



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:	2016.006a-dM	(to be completed by ICTV officers)			
Short title: One new genus (<i>Ledantevirus</i>) including 14 new species in the family <i>Rhabdoviridae</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"/>	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:

10 members have advised support for the proposal; 2 members have not responded.

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	2016.006aM	(assigned by ICTV officers)
To create 14 new species within:		
Genus:	<i>Ledantevirus (new)</i>	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.
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>Nkolbisson ledantevirus</i>	Nkolbisson virus (NKOV; YM 31-65)	KM205017
<i>Barur ledantevirus</i>	Barur virus (BARV; 6235)	KM204983
<i>Fukuoka ledantevirus</i>	Fukuoka virus (FUKV; FUK-11)	KM205001
<i>Nishimuro ledantevirus</i>	Nishimuro virus (NISV)	AB609604
<i>Kern Canyon ledantevirus</i>	Kern Canyon virus (KCV; M03790)	KM204992
<i>Keuraliba ledantevirus</i>	Keuraliba virus (KEUV; DakAnD5314)	KM205021
<i>Yongjia ledantevirus</i>	Yongjia tick virus 2 (YTV-2; YJ1-2)	KM817662
<i>Le Dantec ledantevirus</i>	Le Dantec virus (LDV; DakHD763)	KM205006
<i>Wuhan ledantevirus</i>	Wuhan louse fly virus 5 (WLFV-5; BFJSC-5)	KM817654
<i>Mount Elgon bat ledantevirus</i>	Mount Elgon bat virus (MEBV; BP846)	KM205026
<i>Kumasi ledantevirus</i>	Kumasi rhabdovirus (KRV; M35)	KJ179955
<i>Oita ledantevirus</i>	Oita virus (OITAV; 296-1972)	KM204998
<i>Fikirini ledantevirus</i>	Fikirini rhabdovirus (FKRV; KEN352)	KC676792
<i>Kolente ledantevirus</i>	Kolente virus (KOLEV; DakArK7292)	KC984953

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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 <p>Species demarcation criteria will be defined as follows (see also module 3): Viruses assigned to different species within the genus <i>Ledantevirus</i> have several of the following characteristics: A) minimum amino acid sequence divergence of 7% in L proteins; B) minimum amino acid sequence divergence of 15% in G proteins; C) significant differences in genome organization as evidenced by numbers and locations of ORFs; D) can be distinguished in serological tests; and E) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.</p>
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The viruses assigned to the new genus form a monophyletic group based on well-supported ML trees generated from complete N protein and L protein sequences^{1, 2}. Known characteristics of the viruses are summarized here. The basis of assignment of the viruses to 14 distinct species is described under the genus proposal (**module 3**).

Nkolbisson ledantevirus

Nkolbisson virus (NKOV) was first isolated in Cameroon in 1965 from mosquitoes (*Eretmapodites leucopus*)³. The virus was subsequently isolated from anthropophilic culicine mosquitoes in Côte d'Ivoire and human serum obtained from the Central African Republic⁴. NKOV cross-reacts weakly in complement-fixation (CF) tests and/or indirect immunofluorescence assays (IFA) with BARV, FUKV, KEUV and KCV^{5, 6}. Complete coding regions (10,942 nt) of the NKOV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1, 2}. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) with short inter-genic regions (1–4 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate NKOV is most closely related to NISV, BARV and FUKV (**Figure 2; Figure 3**)^{1, 2}. In some reports Gossas virus (*Bunyaviridae; Nairovirus*) was misidentified as NKOV. This was subsequently corrected^{2, 7}.

Barur ledantevirus

Barur virus (BARV) was isolated in India from ticks and a roof rat (*Rattus rattus*), in Kenya from ticks, fleas and mosquitoes of several species⁸, and in Somalia from ticks⁹. BARV cross-reacts strongly in CF and IFA tests with FUKV, and weakly with KCV, NKOV and KOLEV^{5, 6}. Complete coding regions (10,853 nt) of the NKOV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1, 2}. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) with short inter-genic regions (1–2 nt). A small ORF occurs in an alternative reading frame in the G gene but it is not known if it is expressed. Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate BARV is most closely related to NISV, NKOV and FUKV (**Figure 2; Figure 3**)^{1, 2}.

Fukuoka ledantevirus

Fukuoka virus (FUKV) was first isolated in Japan in 1982 from mosquitoes (*Culex tritaeniorhynchus*) and biting midges (*Culicoides punctatus*), and subsequently from sentinel cattle with mild febrile illnesses and leukopenia resembling bovine ephemeral fever¹⁰. FUKV cross-reacts strongly in CF and IFA tests with BARV, and weakly with KCV, NKOV, KOLEV and MEBV^{5, 6}. The complete FUKV genome (10,863 nt) has been sequenced (**Figure 1A**)^{1, 2}. The genome comprises 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L). Uniquely amongst the ledanteviruses, an alternative ORF in the M gene encodes a small double-membrane-spanning Mx protein (86 aa; 10.4 kDa) (**Figure 1C**). Its characteristic structural features strongly suggest that it is expressed. All inter-genic regions are short (1–2 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate FUKV is most closely related to NISV, BARV and NKOV (**Figure 2; Figure 3**)^{1, 2}.

Nishimuro ledantevirus

Nishimuro virus (NISV) was isolated in Japan in 2009 from a wild boar (*Sus scrofa*). It has also been called wild boar rhabdovirus 1 (WBRV1)¹¹. Neutralising antibodies to NISV have been detected in wild boar and domestic pigs in Japan¹¹. Complete coding regions (10,881 nt) of the NISV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{2, 11}.

The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) with short inter-genic regions (1–2 nt). A small ORF occurs in an alternative reading frame in the N gene but it is not known if it is expressed. Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate NISV is most closely related to NKOV, BARV and FUKV (**Figure 2; Figure 3**)².

Yongjia ledantavirus

Yongjia tick virus 2 (YTV-2) was detected by NGS in a pool of hard ticks (*Haemaphysalis hystricis*) collected from wild or domestic animals in Zhejiang Province, China, between 2011 and 2013¹². No virus isolate is yet available. The complete YTV-2 genome (10,833 nt) has been sequenced (**Figure 1A**)¹². The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) with short inter-genic regions (1–2 nt). A small ORF occurs in an alternative reading frame in the G gene but it is not known if it is expressed. Phylogenetic analysis of L protein sequences indicates that YTV-2 lies centrally in the ledantavirus clade and shares a common ancestor with NKOV, BARV, FUKV and NISV. YTV-2 shares similar levels of amino acid sequence identity in the N, L and G proteins with all other ledantaviruses. (**Figure 2; Figure 3**).

Kern Canyon ledantavirus

Kern Canyon virus (KCV) was isolated in California in 1956 from a mouse-eared bat (*Myotis yumanensis*)^{13, 14}. It cross-reacts weakly in CF and IFA tests with FUKV and NKOV^{5, 6}. Complete coding regions (11,528 nt) of the KCV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1, 2}. The genome comprises 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and an additional transcriptional unit (U1) encoding a small protein (77 aa; 8.8 kDa) between the G and L genes^{1, 2}. The KCV U1 protein shares a low but detectable level of sequence homology with the U1 proteins of KEUV and LDV (**Figure 1B**). The U1 gene is transcribed *in vitro*². Inter-genic regions are all short (2 nt) except between the U1 and L genes (17 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate KCV is most closely related to KEUV and LDV (**Figure 2; Figure 3**)^{1, 2}.

Keuraliba ledantavirus

Keuraliba virus (KEUV) was isolated in 1968 from the liver of a gerbil (*Tatera kempi*) in Senegal and was subsequently isolated on several occasions from rodents of other species¹⁵. It was shown initially to cross-react weakly in CF tests with several vesiculoviruses¹⁶ but subsequently shown to be closely related to LDV¹⁷. Complete coding regions (11,457 nt) of the KEUV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1, 2}. The genome comprises 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and an additional transcriptional unit (U1) encoding a small protein (64 aa; 7.3 kDa) between the G and L genes^{1, 2}. The KEUV U1 protein shares 57.8% amino acid sequence identity with the LDV U1 protein (**Figure 1B**). A small ORF occurs in an alternative reading frame in the G gene but it is not known if it is expressed. All inter-genic regions are short (2 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate KEUV is most closely related to LDV and more distantly to KCV (**Figure 2; Figure 3**)^{1, 2}.

Le Dantec ledantavirus

Le Dantec virus (LDV) was isolated in 1965 in Senegal, from the blood of a 10-year-old girl with acute febrile illness and signs of hepatosplenomegaly¹⁷. RNA from an LDV-like virus has also been detected in a serotine bat (*Eptesicus isabellinus*) from Spain¹⁸. LDV cross-react

strongly in complement-fixation (CF) tests with KEUV¹⁶. Complete coding regions (11,450 nt) of the KEUV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1,2}. The genome comprises 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and an additional transcriptional unit (U1) encoding a small protein (64 aa; 7.4 kDa) between the G and L genes^{1,2}. The U1 gene is transcribed *in vitro*². The LDV U1 protein shares 57.8% amino acid sequence identity with the KEUV U1 protein (**Figure 1B**). A small ORF occurs in an alternative reading frame in the N gene but it is not known if it is expressed. All inter-genic regions are short (2 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate LDV is most closely related to KEUV and more distantly to KCV (**Figure 2; Figure 3**)^{1,2}.

Mount Elgon bat ledantevirus

Mount Elgon bat virus (MEBV) was isolated in Kenya in 1964 from a Hildebrandt's horseshoe bat (*Rhinolophus hildebrandtii*)¹⁹. MEBV cross-reacts weakly in CF tests with FUKV⁵.

Complete coding regions (10,941 nt) of the MEBV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1,2}. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L)^{1,2}. Inter-genic regions are short (1–2 nt) except that the start of the M gene overlaps the end of the preceding P gene by 28 nt. Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate MEBV is most closely related to WLFV-5, OITAV, KRV, FKRV and KOLEV (**Figure 2; Figure 3**)^{1,2}.

Wuhan ledantevirus

Wuhan louse fly virus 5 (WLFV-5) was detected by NGS in pool of louse flies (Hippoboscidae, unidentified species) removed from the skin of bats (unidentified species) collected in Hubei Province, China, between 2011 and 2013¹². No virus isolate is yet available. Complete coding regions (11,103 nt) have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)¹². The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) with short inter-genic regions (2–10 nt), except that the M gene overlaps the end of the preceding P gene by 25 nt. A small ORF occurs in an alternative reading frame in the N gene but it is not known if it is expressed. Phylogenetic analysis of L protein sequences and amino acid sequence identity in the N, L and G proteins indicate WLFV-5 is most closely related to MEBV (**Figure 2; Figure 3**).

Kumasi ledantevirus

Kumasi rhabdovirus (KRV) was isolated in 2011 in Ghana in from the spleen of a straw-coloured fruit bat (*Eidolon helvum*)²⁰. Serological relationships with other rhabdoviruses have not yet been described. The complete KRV genome (11,072 nt) has been sequenced (**Figure 1A**)²⁰. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L). Inter-genic regions are short (1–3 nt). Phylogenetic analysis of L gene and L protein sequences, and amino acid sequence identity in the N, L and G proteins indicate KRV is most closely related to MEBV, OITAV, FKRV and KOLEV (**Figure 2; Figure 3**)²⁰.

Oita ledantevirus

Oita virus (OITAV) was isolated in Japan in 1972 from a little Japanese horseshoe bat (*Rhinolophus cornutus*)²¹. Complete coding regions (11,355 nt) of the OITAV genome have been sequenced with only the 3' and 5' ends incomplete (**Figure 1A**)^{1,2}. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L)^{1,2}. A small ORF occurs in an alternative reading frame in the L gene but it is not known if it

is expressed. Inter-genic regions are relatively short (1–9 nt). Phylogenetic analysis of N protein and L protein sequences and amino acid sequence identity in the N, L and G proteins indicate OITAV is most closely related to KRV, MEBV, FKRV and KOLEV (**Figure 2; Figure 3**)^{1, 2}.

Fikirini ledantavirus

Fikirini virus (FKRV) was isolated in Kenya in 2011 from a stripes leaf-nosed bat (*Hipposideros vittatus*)²². Serological relationships with other rhabdoviruses have not yet been described. The complete FKRV genome (11,139 nt) has been sequenced (**Figure 1A**)²². The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L). Two small ORF occurs in alternative reading frames in the G gene but it is not known if they are expressed. Inter-genic regions are short (2 nt) except that the start of the M gene overlaps the end of the preceding P gene by 23 nt. Phylogenetic analysis of L gene and L protein sequences, and amino acid sequence identity in the N, L and G proteins indicate FKRV is most closely related to KOLEV and more distantly to OITAV, KRV and MEBV (**Figure 2; Figure 3**)^{1, 22}.

Kolente ledantavirus

Kolente virus (KOLEV) was isolated in Guinea in 1985 from a Jones's leaf-nosed bat (*Hipposideros jonesi*) and a pool of ticks (*Amblyomma (Theileriella) variegatum*)⁵. KOLEV cross-reacts weakly in CF tests BARV and FUKV⁵. The complete KOLEV genome (11,120 nt) has been sequenced (**Figure 1A**)⁵. The genome comprises only 5 genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L). A small ORF occurs in an alternative reading frame in the P gene but it is not known if it is expressed. Inter-genic regions are short (2 nt) except that the start of the M gene overlaps the end of the preceding P gene by 23 nt. Phylogenetic analysis of L gene and L protein sequences, and amino acid sequence identity in the N, L and G proteins indicate FKRV is most closely related to KOLEV and more distantly to OITAV, KRV and MEBV (**Figure 2; Figure 3**)^{1, 2, 5}.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	2016.006bM	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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 family is specified, enter “ unassigned ” in the family box
Family:	<i>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	

naming a new genus

Code	2016.006cM	(assigned by ICTV officers)
To name the new genus: <i>Ledantevirus</i>		

Assigning the type species and other species to a new genus

Code	2016.006dM	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Le Dantec ledantevirus</i>		Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered
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). Please enter here the TOTAL number of species (including the type species) that the genus will contain:		
14 species: <i>Nkolbisson ledantevirus</i> <i>Barur ledantevirus</i> <i>Fukuoka ledantevirus</i> <i>Nishimuro ledantevirus</i> <i>Yongjia ledantevirus</i> <i>Kern Canyon ledantevirus</i> <i>Keuraliba ledentevirus</i> <i>Le Dantec ledantevirus</i> (type species) <i>Mount Elgon bat ledantevirus</i> <i>Wuhan ledantevirus</i> <i>Kumasi ledantevirus</i> <i>Oita ledantevirus</i> <i>Fikirini ledantevirus</i> <i>Kolente ledantevirus</i>		

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 rhabdovirus genera but many rhabdoviruses remain unclassified. Here, we propose the establishment of a new genus (*Ledantevirus*) that will comprise 14 new species. Viruses assigned

to the genus infect mammals. Many have been isolated from bats or rodents. Some (or all) may be transmitted by arthropods. The viruses form a distinct clade in a well-supported (BSP \geq 85) tree based on full-length L protein (RdRp) sequences (**Figure 2**). The clade is linked phylogenetically to the approved genera *Perhavirus* and *Sprivivirus* (infecting fish), and more distantly to the genus *Vesiculovirus* (infecting mammals).

Viruses assigned to the proposed genus form a monophyletic group based on phylogenetic analysis of complete N protein and L protein sequences^{1,2} (see also **Figure 2**). Full genome nucleotide sequence identities between the members vary from 44.8% to 79.5% and L protein amino acid sequence identities vary from 46.7% to 92.2%, falling well within the range seen for other genera in the *Rhabdoviridae*². Serological cross-reactions (CF, indirect fluorescence antibody or ELISA) have been reported between various members of the genus. These include: [LDV and KEUV]; [KCV, BARV, FUKV, NKOV and KEUV]; [KOLEV, BARV and FUKV]; and [FUKV, BARV and MEBV]^{5,6,16}. The genome organizations of the viruses are similar, comprising five open reading frames (ORFs) encoding the structural proteins (N, P, M, G and L) and concise intergenic regions (**Figure 1A**). A small additional ORF between the G and L occurs as an independent transcriptional unit in three of the viruses (LDV, KEUV and KCV) and an alternative ORF encoding a putative double-membrane-spanning protein occurs in the M gene of one of the viruses (FUKV)^{1,2}.

Origin of the new genus name:

Derived from the name of the virus assigned as the type species (Le Dantec virus; species *Le Dantec ledantevirus*).

Reasons to justify the choice of type species:

Le Dantec virus is one of several viruses in the new genus for which a partial characterization has been conducted. LDV is particular interest as it is the only virus in the genus that has yet been associated with clinical disease in humans. The Le Dantec serogroup is one of two serogroups to which several of the viruses in the new genus have previously been assigned.

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 *Ledantevirus* have several of the following characteristics: A) minimum amino acid sequence divergence of 7% in L proteins; B) minimum amino acid sequence divergence of 15% in G proteins; C) significant differences in genome organization as evidenced by numbers and locations of ORFs; D) can be distinguished in serological tests; and E) occupy different ecological niches as evidenced by differences in hosts and or arthropod vectors.

All proposed members meet criteria A and B. The viruses each meet the other criteria to varying extents based on available data. Phylogenetically, the viruses fall into three sub-clades and so descriptions of relationships between the viruses are described on that basis.

Sub-clade A (FUKV, BARV, NISV, NKOV and YTV-2)

Based on amino acid sequence divergence, FUKV, BARV and NISV are the most closely related ledanteviruses (94.7-96.6% identity in the N protein; 88.0-92.4% identity in the L protein; 78.4-85.9% identity in the G protein); NKOV and YTV-2 more distantly related to the other viruses (52.8-77.1% identity in the N protein; 54.4-61.9% identity in the L protein; 40.6-52.1% identity in the G protein). FUKV and BARV are the most closely related; however, FUKV varies in genome organization from BARV, NISV NKOV and YTV-2 in that it encodes a small double-

membrane-spanning protein (86 aa) as an alternative ORF in the M gene. BARV, FUKV and NKOV cross-react in CF tests but are distinguishable. The viruses also appear to vary in ecology: NKOV was isolated from culicine mosquitoes in Western and Central Africa; FUKV was isolated from culicine mosquitoes, biting midges (culicoides) and diseased cattle in Japan; and BARV was isolated from ticks and a roof rat (*Rattus rattus*) in India, and ticks, fleas and mosquitoes in East Africa. NISV was isolated from a wild boar (*Sus scrofa*) in Japan. YTV-2 was detected in ticks in China.

Sub-clade B (KEUV, LDV and KCV)

KEUV, LDV and KCV differ from other members of the genus in that they each contain an ORF encoding a small protein (64–77 aa) as an additional transcriptional unit between the G and L genes. KEUV and LDV are the most closely related members of this sub-clade (80.5% identity in N, 81.3% identity in L and 72.5% identity in G), falling well outside the minimum sequence divergence limits. KEUV and LDV cross-react in CF tests but are distinguishable. KCV does not cross-react with KEUV or LDV in CF tests. KEUV and KCV vary in ecology: KEUV has been isolated from rodents in Africa; KCV has been isolated from bats in North America. LDV has been isolated only from a human; its natural reservoir is unknown.

Sub-clade C (MEBV, WLFV-5, KRV, OITAV, FKRV and KOLEV)

Viruses in this sub-clade are significantly divergent in amino acid sequence in the L protein (53.3–74.2% identity in the N protein; 55.1–75.7% in the L protein; 27.3–51.5% identity in the G protein). The viruses each have a similar and simple genome organization. No cross-reaction was detected in CF tests between KOLEV and OITV; other viruses have not been tested. The viruses appear to have similar but distinct ecologies. KOLEV and FKRV were each were isolated from roundleaf bats of different species in Guinea; KOLEV has also been isolated from ticks. KRV was isolated in from a straw-coloured fruit bat in Ghana. OITAV was isolated from a horseshoe bat in Japan, whereas MEBV was isolated from a horseshoe bat of different species in Kenya. WLFV-5 was isolated from louse flies feeding on bats in China.

MODULE 10: **APPENDIX**: supporting material

References:

1. 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.
2. Blasdell KR, Guzman H, Widen SG, Firth C, Wood TG, Holmes EC, Tesh RB, Vasilakis N, Walker PJ, 2015. Ledantavirus: A proposed new genus in the *Rhabdoviridae* has a strong ecological association with bats. American Journal of Tropical Medicine and Hygiene 92: 405-410.
3. Salaun JJ, Rickenba.A, Bres P, Brottes H, Germain M, Eouzan JP, Ferrara L, 1969. Nkolbisson virus (Ym31/65) a novel arborvirus prototype isolated in Cameroon. Annales de l'Institut Pasteur 116: 254-260.
4. Ndiaye M, Saluzzo JF, Digoutte JP, Mattei X, 1987. Identification of Nkolbisson virus by electronic microscopy. Annales de l'Institut Pasteur - Virology 138: 517-521.
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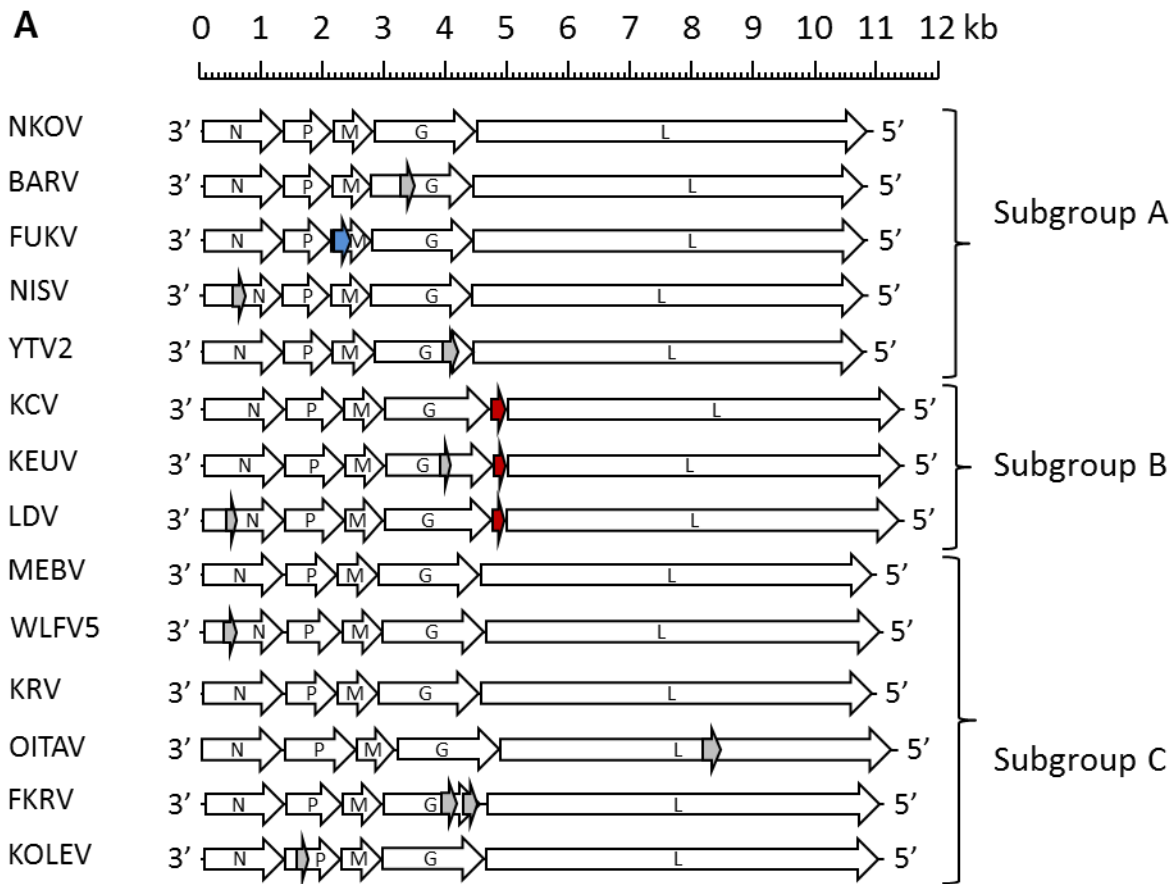
References:

6. 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.
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Annex:



B

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KEUV_U1 MFCSSFIYIISHHTLSQLSSNQRRETF FALMKEV---LDVTGGVIDRVDLVR-----RG-DGSMEMI---MTIIGR
LDV_U1  MFYSVIQIYISSHTLSNLSNDSERRMTFY NLMKDI---LTITGGSIESVNFIR-----RG-DGSMEIN---MYIVPI
          *** : *** **:*:*:* ** : *** : ** : * : *** * : * : * : * : * : * : * : * : * : * :
KCV_U1  M--SVKVSSESGKEMKLLADKATQTKWCCCKRNVGVQVTIRGQRKKKVTFFDEPEEFYIQGEDGLLHLYEKEQVSIGV
          * *      * : : * .. : : : : : : : * . * : . : * * * : : : :

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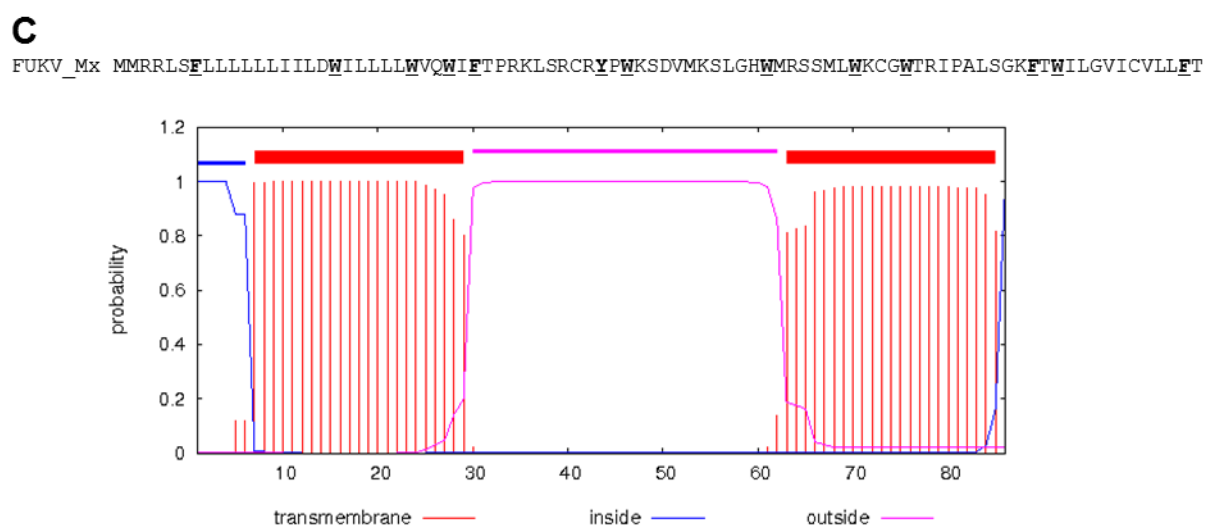


Figure 1. (A) Schematic representation of ledantevirus genome organizations showing the locations of all open reading frames (ORFs) > 180 nt. Red denotes the U1 ORFs of KCV, KEUV and LDV, blue denotes the FUKV Mx ORF and grey denotes other possible ORFs. **(B)** Alignment of the U1 proteins of KEUV, LDV and KCV. **(C)** Sequence of the FUKV Mx protein and its predicted membrane topology (TMHMM; <http://web.expasy.org>). Adapted from Blasdel *et al.* (2015) *Am J Trop Med Hyg* 92: 405-410.

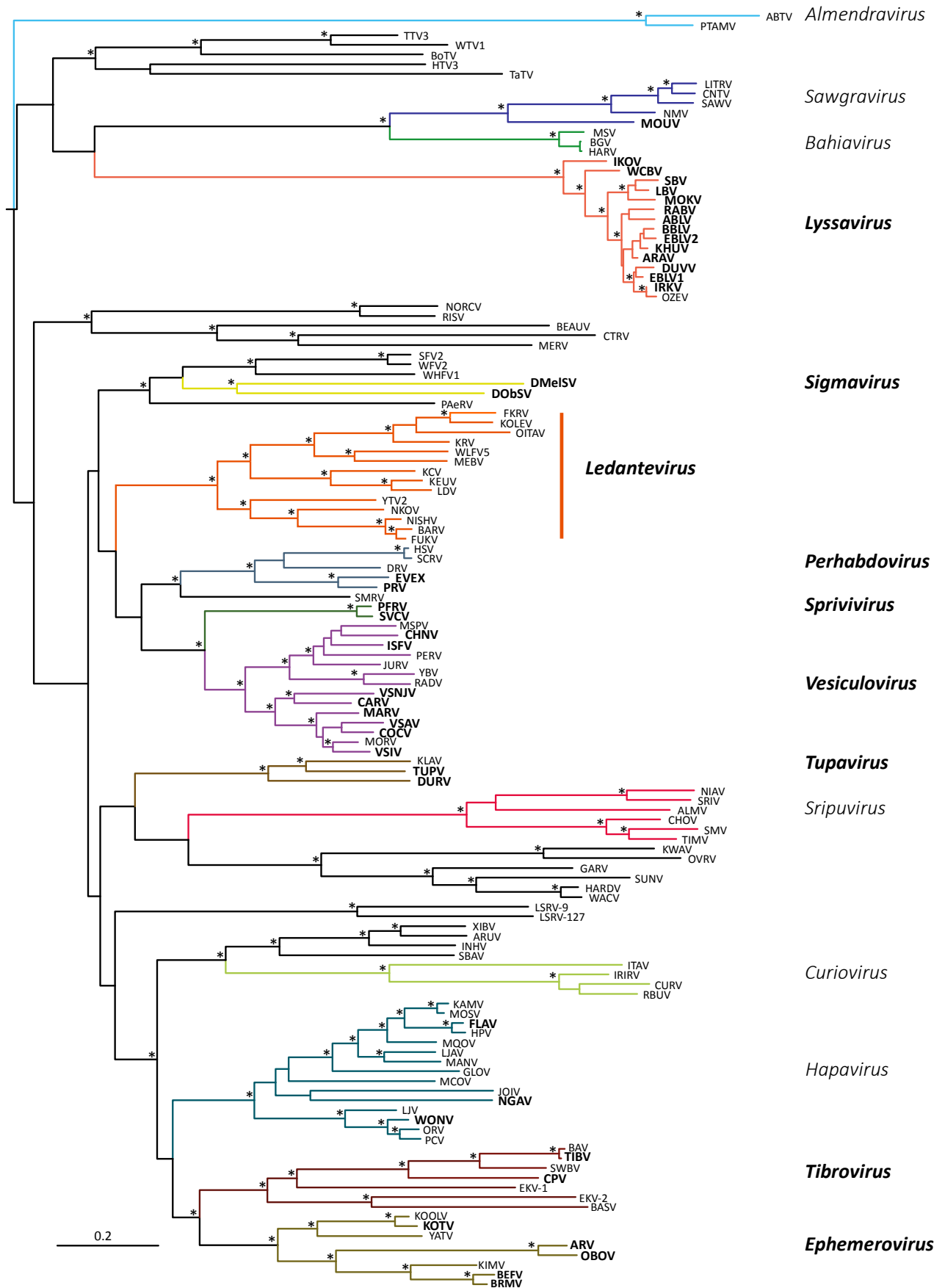


Figure 2. ML phylogenetic tree of 132 animal rhabdovirus L protein sequences. Branches are colour-coded according to existing genera (named in bold italics) or proposed new genera (named light italics) Walker et al. (2015) PLoS Pathogens 11 (2): e10046646¹. The clade representing the proposed new genus *Ledantevirus* 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 (2): e10046646¹. Virus abbreviations and Genbank accession numbers are as listed in Table 1.

Figure 3A. Ledantevirus N protein amino acid sequence identity (as estimated in MEGA6 by p-distance).

	NKOV	NISV	BARV	FUKV	YTV-2	KCV	KEUV	LDV	MEBV	WLFV5	KRV	OITAV	FKRV	KOLEV
NKOV	100													
NISV	75.9	100												
BARV	76.4	94.7	100											
FUKV	77.1	95.7	96.6	100										
YTV2	54.0	52.8	52.8	53.0	100									
KCV	41.2	39.5	40.5	40.7	40.7	100								
KEUV	40.7	40.0	39.8	40.2	39.3	47.7	100							
LDV	39.8	39.5	39.5	40.0	39.8	48.7	80.5	100						
MEBV	41.4	42.4	42.9	42.7	40.7	38.3	41.7	40.5	100					
WLFV5	38.8	39.3	38.8	39.0	36.4	37.6	39.0	37.8	73.0	100				
KRV	42.7	41.2	43.1	42.2	40.2	38.1	39.5	39.0	60.7	59.3	100			
OITAV	38.6	37.3	38.1	37.8	37.6	39.3	39.0	39.5	55.7	53.3	59.3	100		
FKRV	40.2	40.5	40.5	40.2	41.0	37.1	36.9	37.6	61.0	57.6	60.7	57.8	100	
KOLEV	41.4	41.7	41.4	41.4	41.4	38.6	38.3	40.0	62.7	63.1	64.1	58.6	74.2	100

Figure 3B. Ledantevirus L protein amino acid sequence identity (as estimated in MEGA6 by p-distance).

	NKOV	NISV	BARV	FUKV	YTV2	KCV	KEUV	LDV	MEBV	WLFV5	KRV	OITAV	FKRV	KOLEV
NKOV	100													
NISV	61.5	100												
BARV	61.7	88.0	100											
FUKV	61.9	89.4	92.4	100										
YTV2	54.8	54.7	54.4	54.5	100									
KCV	51.5	51.3	50.6	51.2	50.8	100								
KEUV	51.5	51.8	51.1	51.8	50.8	63.3	100							
LDV	51.0	50.4	50.4	50.8	50.8	63.1	81.3	100						
MEBV	49.0	49.0	49.1	49.0	48.0	49.5	49.8	49.2	100					
WLFV5	48.2	48.4	48.2	48.3	47.0	48.8	49.5	49.6	62.2	100				
KRV	47.5	47.4	47.8	47.8	48.7	49.1	49.4	49.2	56.2	55.9	100			
OITAV	48.1	48.1	48.3	48.4	47.4	49.2	48.2	48.0	55.1	56.0	63.8	100		
FKRV	47.4	48.2	48.1	48.1	47.3	48.8	48.4	47.7	55.3	54.3	62.3	62.6	100	
KOLEV	48.6	48.2	47.9	48.7	48.5	49.4	49.8	48.8	55.6	54.8	63.3	62.7	75.7	100

Figure 3C. Ledantevirus G protein amino acid sequence identity (as estimated in MEGA6 by p-distance).

	NKOV	NISV	BARV	FUKV	YTV2	KCV	KEUV	LDV	MEBV	WLFV5	KRV	OITAV	FKRV	KOLEV
NKOV	100													
NISV	52.1	100												
BARV	49.3	78.4	100											
FUKV	49.7	79.0	85.9	100										
YTV2	41.2	41.0	40.6	42.4	100									
KCV	34.9	35.4	37.2	38.0	38.2	100								
KEUV	34.5	34.1	33.9	34.7	35.6	51.7	100							
LDV	34.3	33.9	34.1	34.9	35.2	52.1	72.5	100						
MEBV	30.3	29.5	28.3	28.9	32.7	33.1	31.5	32.9	100					
WLFV5	33.3	29.9	30.3	30.5	30.5	32.1	31.9	31.3	45.9	100				
KRV	25.1	25.7	26.7	27.7	27.5	29.1	26.3	26.7	27.3	26.7	100			
OITAV	28.7	28.3	28.1	27.7	28.9	27.3	27.7	26.3	30.5	31.5	33.9	100		
FKRV	27.7	25.7	26.9	26.3	28.9	26.9	29.1	28.9	33.7	30.3	34.1	44.0	100	
KOLEV	30.3	27.9	28.7	29.1	29.7	28.7	29.1	30.3	31.5	32.7	35.2	40.8	51.5	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 species	<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
Ozerno 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	YYY1-8	not classified		12291+	KM817635
Wuhan fly virus 2	WFV2	YYY1-3	not classified		12247+	KM817646
Wuhan house fly virus 1	WHFV1	YYY2-4	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	<i>Ledantivirus*</i>	<i>Fikirini ledantivirus</i>	11139+	KC676792
Kolente virus	KOLEV	DakArK7292	<i>Ledantivirus*</i>	<i>Kolente ledantivirus</i>	11120	KC984953
Oita virus	OITAV	296-1972	<i>Ledantivirus*</i>	<i>Oita ledantivirus</i>	11355+	KM204998
Kumasi rhabdovirus	KRV	M35	<i>Ledantivirus*</i>	<i>Kumasi ledantivirus</i>	11072	KJ179955
Wuhan louse fly virus 5	WLFV-5	BFJSC-5	<i>Ledantivirus*</i>	<i>Wuhan ledantivirus</i>	11103+	KM817654
Mount Elgon bat virus	MEBV	BP846	<i>Ledantivirus*</i>	<i>Mount Elgon bat ledantivirus</i>	10941+	KM205026
Kern Canyon virus	KCV	M03790	<i>Ledantivirus*</i>	<i>Kern Canyon ledantivirus</i>	11528+	KM204992
Le Dantec virus	LDV	DakHD763	<i>Ledantivirus*</i>	<i>Le Dantec ledantivirus</i>	11450+	KM205006
Yongjia tick virus 2	YTV-2	YJ1-2	<i>Ledantivirus*</i>	<i>Yongjia ledantivirus</i>	10833	KM817662
Nkolbisson virus	NKOV	YM 31-65	<i>Ledantivirus*</i>	<i>Nkolbisson ledantivirus</i>	10942+	KM205017
Nishimuro virus	NISV		<i>Ledantivirus*</i>	<i>Nishimuro ledantivirus</i>	10881+	AB609604
Barur virus	BARV	6235	<i>Ledantivirus*</i>	<i>Barur ledantivirus</i>	10853+	KM204983
Fukuoka virus	FUKV	FUK-11	<i>Ledantivirus*</i>	<i>Fukuoka ledantivirus</i>	10863	KM205001
Keuraliba virus	KEUV	DakAnD5314	<i>Ledantivirus*</i>	<i>Keuraliba ledantivirus</i>	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	VSIV	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>	Durham tupavirus	11092+	FJ952155
Niakha virus	NIAV	DakArD88909	not classified		11124	KC585008
Sripur virus	SRIV	733646	not classified		11290+	KM205023
Almpiwat 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	not available
Kwatta virus	KWAV	A-57	not classified		11211+	KM204985
Oak Vale virus	OVV	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 species	<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 species	<i>Ngaingan virus</i>	15764	NC013955
La Joya virus	LJV	J-134	not classified		15721	KM204986
Wongabel virus	WONV	CS264	unassigned species	<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.