



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:	2016.008aM	(to be completed by ICTV officers)			
Short title: 4 new species in the genus <i>Tibrovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input type="checkbox"/>	5 <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	2016.008aM	(assigned by ICTV officers)
To create 4 new species within:		
Genus:	<i>Tibrovirus</i>	Fill in all that apply. <ul style="list-style-type: none"> • 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.
Subfamily:		
Family:	<i>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)
<i>Sweetwater Branch tibrovirus</i>	Sweetwater Branch virus (SWBV; UF-11)	KM204997
<i>Bas-Congo tibrovirus</i>	Bas-Congo virus (BASV)	JX297815
<i>Ekpoma 1 tibrovirus</i>	Ekpoma virus 1 (EKV-1)	KP324827
<i>Ekpoma 2 tibrovirus</i>	Ekpoma virus 2 (EKV-2)	KP324828

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:

“The species demarcation criteria are based on low-level or no cross-reaction in virus-neutralisation tests supported by phylogenetic analysis and genetic diversity estimations using L and N gene sequences to establish that the species represents a distinct lineage. Typically, there will be <5% amino acid sequence diversity (divergence) within species and >20% diversity (divergence) between species.” (Tibrovirus genus proposal, ICTV, 2011)

Like the viruses that have been assigned to existing species (*Tibrogargan tibrovirus* and *Coastal Plains tibrovirus*), the viruses we propose here to be assigned to new species in the genus *Tibrovirus* share the same unique genome organisation (3′N-P-M-U1-U2-G-U3-L5′), comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L), and three additional genes encoding long ORFs (U1, U2 and U3) (**Figure 1**). ORF U1 and ORF U2 encode small proteins with unknown functions; ORF U3 encodes a small viroporin-like transmembrane protein. Each ORF lies within an independent transcriptional unit bounded by consensus transcription initiation and transcription termination/polyadenylation sequences. The viruses also form a monophyletic clade in a maximum likelihood tree inferred from complete L protein sequences of 132 animal rhabdoviruses (**Figure 2**). Species are demarcated according to the criteria specified above, including amino acid sequence divergence in the N and L proteins (**Figure 3**).

a. *Sweetwater Branch tibrovirus*

Sweetwater Branch virus (SWBV) strain UF-11 was isolated in 1981 from biting midges (*Culicoides insignis*) collected near water buffalo (*Bubalus bubalis*) in Florida, USA¹. It was isolated at a similar time and location to Bivens Arm virus (BAV) strain UF-10 which was also isolated from *C. insignis*. SWBV is antigenically related to BAV which cross-reacts strongly in plaque-reduction neutralisation tests with Tibrogargan virus (TIBV; type species *Tibrogargan tibrovirus*); however, there is no significant cross-neutralisation between SWBV and TIBV or BAV¹. Complete coding regions (13,141 nt) of the SWBV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1**)². The genome organisation is the same as other tibroviruses (3'N-P-M-U1-U2-G-U3-L5'). Phylogenetic analysis of L protein sequences indicates that SWBV lies centrally on the tibrovirus clade and is distinct from TIBV and Coastal Plains virus (CPV; species *Coastal Plains tibrovirus*) (**Figure 2**)². Amino acid sequence identities indicate that SWBV is most closely related to TIBV and CPV in the N (76.0% and 70.0%), G (65.7% and 59.5%) and L (65.6% and 57.4%) proteins, respectively (**Figure 3**). These levels of sequence divergence exceed 20% and so SWBV should be assigned to a new species.

b. *Bas-Congo tibrovirus*

Bas-Congo virus (BASV) was detected by next generation sequencing (NGS) in an acute phase serum sample from a human patient from the Democratic Republic of Congo with severe haemorrhagic fever³. No virus isolate is available. A partial genome sequence has been obtained (11892 nt) including all coding regions except the N and L genes for which extreme terminal sequences are absent (**Figure 1**)³. The genome organisation is the same as that of other tibroviruses (3'N-P-M-U1-U2-G-U3-L5'). Phylogenetic analysis of L protein sequences indicates that BASV lies on a deeply rooted branch of the tibrovirus clade and is most closely related to Ekpoma virus-2 (EKV-2) which was detected by metagenomics analysis of blood from a healthy human in Nigeria (**Figure 2**)⁴. Amino acid sequence identities indicate that BASV shares similar levels of homology in the N (39.5-46.0%), G (29.5-35.7%) and L (44.4-51.8%) proteins with other tibroviruses (**Figure 3**). These levels of sequence divergence exceed 20% and so BASV should be assigned to a new species.

c. *Ekpoma-1 tibrovirus*

Ekpoma virus-1 (EKV-1) was detected by NGS in a blood sample from a healthy human in Nigeria⁴. A partial genome sequence has been obtained (12659 nt) including complete coding regions with only the 3' and 5' ends incomplete (**Figure 1**)⁴. The genome organisation is the same as that of other tibroviruses (3'N-P-M-U1-U2-G-U3-L5'). Phylogenetic analysis of L protein sequences indicates that EKV-1 lies centrally on a deeply rooted branch of the tibrovirus clade (**Figure 2**)⁴. Amino acid sequence identities indicate that EKV-1 shares similar levels of homology in the N (40.8-48.8%), G (29.0-38.3%) and L (43.8-51.8%) proteins with other tibroviruses (**Figure 3**). These levels of sequence divergence exceed 20% and so EKV-1 should be assigned to a new species.

d. *Ekpoma-2 tibrovirus*

Ekpoma virus-2 (EKV-2) was detected by NGS in a blood sample from a healthy human in Nigeria⁴. A partial genome sequence has been obtained (12674 nt) including complete coding regions with only the 3' and 5' ends incomplete (**Figure 1**)⁴. The genome organisation is the same as that of other tibroviruses (3'N-P-M-U1-U2-G-U3-L5'). Phylogenetic analysis of L protein sequences indicates that EKV-2 lies centrally on a deeply rooted branch of the tibrovirus clade and is most closely related to BASV (**Figure**

2)⁴. Amino acid sequence identities indicate that EKV-2 shares similar levels of homology in the N (38.9-46.0%), G (29.0-35.7%) and L (44.8-49.1%) proteins with other tibroviruses (**Figure 3**). The levels of sequence divergence exceed 20% and so EKV-2 should be assigned to a new species.

NOTE:

Bivens Arm virus (BAV) strain UF-10 was isolated in 1981 from biting midges (*Culicoides insignis*) collected near water buffalo (*Bubalus bubalis*) in Florida, USA¹. It cross-reacts with TIBV and CPV in complement-fixation and indirect immunofluorescence tests⁵ and is indistinguishable from TIBV in plaque-reduction neutralisation tests¹. Complete coding regions (13,296 nt) of the BAV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1**)^{6,7}. It shares the same genome organisation with TIBV and other tibroviruses (3'N-P-M-U1-U2-G-U3-L5'). Phylogenetic analysis of L protein sequences indicates that BAV is very closely related to TIBV (**Figure 2**). The genomes of BAV and TIBV share 92.5% nucleotide sequence identity. Amino acid sequence identities between BAV and TIBV proteins are: N protein (99.0%), G protein (96.9%) and L protein (97.3%) (**Figure 3**). These levels of sequence divergence are less than 5% and so BAV and TIBV should be assigned to the same species (*Tibrogargan tibrovirus*).

References:

1. Gibbs EPJ, Calisher CH, Tesh RB, Lazuick JS, Bowen R, Greiner EC, 1989. Bivens Arm virus: A new rhabdovirus isolated from *Culicoides insignis* in Florida and related to Tibrogargan virus of Australia. *Veterinary Microbiology* 19: 141-150.
2. Walker PJ, Widen SG, Firth C, Blasdell KR, Wood TG, Travassos da Rosa AP, Guzman H, Tesh RB, Vasilakis N, 2015. Genomic characterization of Yogue, Kasokero, Issyk-Kul, Keterah, Gossas, and Thiafora viruses: nairoviruses naturally infecting bats, shrews, and ticks. *American Journal of Tropical Medicine and Hygiene* 93: 1041-1051.
3. Grard G, Fair JN, Lee D, Slikas E, Steffen I, Muyembe J-J, Sittler T, Veeraraghavan N, Ruby JG, Wang C, Makuwa M, Mulembakani P, Tesh RB, Mazet J, Rimoin AW, Taylor T, Schneider BS, Simmons G, Delwart E, Wolfe ND, Chiu CY, Leroy EM, 2012. A novel rhabdovirus associated with acute hemorrhagic fever in Central Africa. *PLoS Pathogens* 8: e1002924.
4. Stremlau MH, Andersen KG, Folarin OA, Grove JN, Odiya I, Ehiane PE, Omoniwa O, Omoregie O, Jiang PP, Yozwiak NL, Matranga CB, Yang X, Gire SK, Winnicki S, Tariyal R, Schaffner SF, Okokhere PO, Okogbenin S, Akpede GO, Asogun DA, Agbonlahor DE, Walker PJ, Tesh RB, Levin JZ, Garry RF, Sabeti PC, Happi CT, 2015. Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. *PLoS Neglected Tropical Diseases* 9: e0003631.
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. Walker PJ, Firth C, Widen SG, Blasdell 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.
7. Lauck M, Yu SQ, Cai Y, Hensley LE, Chiu CY, O'Connor DH, Kuhn JH, 2015. Genome sequence of Bivens Arm virus, a tibrovirus belonging to the species Tibrogargan virus (Mononegavirales: Rhabdoviridae). *Genome Announcements* 3: e00089-15.

Annex:

Figure 1. Genome organisations of tibroviruses. ORF U1 (turquoise), ORF U2 (navy blue) and ORF U3 (yellow) are highlighted. ORF U1 and ORF U2 encode small proteins of unknown function and ORF U3 encodes a small viroporin-like transmembrane protein.

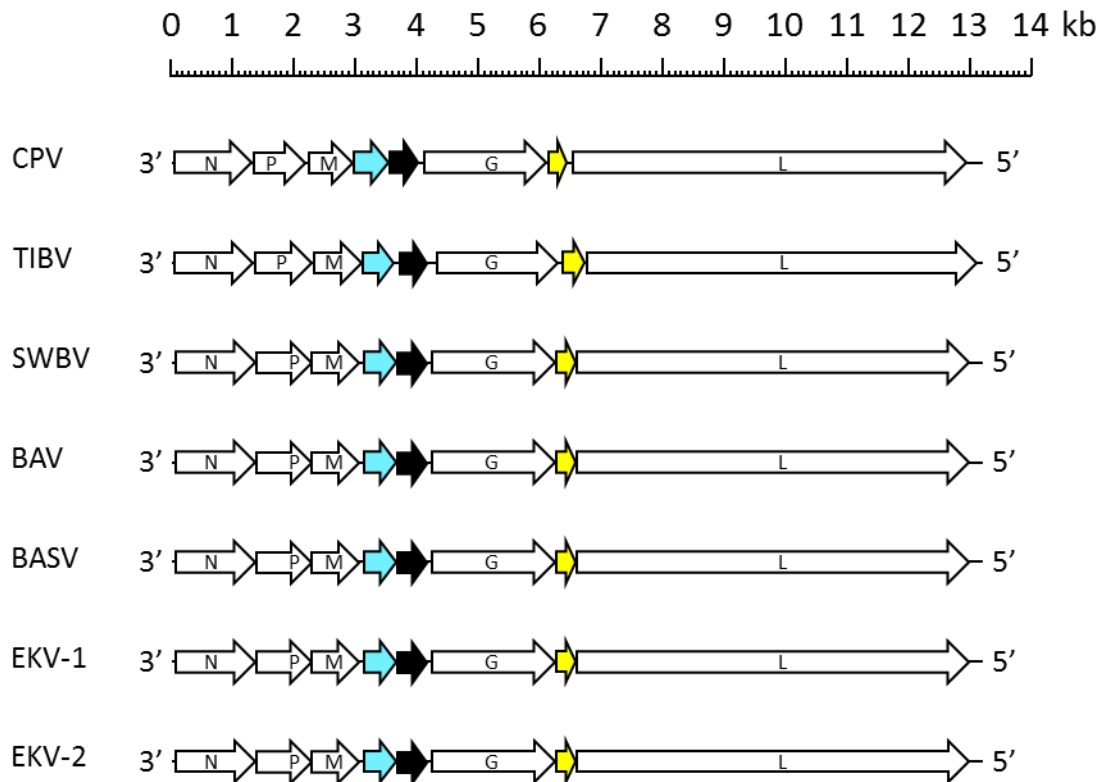


Figure 2. ML phylogenetic tree of 132 animal rhabdovirus L protein sequences. Branches are colour-coded according to existing genera (named in bold italics) or proposed new genera (named light italics) according to Walker et al. (2015) PLoS Pathogens 11: e10046642⁶. The clade representing the proposed new genus *Tibrovirus* 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 *Bahivavirus*) that comprise viruses isolated from mosquitoes. The ML tree was generated as described in Walker et al. (2015) PLoS Pathogens 11: e10046642⁶. Virus abbreviations and Genbank accession numbers are as listed in **Table 1**.

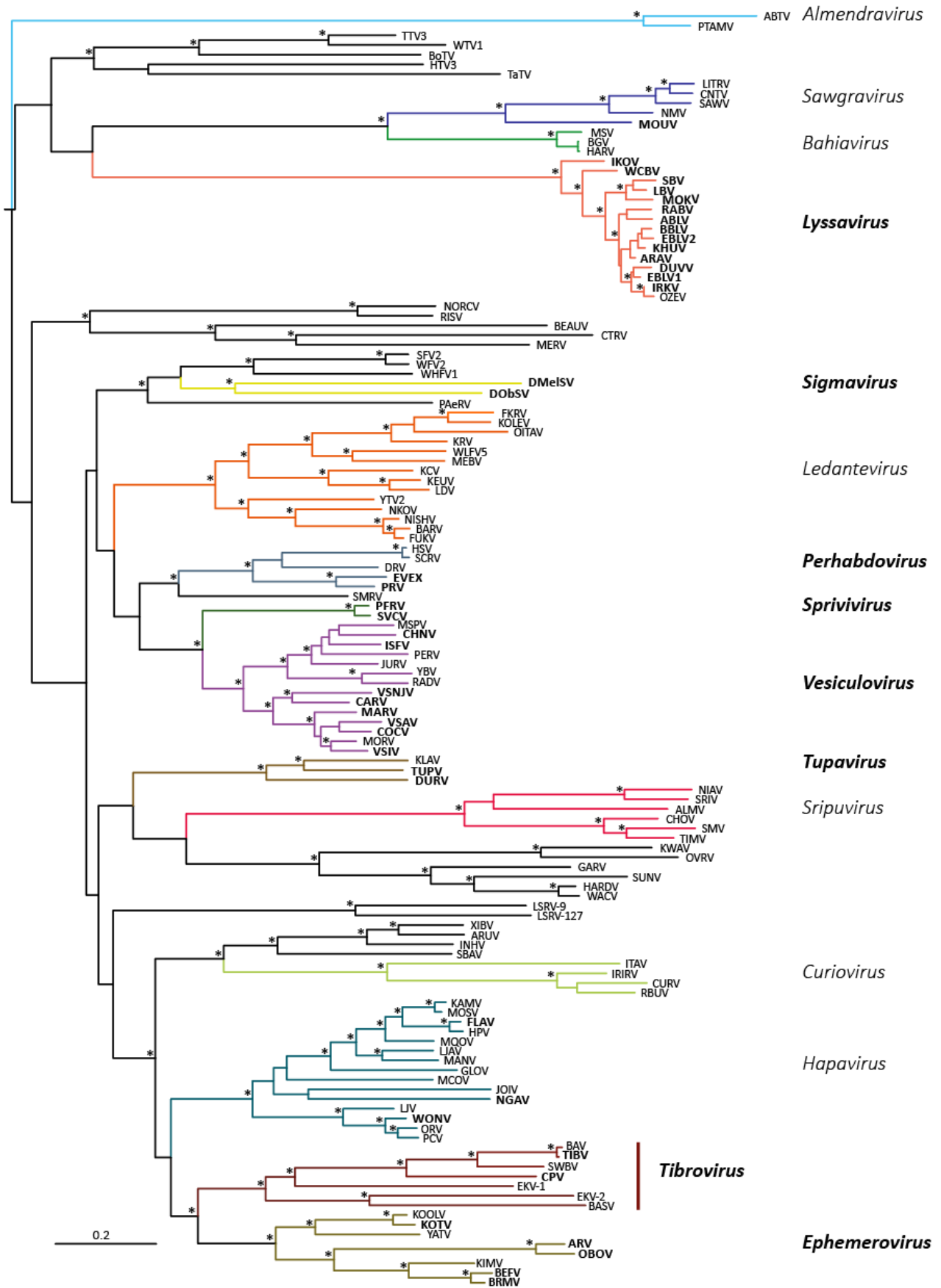


Figure 3A. Amino acid sequence identities (p-distance) of partial N protein sequences as determined in MEGA 6.0.

	TIBV	BAV	SWBV	CPV	EKV-1	EKV-2	BASV
TIBV	100						
BAV	99.0	100					
SWBV	76.0	76.8	100				
CPV	68.5	69.0	70.0	100			
EKV-1	48.5	48.8	46.5	46.3	100		
EKV-2	41.3	41.3	39.8	41.3	42.0	100	
BASV	40.0	40.3	39.5	40.8	40.8	46.0	100

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

	TIBV	BAV	SWBV	CPV	EKV-1	EKV-2	BASV
TIBV	100						
BAV	96.9	100					
SWBV	65.7	65.0	100				
CPV	58.5	58.3	59.5	100			
EKV-1	38.1	38.3	36.9	34.6	100		
EKV-2	32.8	33.1	31.6	32.9	29.0	100	
BASV	32.2	32.2	30.5	29.5	32.2	35.7	100

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

	TIBV	BAV	SWBV	CPV	EKV-1	EKV-2	BASV
TIBV	100						
BAV	97.3	100					
SWBV	65.6	65.2	100				
CPV	57.8	57.8	57.4	100			
EKV-1	43.8	44.0	44.0	43.1	100		
EKV-2	46.1	46.1	47.0	49.1	44.8	100	
BASV	44.1	44.1	46.1	44.4	51.8	45.9	100

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	IKOV	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	DObSV	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	Vesiculovirus	Isfahan vesiculovirus	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 Phl-166	not classified		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	not classified		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
Irtiri 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
Ngaining virus	NGAV	MRM14556	unassigned	Ngaining 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	Tibrovirus*	Tibrogargan tibrovirus	13288+	KM205019
Tibrogargan virus	TIBV	CS132	Tibrovirus	Tibrogargan tibrovirus	13298	GQ294472
Sweetwater Branch virus	SWBV	UF-11	Tibrovirus*	Sweetwater Branch tibrovirus	13141+	KM204997
Coastal Plains virus	CPV	DPP53	Tibrovirus	Coastal Plains tibrovirus	13203	GQ294473
Ekpoma virus-1	EKV-1		Tibrovirus*	Ekpoma-1 tibrovirus	12,659+	KP324827
Ekpoma virus-2	EKV-2		Tibrovirus*	Ekpoma-2 tibrovirus	12,674+	KP324828
Bas-Congo virus	BASV	BASV-1	Tibrovirus*	Bas-Congo tibrovirus	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.