



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**

<b>Code assigned:</b>	<b>2016.007a-dM</b>	(to be completed by ICTV officers)			
<b>Short title:</b> One new genus ( <i>Sripuvirus</i> ) in the family <i>Rhabdoviridae</i> , including 5 new species. (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input checked="" type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

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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:**

All members have reviewed the proposal advised their support.

Date first submitted to ICTV:

June 2016

Date of this revision (if different to above):

**ICTV-EC comments and response of the proposer:**

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## 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	<b>2016.007aM</b>	(assigned by ICTV officers)
<b>To create 5 new species within:</b>		
Genus:	<i>Sripuvirus</i> (new)	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Niakha sripuvirus</i> (reassigned)	Niakha virus (NIAV; DakArD88909)	KC585008
<i>Sripur sripuvirus</i>	Sripur virus (SRIV; 733646)	KM205023
<i>Almpiwar sripuvirus</i>	Almpiwar virus (ALMV; MRM4059)	KJ399977
<i>Chaco sripuvirus</i>	Chaco virus (CHOV; BeAn42217)	KM205000
<i>Sena Madureira sripuvirus</i>	Sena Madureira virus (SMV; BeAn303197)	KM205004

### 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 will be defined as follows (see also module 3):

Viruses assigned to different species within the genus *Sripuvirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; D) significant differences in genome organization as evidenced by numbers and locations of ORFs; E) can be distinguished in virus neutralisation tests; and F) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.

The viruses assigned to the new genus *Sripuvirus* have genomes (**Figure 1**) containing the five canonical rhabdovirus structural protein genes (N, P, M, G and L) and multiple additional long ORFs. They share the common features of: i) a consecutive ORF (Mx) in the M gene for which the initiation codon overlaps the termination codon of the M ORF; and ii) an ORF (Gx) in an alternative reading frame near the start of the G gene. Mx ORFs encode small basic proteins; Gx ORFs encode small double-membrane-spanning proteins (**Figure 2**). Sripuviruses form a monophyletic group based on well-supported ML trees generated from complete L protein sequences (**Figure 3**). Known characteristics of the viruses of taxonomic significance are

summarized here. The basis of assignment of the viruses as 5 distinct species in this genus is described under the genus proposal (**module 3**).

### ***Niakha sripuvirus***

Niakha virus (NIAV) was isolated from a mixed pool of 200 sandflies (*Phlebotomus duboscqi* and *Sergentomyia* sp.) collected at Niakha in Senegal in 1992<sup>1</sup>. It was found to be unrelated by complement-fixation tests to 23 other rhabdoviruses, including 19 that had been isolated previously in Africa<sup>2</sup>. The complete NIAV genome (11,124 nt) has been sequenced (**Figure 1**)<sup>2</sup>. The genome is typical of sripuviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and three other long ORFs<sup>3</sup>. The Mx ORF (also called U1) lies in the M gene with the initiation codon overlapping the termination codon of the M ORF; it encodes an 81-aa basic protein (9.4 kDa) (**Figure 2**). The Gx ORF (also called U2) lies in an alternative reading frame near the start of the G gene; it encodes a 97-aa double-membrane-spanning protein (10.8 kDa) (**Figure 2**). The Lx ORF (also called U3) lies in an alternative reading frame near the start of the L gene; it encodes a 51-aa highly basic protein (6.4 kDa). Phylogenetic analysis of L protein sequences (**Figure 3**)<sup>3</sup> and amino acid sequence identity in the N, L and G proteins (**Figure 4**) indicate that NIAV lies in the sripuvirus clade and is most closely related to Sripur virus (SRIV).

### ***Sripur sripuvirus***

Sripur virus (SRIV) was isolated from sandflies (*Sergentomyia* sp.) collected in Asansol, West Bengal, India in 1973<sup>4</sup>. It was found to be unrelated by indirect immunofluorescence to 89 rhabdoviruses tested, including Almpiwar virus (ALMV)<sup>5</sup>. Complete coding regions (11,290 nt) of the SRIV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1**)<sup>3</sup>. The genome is typical of sripuviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and six other long ORFs. ORF Nx and ORF Ny lie in alternative reading frames in the N gene; they encode small proteins (62-aa and 64-aa, respectively) for which the initiation codons are in unfavourable Kozak context and so they may not be expressed. The U1 ORF lies in an independent transcriptional unit (gene) between the N gene and P gene; it encodes a 66-aa protein (8.0 kDa). The Px ORF lies in an alternative reading frame near the start of the P gene; it encodes a 183-aa highly basic protein (21.9 kDa). The Mx ORF lies in the M gene with the initiation codon overlapping the termination codon of the M ORF; it encodes an 80-aa basic protein (9.7 kDa) (**Figure 2**). The Gx ORF lies in an alternative reading frame near the start of the G gene; it encodes a 99-aa double-membrane-spanning protein (11.1 kDa) (**Figure 2**). Phylogenetic analysis of L protein sequences (**Figure 3**)<sup>3</sup> and amino acid sequence identity in the N, L and G proteins (**Figure 4**) indicate that SRIV lies in the sripuvirus clade and is most closely related to NIAV.

### ***Almpiwar sripuvirus***

Almpiwar virus (ALMV) was isolated from a skink (*Ablepharus boutonii virgatus*) trapped at Kowanyama, Queensland, Australia, in 1966<sup>4,6</sup>. It was found to be unrelated by indirect immunofluorescence tests to 89 rhabdoviruses, including Sripur virus (SRIV)<sup>5</sup>. The complete ALMV genome (11,156 nt) has been sequenced (**Figure 1**)<sup>7</sup>. The genome is typical of sripuviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and four other long ORFs. ORF Nx lies in an alternative reading frame towards the end of the N gene; it encodes a 102-aa highly basic protein (12.2 kDa) for which the initiation codon is in favourable Kozak context. The Px ORF lies in an alternative reading frame near the start of the P gene; it encodes a 126-aa highly basic protein (15.4 kDa). The Mx ORF lies in the M gene with the initiation codon overlapping the termination codon of the M ORF; it encodes a 79-aa basic protein (9.5 kDa) (**Figure 2**). The Gx ORF lies in an alternative reading frame near the start of the G gene; it encodes a 94-aa double-membrane-spanning

protein (10.4 kDa) (**Figure 2**). Phylogenetic analysis of L protein sequences indicates that ALMV lies centrally in the sripuvirus clade (**Figure 3**) and amino acid sequence identity in the N, L and G proteins (**Figure 4**) indicate ALMV shares similar levels of identity with all other sripuviruses.

#### ***Chaco sripuvirus***

Chaco virus (CHOV) was isolated from a lizard (*Ameiva ameiva ameiva*) near Belem, Para, Brazil in 1962<sup>8</sup>. CHOV was found to cross-react in CF tests with Timbo virus (TIMV) which was isolated from the same species of lizard at the same location approximately one week earlier<sup>8,9</sup> and with Sena Madureira virus (SMV; see below)<sup>5,10</sup>. Complete coding regions (11,397 nt) of the CHOV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1**)<sup>3</sup>. The genome is typical of sripuviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and three other long ORFs. ORF U1 lies in an independent transcriptional unit (gene) between the N gene and P gene; it encodes a highly acidic 115-aa protein (13.6 kDa) (**Figure 2**). The Mx ORF lies in the M gene with the initiation codon overlapping the termination codon of the M ORF; it encodes a 79-aa basic protein (9.5 kDa) (**Figure 2**). The Gx ORF lies in an alternative reading frame near the start of the G gene; it encodes a 99-aa double-membrane-spanning protein (10.9 kDa) (**Figure 2**). Phylogenetic analysis of L protein sequences (**Figure 3**)<sup>3</sup> and amino acid sequence identity in the N, L and G proteins (**Figure 4**) indicate that CHOV lies in the sripuvirus clade and is most closely related to SMV and TIMV.

#### ***Sena Madureira sripuvirus***

Sena Madureira virus (SMV) was isolated from a lizard (*Ameiva ameiva ameiva*) at Sena Madureira, Acre, Brazil, in 1976<sup>4</sup>. SMV was found to cross-react in CF tests with CHOV and TIMV<sup>10</sup>. Complete coding regions (11,422 nt) of the SMV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1**)<sup>3</sup>. The genome is typical of sripuviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and three other long ORFs. ORF U1 lies in an independent transcriptional unit (gene) between the N gene and P gene; it encodes a highly acidic 115-aa protein (13.7 kDa) (**Figure 2**). The Mx ORF lies in the M gene with the initiation codon overlapping the termination codon of the M ORF; it encodes a 79-aa basic protein (9.4 kDa) (**Figure 2**). The Gx ORF lies in an alternative reading frame near the start of the G gene; it encodes a 99-aa double-membrane-spanning protein (10.7 kDa) (**Figure 2**). Phylogenetic analysis of L protein sequences (**Figure 3**)<sup>3</sup> and amino acid sequence identity in the N, L and G proteins (**Figure 4**) indicate that SMV lies in the sripuvirus clade and is most closely related to CHOV and TIMV.

Each of these viruses meet species demarcation criteria A, B, C, D and F. No neutralisation test data are yet available but lack of cross reactivity in CF and IFA tests suggest that species demarcation criterion E would also be met if tested.

**Note: Although Timbo virus (TIMV) is related antigenically to CHOV and SMV<sup>8,10</sup>, and phylogenetic analysis of L protein sequences (Figure 3) indicate that it falls within the sripuvirus clade, it has not been assigned to a new species in this proposal as the complete coding-sequence is not yet available.**

### MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	<b>2016.007bM</b>	(assigned by ICTV officers)
<b>To create a new genus within:</b>		
Subfamily:		Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no family is specified, enter “ <b>unassigned</b> ” in the family box
Family:	<i>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	

naming a new genus

Code	<b>2016.007cM</b>	(assigned by ICTV officers)
<b>To name the new genus: <i>Sripuvirus</i></b>		

Assigning the type species and other species to a new genus

Code	<b>2016.007dM</b>	(assigned by ICTV officers)
<b>To designate the following as the type species of the new genus</b>		
<i>Niakha sripuvirus</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
<p>The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). <b>Please enter here the TOTAL number of species (including the type species) that the genus will contain:</b></p> <p><b>5 Species:</b>  <i>Niakha sripuvirus</i> (type species)  <i>Sripur sripuvirus</i>  <i>Almpiwar sripuvirus</i>  <i>Chaco sripuvirus</i>  <i>Sena Madureira sripuvirus</i></p>		

#### **Reasons to justify the creation of a new genus:**

Additional material in support of this proposal may be presented in the Appendix, Module 9

The *Rhabdoviridae* is a large and diverse family of viruses. There are currently 11 approved genera in the *Rhabdoviridae*. However, many rhabdoviruses remain unclassified. Here, we propose the establishment of a new genus (*Sripuvirus*) that will include 5 new species. Three of the viruses to be assigned to the proposed genus were isolated from reptiles and two were isolated from sandflies (*Phlebotomus duboscqi* and *Sergentomyia* spp.). The viruses form a distinct clade in a well-supported (BSP  $\geq$  85) tree based on full length L protein (RdRp) sequences (**Figure 3**). The clade is linked phylogenetically to the approved genus *Tupavirus* (infecting birds and tree shrew), and to a clade of unclassified viruses that were isolated from birds or mosquitoes or midges (KWAV, OVRV, GARV, SUNV, WACV and HARDV; see **Table 1**). Complete or near-complete genome sequences are known for each of the viruses to be assigned to the genus.

Sripuvirus genomes are similar in size (~11,000 - 11,500 nt) and contain multiple ORFs encoding likely accessory proteins (**Figure 1**). The genomes all feature a consecutive ORF (Mx) in the M gene for which the initiation codon overlaps the termination codon of the M ORF; the Mx ORFs encode small basic proteins. ‘Termination upstream ribosome-binding site’ (TURBS)-like sequence motifs typically occur upstream of the overlapping stop-start codons, suggesting the mechanism for expression<sup>3</sup>. Sripuvirus genomes also feature an alternative ORF (Gx) near the start of the G gene; Gx ORFs encode small double-membrane-spanning proteins. The Gx proteins are likely to be expressed by ‘leaky’ ribosomal scanning<sup>3</sup>.

Antigenic cross-reactions (CF test) have been reported between some members of the genus and these viruses (CHOV and SMV) have been assigned to the Timbo serogroup<sup>10</sup>. TIMV is also a likely member of the genus but its complete genome sequence has not yet been reported.

**Origin of the new genus name:**

The name is derived as a siglum from Sripur virus, one of the foundation members of the genus.

**Reasons to justify the choice of type species:**

Niakha virus (type species *Niakha sripuvirus*) is the best characterized virus in the new genus in terms of ecology, morphology, histopathology, molecular and generic structure and evolutionary analysis<sup>1, 2, 3</sup>.

**Species demarcation criteria in the new genus:**

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

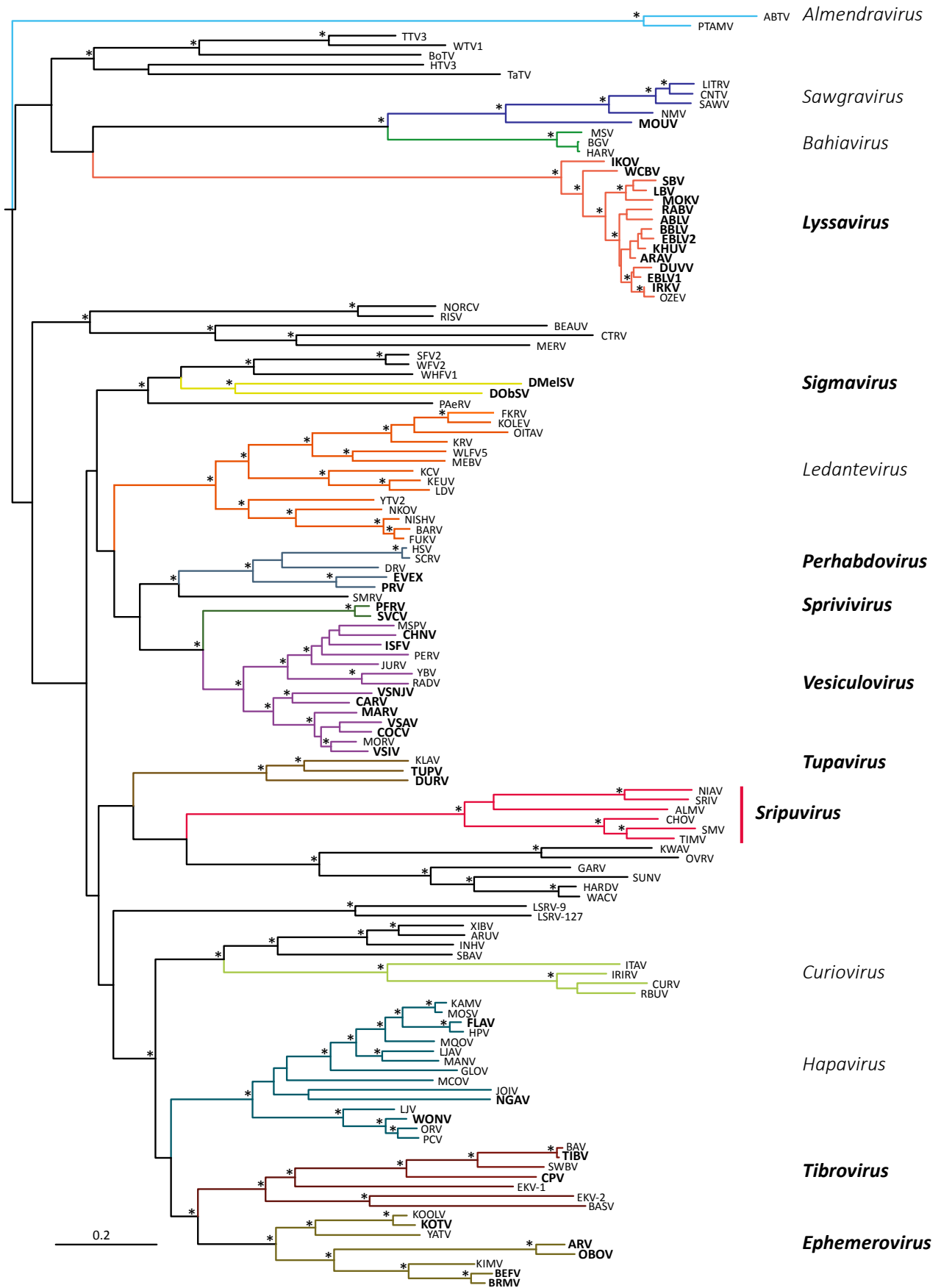
Viruses assigned to different species within the genus *Sripuvirus* display several of the following characteristics: A) minimum amino acid sequence divergence of 5% in N proteins; B) minimum sequence divergence of 10% in the L proteins; C) minimum amino acid sequence divergence of 15% in G proteins; 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.

**References:**

1. Fontenille D, Traore-Lamizana M, Trouillet J, Leclerc A, Mondo M, Ba Y, Digoutte JP, Zeller HG, 1994. First isolations of arboviruses from phlebotomine sand flies in West Africa. *The American Journal of Tropical Medicine and Hygiene* 50: 570-574.
2. Vasilakis N, Widen S, Mayer SV, Seymour R, Wood TG, Popov V, Guzman H, Travassos da Rosa AP, Ghedin E, Holmes EC, Walker PJ, Tesh RB, 2013. Niakha virus: a novel member of the family Rhabdoviridae isolated from phlebotomine sandflies in Senegal. *Virology* 444: 80-89.
3. Walker PJ, Firth C, Widen SG, Blasdel KR, Guzman H, Wood TG, Paradkar PN, Holmes EC, Tesh RB, Vasilakis N, 2015. Evolution of genome size and complexity in the *Rhabdoviridae*. *PLoS Pathogens* 11: e1004664.
4. Karabatsos N, 1985. *International Catalogue of Arboviruses Including Certain other Viruses of Vertebrates*. San Antonio: American Society for Tropical Medicine and Hygiene.
5. Calisher CH, Karabatsos N, Zeller H, Digoutte J-P, Tesh RB, Shope RE, Travassos da Rosa APA, St. George TD, 1989. Antigenic relationships among rhabdoviruses from vertebrates and hematophagous arthropods. *Intervirology* 30: 241-257.
6. Doherty RL, Whitehead RH, Wetters EJ, Gorman BM, Carley JG, 1970. A survey of antibody to 10 arboviruses (Koongol group, Mapputta group and ungrouped) isolated in Queensland. *Transactions of the Royal Society for Tropical Medicine and Hygiene* 64: 748-753.
7. McAllister J, Gauci PJ, Mitchell IR, Boyle DB, Bulach DM, Weir RP, Melville LF, Davis SS, Gubala AJ, 2014. Genomic characterisation of Almpiwar virus, Harrison Dam virus and Walkabout Creek virus; three novel rhabdoviruses from northern Australia. *Virology Reports* 3: 1-17.
8. Causey OR, Shope RE, Bensabath G, 1966. Marco, Timbo, and Chaco, newly recognized arboviruses from lizards of Brazil. *American Journal Tropical Medicine and Hygiene* 15: 239-243.
9. Monath TP, Cropp CB, Frazier CL, Murphy FA, Whitfield SG, 1979. Viruses isolated from reptiles: identification of three new members of the family *Rhabdoviridae*. *Archives of Virology* 60: 1-12.
10. Tesh RB, Travassos da Rosa APA, Travassos da Rosa JS, 1983. Antigenic relationship among rhabdoviruses infecting terrestrial vertebrates. *Journal of General Virology* 64: 169-176.







**Figure 3.** ML phylogenetic tree of 132 animal rhabdovirus L protein sequences. Branches are colour-coded according to existing genera (named in bold italics) or proposed new genera (named light italics) Walker *et al.* (2015) PLoS Pathogens 11 (2): e1004664<sup>3</sup>. The clade representing the proposed new genus *Sripuvirus* is highlighted. Horizontal branch lengths are drawn to a scale of

amino acid substitutions/site, and all bootstrap support values (BSP)  $\geq 75\%$  are shown by the \* symbol. The tree is rooted 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. *Cytorhabdovirus*, *novirhabdovirus* and *nucleorhabdovirus* outgroup sequences were excluded from the tree as they were too divergent to establish a reliable rooting. The tree is therefore rooted arbitrarily on one of two basal clades (potential new genera *Almendravirus* and *Bahiavirus*) that comprise viruses isolated from mosquitoes. The ML tree was generated as described in Walker *et al.* (2015) PLoS Pathogens 11 (2): e1004664<sup>3</sup>. Virus abbreviations and GenBank accession numbers are as listed in **Table 1**.

	NIAV	SRIV	ALMV	CHOV	SMV
NIAV	100				
SRIV	64.3	100			
ALMV	35.0	35.0	100		
CHOV	29.9	31.8	31.8	100	
SMV	31.1	33.0	30.1	74.0	100

**Figure 4A.** Sripuvirus N protein amino acid sequence identity (%; as estimated in MEGA6 by p-distance).

	NIAV	SRIV	ALMV	CHOV	SMV
NIAV	100				
SRIV	67.1	100			
ALMV	48.9	49.4	100		
CHOV	47.9	48.1	48.2	100	
SMV	47.6	47.6	48.1	70.7	100

**Figure 4B.** Sripuvirus L protein amino acid sequence identity (%; as estimated in MEGA6 by p-distance).

	NIAV	SRIV	ALMV	CHOV	SMV
NIAV	100				
SRIV	62.5	100			
ALMV	45.6	47.0	100		
CHOV	39.7	40.1	41.5	100	
SMV	40.9	42.1	41.5	66.5	100

**Figure 4C.** Sripuvirus G protein amino acid sequence identity (%; as estimated in MEGA6 by p-distance).

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

Virus	Abbrev.	Strain	Rhabdovirus genus	Species	Genome size (nt)	GenBank accession
Arboretum virus	ABTV	LO-121	not classified		11492	KC994644
Puerto Almendras virus	PTAMV	LO-39	not classified		11876	KF534749
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
Moussa virus	MOUV	D24	unassigned sp.	<i>Moussa virus</i>	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	I KOV	RV2508	<i>Lyssavirus</i>	<i>Ikoma lyssavirus</i>	11902	JX193798
West Caucasian bat virus	WCBV	NZ86	<i>Lyssavirus</i>	<i>West Caucasian bat lyssavirus</i>	12278	EF614258
Shimoni bat virus	SBV	N613	<i>Lyssavirus</i>	<i>Shimoni bat lyssavirus</i>	12045	GU170201
Lagos bat virus	LBV	0406SEN	<i>Lyssavirus</i>	<i>Lagos bat lyssavirus</i>	12016	EU293108
Mokola virus	MOKV	RV1035	<i>Lyssavirus</i>	<i>Mokola lyssavirus</i>	11939	KF155006
rabies virus	RABV	HN10	<i>Lyssavirus</i>	<i>Rabies lyssavirus</i>	11932	EU643590
Australian bat lyssavirus	ABLV	96-1256	<i>Lyssavirus</i>	<i>Australian bat lyssavirus</i>	11918	AF081020
Bokeloh bat lyssavirus	BBLV	21961	<i>Lyssavirus</i>	<i>Bokeloh bat lyssavirus</i>	11900	JF311903
European bat lyssavirus 2	EBLV2	RV1333	<i>Lyssavirus</i>	<i>European bat lyssavirus 2</i>	11930	EF157977
Khujand virus	KHUV		<i>Lyssavirus</i>	<i>Khujand lyssavirus</i>	11903	EF614261
Aravan virus	ARAV		<i>Lyssavirus</i>	<i>Aravan lyssavirus</i>	11918	EF614259
Duvenhage virus	DUVV	86132SA	<i>Lyssavirus</i>	<i>Duvenhage lyssavirus</i>	11976	EU293119
European bat lyssavirus 1	EBLV1	RV9	<i>Lyssavirus</i>	<i>European bat lyssavirus 1</i>	11966	EF157976
Irkut virus	IRKV	J426	<i>Lyssavirus</i>	<i>Irkut lyssavirus</i>	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	SY1-8	not classified		12291+	KM817635
Wuhan fly virus 2	WV2	SY1-3	not classified		12247+	KM817646
Wuhan house fly virus 1	WHFV1	SY2-4	not classified		12651+	KM817648
Drosophila melanogaster sigmavirus	DMelSV	HAP23	<i>Sigmavirus</i>	<i>Drosophila melanogaster sigmavirus</i>	12390+	GQ375258
Drosophila obscura sigmavirus	DObsSV	10A	<i>Sigmavirus</i>	<i>Drosophila obscura sigmavirus</i>	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	<i>Perhabdovirus</i>	<i>Anguillid perhabdovirus</i>	11806	FN557213
perch rhabdovirus	PRV	J424	<i>Perhabdovirus</i>	<i>Perch perhabdovirus</i>	11487+	JX679246
Scophthalmus maximus rhabdovirus	SMRV		not classified		11492	HQ003891
pike fry rhabdovirus	PFRV	F4	<i>Sprivivirus</i>	<i>Pike fry sprivivirus</i>	11097	FJ872827
spring viremia of carp virus	SVCV	VR-1390	<i>Sprivivirus</i>	<i>Carp sprivivirus</i>	11019	AJ318079
Malpais Spring virus	MSPV	85-488NM	not classified		11019	KC412247
Chandipura virus	CHNV	CIN0451	<i>Vesiculovirus</i>	<i>Chandipura vesiculovirus</i>	11120	GU212856
Isfahan virus	ISFV	91026-167	<i>Vesiculovirus</i>	<i>Isfahan vesiculovirus</i>	11088	AJ810084

Perinet virus	PERV	DakArMg802	not classified		11103+	HM566195
Jurona virus	JURV	BeAr40578	not classified		11121+	KM204996
Yug Bogdanovac virus	YBV	Yu4-76	not classified		11202	JF911700
Radi virus	RADV	ISS PhI-166	not classified		11068+	KM205024
vesicular stomatitis New Jersey virus	VSNJV	NJ89GAS	<i>Vesiculovirus</i>	<i>New Jersey vesiculovirus</i>	11123	JX121110
Carajas virus	CARV	BeAr411391	<i>Vesiculovirus</i>	<i>Carajas vesiculovirus</i>	10716+	KM205015
Maraba virus	MARV	BeAr411459	<i>Vesiculovirus</i>	<i>Maraba vesiculovirus</i>	11135	HQ660076
vesicular stomatitis Alagoas virus	VSAV	Indiana 3	<i>Vesiculovirus</i>	<i>Alagoas vesiculovirus</i>	11070	EU373658
Cocal virus	COCV	TRVL40233	<i>Vesiculovirus</i>	<i>Cocal vesiculovirus</i>	11003	EU373657
Morreton virus	MORV	CoAr191048	not classified		11181+	KM205007
vesicular stomatitis Indiana virus	VSVI	98COE	<i>Vesiculovirus</i>	<i>Indiana vesiculovirus</i>	11161	AF473864
Klamath virus	KLAV	M-1056	not classified		11478+	KM204999
tupaia rhabdovirus	TUPV		<i>Tupavirus</i>	<i>Tupaia tupavirus</i>	11440	AY840978
Durham virus	DURV	CC228-C5	<i>Tupavirus</i>	<i>Durham tupavirus</i>	11092+	FJ952155
Niakha virus	NAV	DakArD88909	<i>Sripuvirus*</i>	<i>Niakha sripuvirus</i>	11124	KC585008
Sripur virus	SRIV	733646	<i>Sripuvirus*</i>	<i>Sripur sripuvirus</i>	11290+	KM205023
Almpiwar virus	ALMV	MRM4059	<i>Sripuvirus*</i>	<i>Almpiwar sripuvirus</i>	11156	KJ399977
Chaco virus	CHOV	BeAn42217	<i>Sripuvirus*</i>	<i>Chaco sripuvirus</i>	11397+	KM205000
Sena Madureira virus	SMV	BeAn303197	<i>Sripuvirus*</i>	<i>Sena Madureira sripuvirus</i>	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
Iri virus	IRIV	BeAr408005	not classified		13070	KM204995
Curionopolis virus	CURV	BeAr440009	not classified		13170	KM204994
Rochambeau virus	RBV	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 sp.	<i>Flanders virus</i>	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 sp.	<i>Ngaingan virus</i>	15764	NC013955
La Joya virus	LJV	J-134	not classified		15721	KM204986
Wongabel virus	WONV	CS264	unassigned sp.	<i>Wongabel virus</i>	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	<i>Tibrovirus</i>	<i>Tibrogargan tibrovirus</i>	13298	GQ294472
Sweetwater Branch virus	SWBV	UF-11	not classified		13141+	KM204997
Coastal Plains virus	CPV	DPP53	<i>Tibrovirus</i>	<i>Coastal Plains tibrovirus</i>	13203	GQ294473
Ekpoma-1 virus	EKV-1		not classified		12,659+	KP324827
Ekpoma-2 virus	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	<i>Ephemerovirus</i>	<i>Kotonkan ephemerovirus</i>	15870	HM474855
Yata virus	YATV	DakArB2181	not classified		14479	KM085030
Adelaide River virus	ARV	DPP61	<i>Ephemerovirus</i>	<i>Adelaide River ephemerovirus</i>	14627	JN935380
Obodhiang virus	OBOV	SudAr1154-64	<i>Ephemerovirus</i>	<i>Obodhiang ephemerovirus</i>	14717	HM856902
Kimberley virus	KIMV	CS368	not classified		15442	JQ941664
bovine ephemeral fever virus	BEFV	BB7721	<i>Ephemerovirus</i>	<i>Bovine fever ephemerovirus</i>	14900	AF234533
Berrimah virus	BRMV	DPP63	<i>Ephemerovirus</i>	<i>Berrimah ephemerovirus</i>	15024	HM461974

\* Taxonomic assignments proposed here.

+ Complete coding sequences only.