV	FUK-11	not classified		10863	KM205001
Keuraliba virus	KEUV	DakAnD5314	not classified		11457+	KM205021
hybrid snakehead virus	HSV	C1207	not classified		11545	KC519324
Siniperca chuatsi rhabdovirus	SCRV		not classified		11545	DQ399789
dolphin rhabdovirus	DRV	pxV1	not classified		11141	KF958252
eel virus European X	EVEX	153311	*Perhabdovirus*	*Anguillid perhabdovirus*	11806	FN557213
perch rhabdovirus	PRV	J424	*Perhabdovirus*	*Perch perhabdovirus*	11487+	JX679246

Scophthalmus maximus rhabdovirus	SMRV		not classified		11492	HQ003891
pike fry rhabdovirus	PFRV	F4	*Sprivivirus*	*Pike fry sprivivirus*	11097	FJ872827
spring viremia of carp virus	SVCV	VR-1390	*Sprivivirus*	*Carp sprivivirus*	11019	AJ318079
Wuhan louse fly virus 11	WLFV11	BFJSC-9	not classified		partial	KM817658
Malpais Spring virus	MSPV	85-488NM	*Vesiculovirus**	*Malpais Spring vesiculovirus*	11019	KC412247
Chandipura virus	CHNV	CIN0451	*Vesiculovirus*	*Chandipura vesiculovirus*	11120	GU212856
Isfahan virus	ISFV	91026-167	*Vesiculovirus*	*Isfahan vesiculovirus*	11088	AJ810084
Perinet virus	PERV	DakArMg802	*Vesiculovirus**	*Perinet vesiculovirus*	11103+	HM566195
Piry virus	PIRV	BeAn24232	*Vesiculovirus*	*Piry vesiculovirus*	partial	D26175
Jurona virus	JURV	BeAr40578	*Vesiculovirus**	*Jurona vesiculovirus*	11121+	KM204996
Yug Bogdanovac virus	YBV	Yu4-76	*Vesiculovirus**	*Yug Bogdanovac vesiculovirus*	11202	JF911700
American bat vesiculovirus	ABVV	TFFN-2013	*Vesiculovirus**	*American bat vesiculovirus*	10651+	JX569193
Radi virus	RADV	ISS Phl-166	*Vesiculovirus**	*Radi vesiculovirus*	11068+	KM205024
vesicular stomatitis New Jersey virus	VSNJV	NJ89GAS	*Vesiculovirus*	*New Jersey vesiculovirus*	11123	JX121110
Carajas virus	CARV	BeAr411391	*Vesiculovirus*	*Carajas vesiculovirus*	10716+	KM205015
Maraba virus	MARV	BeAr411459	*Vesiculovirus*	*Maraba vesiculovirus*	11135	HQ660076
vesicular stomatitis Alagoas virus	VSAV	Indiana 3	*Vesiculovirus*	*Alagoas vesiculovirus*	11070	EU373658
Cocal virus	COCV	TRVL40233	*Vesiculovirus*	*Cocal vesiculovirus*	11003	EU373657
Morreton virus	MORV	CoAr191048	*Vesiculovirus**	*Morreton vesiculovirus*	11181+	KM205007
vesicular stomatitis Indiana virus	VSIV	98COE	*Vesiculovirus*	*Indiana vesiculovirus*	11161	AF473864
Klamath virus	KLAV	M-1056	not classified		11478+	KM204999
tupaia rhabdovirus	TUPV		*Tupavirus*	*Tupaia tupavirus*	11440	AY840978
Durham virus	DURV	CC228-C5	*Tupavirus*	Durham tupavirus	11092+	FJ952155
Niakha virus	NIAV	DakArD88909	not classified		11124	KC585008
Sripur virus	SRIV	733646	not classified		11290+	KM205023
Almpiwar virus	ALMV	MRM4059	not classified		11156	KJ399977
Chaco virus	CHOV	BeAn42217	not classified		11397+	KM205000
Sena Madureira virus	SMV	BeAn303197	not classified		11422+	KM205004
Timbo virus	TIMV	BeAn41787	not classified		partial	na
Kwatta virus	KWAV	A-57	not classified		11211+	KM204985
Oak Vale virus	OVRV	K13965	not classified		11220	JF705877
Garba virus	GARV	DakAnB439a	not classified		10821+	KM204982
Sunguru virus	SUNV	UG#41	not classified		11056	KF395226
Harrison Dam virus	HARDV	CS75	not classified		11284+	KJ432573
Walkabout Creek virus	WACV	CS1056	not classified		11214	KJ432572
Lepeophtheirus salmonis rhabdovirus 9	LSRV-9		not classified		11681+	KJ958535
Lepeophtheirus salmonis rhabdovirus 127	LSRV-127		not classified		11519+	KJ958536
Xiburema virus	XIBV	BeAr362159	not classified		12240	KJ636781
Aruac virus	ARUV	TRVL9223	not classified		11906+	KM204987
Inhangapi virus	INHV	BeAr177325	not classified		12026	KM204991
Santa Barbara virus	SBAV	Ar775619	not classified		12162	KM350503
Itacaiunas virus	ITAV	BeAr427036	not classified		12536+	KM204984
Iriri virus	IRIRV	BeAr408005	not classified		13070	KM204995
Curionopolis virus	CURV	BeAr440009	not classified		13170	KM204994
Rochambeau virus	RBUV	CaAr16102	not classified		13593	KM205012
Kamese virus	KAMV	MP6186	not classified		13209	KM204989
Mossuril virus	MOSV	SAAr1995	not classified		13106+	KM204993
Flanders virus	FLAV	61-7484	unassigned	*Flanders virus*	13038	KM205002
Hart Park virus	HPV	AR7C	not classified		13104	KM205011
Mosqueiro virus	MQOV	BeAr185559	not classified		12957	KM205014
Landjia virus	LJAV	DakAnB769d	not classified		13695+	KM205010
Manitoba virus	MANV	Mn936-77	not classified		13784+	KM205008
Gray Lodge virus	GLOV	BFN3187	not classified		12403	KM205022
Marco virus	MCOV	BeAn40290	not classified		13294+	KM205005
Joinjakaka virus	JOIV	AusMK7937	not classified		13155	KM205016
Ngaingan virus	NGAV	MRM14556	unassigned	*Ngaingan virus*	15764	NC013955
La Joya virus	LJV	J-134	not classified		15721	KM204986
Wongabel virus	WONV	CS264	unassigned	*Wongabel virus*	13196	NC011639
Ord River virus	ORV	OR1023	not classified		13189+	KM205025
Parry Creek virus	PCV	OR189	not classified		13205+	KM204988
Bivens Arm virus	BAV	UF-10	not classified		13288+	KM205019
Tibrogargan virus	TIBV	CS132	*Tibrovirus*	*Tibrogargan tibrovirus*	13298	GQ294472
Sweetwater Branch virus	SWBV	UF-11	not classified		13141+	KM204997
Coastal Plains virus	CPV	DPP53	*Tibrovirus*	*Coastal Plains tibrovirus*	13203	GQ294473
Ekpoma virus-1	EKV-1		not classified		12,659+	KP324827
Ekpoma virus-2	EKV-2		not classified		12,674+	KP324828
Bas Congo virus	BASV	BASV-1	not classified		11892+	JX297815
Koolpinyah virus	KOOLV	DPP833/819	not classified		16133	KM085029
Kotonkan virus	KOTV	IbAr23380	*Ephemerovirus*	*Kotonkan ephemerovirus*	15870	HM474855
Yata virus	YATV	DakArB2181	not classified		14479	KM085030

Adelaide River virus	ARV	DPP61	*Ephemerovirus*	*Adelaide River ephemerovirus*	14627	JN935380
Obodhiang virus	OBOV	SudAr1154-64	*Ephemerovirus*	*Obodhiang ephemerovirus*	14717	HM856902
Kimberley virus	KIMV	CS368	not classified		15442	JQ941664
bovine ephemeral fever virus	BEFV	BB7721	*Ephemerovirus*	*Bovine fever ephemerovirus*	14900	AF234533
Berrimah virus	BRMV	DPP63	*Ephemerovirus*	*Berrimah ephemerovirus*	15024	HM461974

* Taxonomic assignments proposed here.
+ Complete coding sequences only.