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:	***2016.003a-dM***	(to be completed by ICTV officers)

Short title: One new genus (*Curiovirus*), including 4 new species, in the family *Rhabdoviridae*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	ICTV *Rhabdoviridae* SG

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

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:

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	***2016.003aM***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Curiovirus*** (new)
Subfamily:	
Family:	***Rhabdoviridae***
Order:	***Mononegavirales***

Fill in all that apply.

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

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Curionopolis curiovirus (type species)	Curionopolis virus (CURV; strain BeAr440009)	KM204994
Iriri curiovirus	Iriri virus (IRIRV; strain BeAr408005)	KM204995
Rochambeau curiovirus	Rochambeau virus (RBUV; strain CaAr16102)	KM205012
Itacaiunas curiovirus	Itacaiunas virus (ITAV; strain BeAr427036)	KM204984

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 *Curiovirus* 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 *Curiovirus* 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) one or more additional long ORFs between the M and G genes; and ii) one or more additional long ORFs between the G and L genes, one of which encodes a viroporin-like protein (**Figures 2-6**). Curioviruses form a monophyletic group based on well-supported ML trees generated from complete L protein sequences (**Figure 7**). Known characteristics of the viruses of taxonomic significance are summarized here. The basis of assignment of the viruses to 4 distinct species in this genus is described under the genus proposal (**module 3**).

Curionopolis curiovirus

Curionopolis virus (CURV) was isolated from a pool of biting midges (*Culicoides* sp.) collected at Serra Norte in Parauapebas, Para State, Brazil, in 1985[1]. CURV was found to be unrelated by complement-fixation tests to 38 other rhabdoviruses[1]. CURV was also reported not to cross-react in CF or indirect immunofluorescence tests with Itacaiunas virus (ITAV; see below). Neutralising antibodies to CURV have been reported in a tufted capuchin (*Cebus apella*) and in a South American coati (*Nasua nasua*)[1]. The complete CURV genome (13,170 nt) has been sequenced (**Figure 1**)[2, 3]. The genome is typical of curioviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and several additional long ORFs located between the M and G genes, and between the G and L genes[2]. ORFs U1, U1x and U2 are located between the M and G genes: ORF U1 encodes an 82-aa (9.3 kDa) acidic protein (**Figure 2**); ORF U1x overlaps ORF1 in the same transcriptional unit and encodes a 68-aa (8.2 kDa) acidic protein (**Figure 3**); ORF U2 lies in an independent transcriptional unit and encodes a 105-aa (11.5 kDa) protein with a predicted N-terminal transmembrane domain (**Figure 4**). ORF U3 and ORF U3x are located between the G and L genes: ORF U3 encodes a 91-aa (10.9 kDa) viroporin-like protein (**Figure 6**); ORF U3x overlaps ORF U3 in the same transcriptional unit and encodes a 115-aa (13.3 kDa) basic protein (**Figure 5**). Phylogenetic analysis of L protein sequences (**Figure 7**)[2] and amino acid sequence identity in the N, L and G proteins (**Figure 8**) indicate that CURV lies in the curiovirus clade and is most closely related to Rochambeau virus (RBUV; see below).

Iriri curiovirus

Iriri virus (IRIRV) was isolated from sandflies (*Lutzomyia* sp.) collected in Altamira, Para State, Brazil, in 1982[4]. The complete IRIRV genome (13,070 nt) has been sequenced (**Figure 1**)[2]. The genome is similar to that of CURV, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and several additional long ORFs located between the M and G genes, and between the G and L genes[2]. ORFs U1, U1x and U2 are located between the M and G genes: ORF U1 encodes an 82-aa (9.5 kDa) acidic protein (**Figure 2**); ORF U1x overlaps ORF1 in the same transcriptional unit and encodes a 65-aa (7.5 kDa) acidic protein (**Figure 3**); ORF U2 lies in an independent transcriptional unit and encodes a 105-aa (11.7 kDa) protein with a predicted N-terminal transmembrane domain (**Figure 4**). ORF U3 and ORF U3x are located between the G and L genes: ORF U3 encodes an 85-aa (9.9 kDa) viroporin-like protein (**Figure 6**); ORF U3x overlaps ORF U3 in the same transcriptional unit and encodes a 115-aa (13.6 kDa) basic protein (**Figure 5**). The IRIRV genome also has a small alternative ORF near the start of the G gene encoding a 60-aa basic protein (7.0 kDa). Phylogenetic analysis of L protein sequences (**Figure 7**)[2] and amino acid sequence identity in the N, L and G proteins (**Figure 8**) indicate that IRIRV lies in the curiovirus clade and is most closely related to CURV and RBUV (see below).

Rochambeau curiovirus

Rochambeau virus (RBUV) was isolated from mosquitoes (*Coquillettidia albicosta*) collected in Paramana, French Guiana, in 1973[5, 6]. It was found to cross-react with rabies virus and Sandjimba virus (uncharacterized rhabdovirus) in indirect immunofluorescence tests[7]. The complete RBUV genome (13,593 nt) has been sequenced (**Figure 1**)[2]. The genome is similar to CURV and IRIRV, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and several additional long ORFs located between the M and G genes, and between the G and L genes[2]. ORFs U1, U1x and U2 are located between the M and G genes: ORF U1 encodes an 82-aa (9.3 kDa) acidic protein (**Figure 2**); ORF U1x overlaps ORF1 in the same transcriptional unit and encodes a 74-aa (8.6 kDa) acidic protein (**Figure 3**); ORF U2 lies in an independent transcriptional unit and encodes a 91-aa (10.0 kDa) protein with a predicted central transmembrane domain (**Figure 4**). ORF U3, ORF U4 and ORF U4x are located between the G and L genes: ORF U3 is unique to RBUV and encodes a 134-aa (15.2 kDa) protein with a predicted central transmembrane domain; ORF U4 encodes a 92-aa (10.9 kDa) viroporin-like protein (**Figure 6**); ORF U4x overlaps ORF U4 in the same transcriptional unit and encodes a 115-aa (13.4 kDa) basic protein (**Figure 5**). Phylogenetic analysis of L protein sequences (**Figure 7**)[2] and amino acid sequence identity in the N, L and G proteins (**Figure 8**) indicate that RBUV lies in the curiovirus clade and is most closely related to CURV and IRIRV.

Itacaiunas curiovirus

Itacaiunas virus (ITAV) was isolated from a pool of biting midges (*Culicoides* sp.) collected at Serra Norte in Parauapebas, Para State, Brazil, in 1984[1]. ITAV was found to be unrelated by complement-fixation tests to 38 other rhabdoviruses[1]. ITAV was also reported not to cross-react in CF or indirect immunofluorescence tests with CURV virus. Complete coding regions (12,536 nt) of the ITAV genome have been sequenced with only the 3´ and 5´ ends incomplete (**Figure 1**)[2]. The genome is typical of curioviruses, comprising five genes encoding the canonical rhabdovirus structural proteins (N, P, M, G and L) and additional long ORFs located between the M and G genes, and between the G and L genes[2]; however, ITAV has fewer additional ORFs than CURV, IRIRV or RBUV. ORF U1 is located between the M and G genes and encodes an 87-aa (9.9 kDa) acidic protein that shares low but identifiable homology with the CURV, IRIRV and RBUV U1 proteins (**Figure 2)**; it also shares identifiable homology with the RBUV U2 protein **(Figure 4B)**. ORF U2 is located between the G and L genes and encodes an 81-aa (9.4 kDa) viroporin-like protein (**Figure 6**). Phylogenetic analysis of L protein sequences (**Figure 7**)[2] and amino acid sequence identity in the N, L and G proteins (**Figure 8**) indicate that CURV lies in the curiovirus clade but is more distantly related to CURV, IRIRV and RBUV.

Each of these viruses meet species demarcation criteria A, B, C and D, establishing them as members of distinct species. Most of the viruses can also be distinguished ecologically (criterion F) but CURV and ITAV were each isolated from biting midges at a similar time and location, suggesting they may share a similar ecology. No neutralisation test data are yet available but CURV and ITAV failed to cross-react in CF tests, suggesting that species demarcation criterion E would also be met if tested.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.003bM***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:		Fill in all that apply.
Family:	***Rhabdoviridae***	
Order:	***Mononegavirales***	

- 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

naming a new genus

Code	***2016.003cM***	(assigned by ICTV officers)

To name the new genus: ***Curiovirus***

Assigning the type species and other species to a new genus

Code	***2016.003dM***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Curionopolis curiovirus	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:**

4 Species:
Curionopolis curiovirus **(type species)**
Iriri curiovirus
Rochambeau curiovirus
Itacaiunas curiovirus

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 (*Curiovirus*) that will include 4 new species. Two of the viruses to be assigned to the proposed genus were isolated from biting midges (*Culicoides* sp.), one was isolated from sandflies (*Lutzomyia* sp.) and one was isolated from mosquitoes (*Coquillettidia albicosta*). Curiovirus genomes are similar in size (~12,600 – 13,600 nt) and contain multiple ORFs encoding likely accessory proteins (**Figure 1**). The genomes all feature: (i) one or more ORFs between the M and G genes encoding proteins that share identifiable sequence identity; and (ii) one or more ORFs between the G and L genes, one of which encodes a class 1A viroporin-like protein. The viruses form a distinct clade in a well-supported (BSP ≥ 85) tree based on full length L protein (RdRp) sequences (**Figure 7**). The clade is linked phylogenetically to a clade of unclassified viruses comprising Inhangapi virus (INHV; isolated from sandflies [*Lutzomyai flaviscutellata*] in Brazil), Aruac virus (ARUV; isolated from mosquitoes [*Trichoprosopon* *theobalbi*] in Thailand), Xiburema virus (XIBV; isolated from mosquitoes [*Sabethes intermedius*] in Brazil) and Santa Barbara virus (SBAV; isolated from an unidentified fly [family Psychodidae] in Brazil). However, the genome organisations of these viruses are diverse and differ from those of the curioviruses. Therefore, we propose to exclude them from the genus at this stage. Antigenic cross-reactions (CF test) have not been reported between members of the genus.

Origin of the new genus name:

The name is derived as a siglum from Curionopolis virus, one of the foundation members of the genus which we assign to the type species. We note the previous suggestion that CURV and ITAV should be assigned to a genus for which the name "*Bracorhabdovirus*" was proposed (Brazilian Amazonian *Culicoides* rhabdoviruses)[1]. However, the four viruses to be assigned to the new genus have a broader host/vector range and geographic distribution than this name suggests. We therefore favour the non-prejudicial genus name *Curiovirus* that has also been proposed in a previous publication[2].

Reasons to justify the choice of type species:

Curionopolis virus (type species ***Curionopolis curiovirus***) is one of the better characterized members of the genus[1, 8].

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 *Curiovirus* 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. Diniz JA, Nunes MR, Travassos da Rosa AP, Cruz AC, de Souza W, Medeiros DB, Chiang JO, Vasconcelos PF, 2006. Characterization of two new rhabdoviruses isolated from midges (Culicoides spp) in the Brazilian Amazon: proposed members of a new genus, Bracorhabdovirus. Archives of Virology 151: 2519-2527.
2. 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.
3. Medeiros DBA, Diniz Júnior JAP, Cardoso JF, Silva SP, da Silva DEA, de Oliveira LF, é Vasconcelos JM, Chiang JO, Dias AA, Nunes MRT, Vianez Júnior JLSG, Vasconcelos PFC, 2014. Nearly complete genome sequence of Curionopolis virus, a culicoides-related rhabdovirus isolated in the Brazilian Amazon region. Genome Announcements 2: e01158-14.
4. Travassos da Rosa JFS, Travassos da Rosa APA, Vasconcelos PFC, Pinheiro FP, Rodrigues SG, Travassos da Rosa ES, Dias LB, Cruz ACR, 1998. Arboviruses isolated in the Evandro Chagas Institute, including some described for the first time in the Brazilian Amazon region, their known hosts, and their pathology for man. Travassos da Rosa APA, Vasconcelos PFC, Travassos da Rosa JFS, eds. An overview of arbovirology in Brazil and neighbouring countries. Belem: Instituto Evandro Chagas, 18-31.
5. Digoutte JP, 1974. Rapport Annuel de l'Institut Pasteur se al Guyane Francaise: 25.
6. Karabatsos N, 1985. International Catalogue of Arboviruses Including Certain other Viruses of Vertebrates. San Antonio: American Society for Tropical Medicine and Hygiene.
7. 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.
8. Diniz JA, Dos Santos ZA, Braga MA, Dias AL, da Silva DE, de Almeida Medeiros DB, de Souza Barros VL, Chiang JO, de Freitas Zoghbi KE, Quaresma JA, Takiya CM, Moura Neto V, de Souza W, da Costa Vasconcelos PF, Diniz CW, 2008. Early and late pathogenic events of newborn mice encephalitis experimentally induced by Itacaiunas and Curionopolis bracorhabdoviruses infection. PLoS One 3: e1733.

Annex:

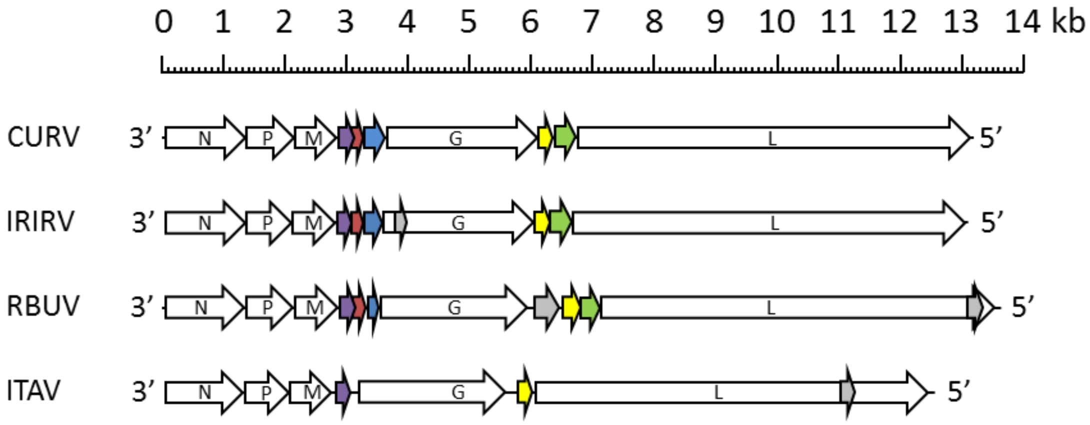

Figure 1. Genome organisations of curioviruses. The U1 (purple), U1x (orange) and U2 (blue) ORFs encode homologous sets of accessory proteins. The U3 ORFs of CURV and IRIRV, the U4 ORF of RBUV and the U2 ORF of ITAV each encode viroporin-like proteins (yellow). The U3x ORFs of CURV and IRIRV, and the RBUV U4x ORF also encode homologous sets of accessory proteins (green). [Note that the ITAV U1 protein also shares identifiable homology with the RBUV U2 protein].

```
CURV_U1         MVPSKTLGERMLVDLLECHCLVEEEETENERLYICTGDPDAIGDLFARACVWLVN-LEAL
IRIRV_U1        MVPSKTLGEKILTDLLEAYCLIIEDEWEEERVYTCEGPPDKVGDLYARTCVWLVN-LEAL
RBUV_U1         MVPSKTLGERILTELLESHALLEEEEFEAERVYICRGNPDQIGALYARACVWLVN-LEAI
                *********::*.:***.:.*: *:* * **:* * * ** :* *:**:****** ***:
ITAV_U1         MDPPSYWVN-------GARPVLLRESYPVGEQFIFRGFTSLLGSLNKANIVNMLEHLQKF
                * *..   :        .  :: .:.    . :   * .. :* *     * ::: *: :

CURV_U1         GCFSPHWDLDHE--EPGRLVISVFP---------
IRIRV_U1        GLITKNWELDHE--EPGRLVIKIYC---------
RBUV_U1         NLLSSNWDLDHE--EPGKLVVTIFA---------
                . :: :*:****  ***:**:.::
ITAV_U1         ASSPIYYKIEDSILEEGAFFVTILDPQNPQHSSV
                   .  :.::..  * * :.:.:
```

Figure 2. Clustal X alignments of curiovirus U1 proteins.

```
CURV_U1x        MKSLGDWLFQYSLDRSLFVTRMFESEEEFLDFYVDLYIACKSVNESIHVTVTRSLIDPFH
IRIRV_U1x       MKSLADWLSKSTVDGPVFITKMFKEENGLIDFYLDLYLEVVPIG--LEVRFCRSVVEPLH
RBUV_U1x        MKSLGSWLSQSSHDVPIYIIKWFEKEEDVVDFYIDLFLNAQEVSKEIVVKFHRSVIDPLY
                ****..** : : * .::: : *:.*: .:***:**::    :.  : * . **:::*::

CURV_U1x        VIFRIWQT------
IRIRV_U1x       VIFIISP-------
RBUV_U1x        VIFEISSGPLSQHP
                *** *
```

Figure 3. Clustal X alignments of CURV, IRIRV and RBUV U1x proteins.

A

```
CURV_U2         MKNTMEAKAVVAGILLLSSLILFPTL---DAQALTILKRTCGDGMMKRVPCKLMDSVENG
IRIRV_U2        MKKTMGAKGRLACIFIG--MVFFSYLRESDQQGFTYIKRTCGDKMMRVIPCNLMDSVKTL
RBUV_U2         MKV----------VFIIY-TLLFSHLNSSE--IFDDEESSCDGNELEKLQC-MLDSLNSG
                **           :::    ::*. *   : : :   : :*..  :. : * ::**::.

CURV_U2         ISARGSCLIFCSSKKKIKGKDGRMRNLCLTGDPRADEIIKCREQILKKKTEI
IRIRV_U2        TGPKGKCLVFCSSKRKIKGRDGKQRDLCLTGDPRSDEVMKCKDKISGTKSP-
RBUV_U2         -GVLESVPQTSTSPQGVGAIISGIEKPSFFLQLFLPFAMAFRDSIV------
                 .   .    .:* : :    .  .. .:  :      :  ::.*
```

B

```
RBUV_U2         MKVVFIIYTLLFSHLNSSEIFDDEESSCDGNE-LEK-LQCMLDSLNSG---GVLESVPQT
ITAV_U1         MD-----PPSYW--VNGARPVLLRESYPVGEQFIFRGFTSLLGSLNKANIVNMLEHLQKF
                *.      .  :  :*.:. .  .**   *:: : : : .:*.***..   .:** : :

RBUV_U2         STSPQGVGAIISGIEKPSFFLQLFLPFAMAFRDSIV
ITAV_U1         ASSPIYYKIEDSILEEGAFFVTILDPQNPQHSSV--
                ::**       * :*: :**: :: *    . .
```

Figure 4. Clustal X alignments of CURV, IRIRV and RBUV U2 proteins (A) and the RBUV U2 protein and the ITAV U1 protein (B).

```
CURV_U3x        MIKIRKEGSSKDDFLFYQKVGERIQNIFPDAINLKVHRSQDGVFILDLTWPPGVSVLLVP
IRIRV_U3x       MIKIRKTQENRDEFSLYQRFGERLVSLFPDSFDFYIKREEGGTIALTLTWPPGLPVLIIP
RBUV_U4x        MIRLVKSKETMEDYLFYRNLGERLVDMFPELFFLSITRSDNGVVSLDLNWRKGTPILLIP
                **:: *  .. ::: :*:..***: .:**: : : : *.:.*.. * *.*  * .:*::*

CURV_U3x        RRLKTVRRFVSERPGRELFLLGDLLYNKMGLKRSQIDTSYEMIHGGKWAIISIYG
IRIRV_U3x       RRLKTSRRFIVYRPGRDLFVIANLLYNVMGLKKSQIDMRYEMINEGKWAIVTLYG
RBUV_U4x        RRLKTQRRFVSYRPGRDIYLVSDFLYGKVGLKKSQIDCTYSLIMKGKAAIISIHG
                ***** ***:  ****:::::.::**. :***:****  *.:*  ** **::::*
```

Figure 5. Clustal X alignments of CURV and IRIRV U3x proteins and RBUV U4x protein.

```
CURV_U3         MESSLEKNILGGAWKDLEKYWKVIERWAQFAFWFFVVIILLKLLKIVLEVSQKILSGCKG
IRIRV_U3        MEKSLEKNFGLDGLKFLEKGWEDFKKSVAVIFWILIVIAIIKVLSFLARVLGQVFRALTF
RBUV_U4         MEPVLEKNWGGNILEGFGKYWVEVRYWVSVSFWFFIGIILIKIIKSLVLIGEKIVSCSGA
                **  ****   .  : : * *  ..  . . **::: * ::*::. :  :  ::.
ITAV_U2         MENKAFGLDDLGAFFKNFITGISNQFNWFFKTVFSLVIIFLLIKILVKFMSGLSNCIAAG

CURV_U3         IRRSTGRVLKRLRKRNQRKIKALDTRVRQQK-
IRIRV_U3        VSEFAGKGVKKLKRVKKRRLKLRKK-------
RBUV_U4         IYSIIKKHCLRIKRTTRRRRKIKKHHHNDPTR
                :     :   :::: .:*: *  .
ITAV_U2         FKIRRQVRHWRNGNEGSRENP
```

Figure 6. Curiovirus viroporin-like proteins (CURV U3, IRIRV U3, RBUV U4 and ITAV U2).

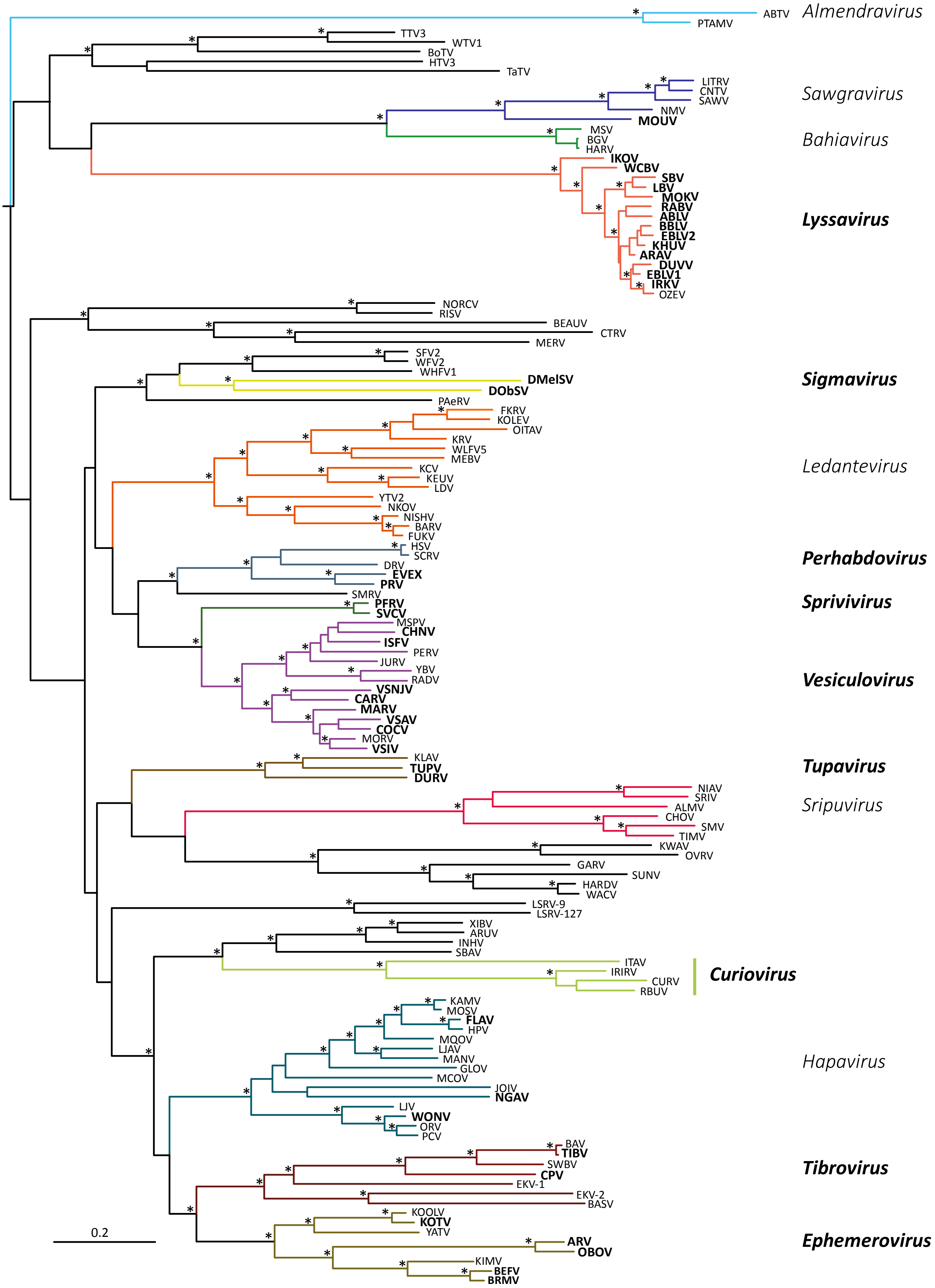

Figure 7. ML phylogenetic tree of 132 animal rhabdovirus L protein sequences. Branches are colour-coded according to existing genera (named in bold italics) or proposed new genera (named light italics) as presented in Walker *et al*. (2015) PLoS Pathogens 11 (2): e1004664[2]. The clade representing the proposed new genus *Curiovirus* is highlighted. Horizontal branch lengths are

drawn to a scale of amino acid substitutions/site, and all bootstrap support values (BSP) ≥ 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[2]. Virus abbreviations and Genbank accession numbers are as listed in **Table 1**.

	CURV	IRIRV	RBUV	ITAV
CURV	100			
IRIRV	76.0	100		
RBUV	81.2	77.2	100	
ITAV	46.6	48.2	46.1	100

Figure 8A. Curiovirus N protein amino acid sequence identity (%; as estimated in MEGA6 by p-distance).

	CURV	IRIRV	RBUV	ITAV
CURV	100			
IRIRV	67.6	100		
RBUV	68.9	66.3	100	
ITAV	47.1	45.8	45.9	100

Figure 8B. Curiovirus L protein amino acid sequence identity (%; as estimated in MEGA6 by p-distance).

	CURV	IRIRV	RBUV	ITAV
CURV	100			
IRIRV	56.2	100		
RBUV	55.8	54.8	100	
ITAV	24.8	25.1	23.1	100

Figure 8C. Curiovirus 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.	*Moussa virus*	11526	FJ985749
Muir Springs virus	MSV	76V-23524	not classified		12580	KM204990
Bahia Grande virus	BGV	TB4-1054	not classified		12639	KM205018
Harlingen virus	HARV	PV01-3828	not classified		12626	KM205003
Ikoma virus	IKOV	RV2508	*Lyssavirus*	*Ikoma lyssavirus*	11902	JX193798
West Caucasian bat virus	WCBV	NZ86	*Lyssavirus*	*West Caucasian bat lyssavirus*	12278	EF614258
Shimoni bat virus	SBV	N613	*Lyssavirus*	*Shimoni bat lyssavirus*	12045	GU170201
Lagos bat virus	LBV	0406SEN	*Lyssavirus*	*Lagos bat lyssavirus*	12016	EU293108
Mokola virus	MOKV	RV1035	*Lyssavirus*	*Mokola lyssavirus*	11939	KF155006
rabies virus	RABV	HN10	*Lyssavirus*	*Rabies lyssavirus*	11932	EU643590
Australian bat lyssavirus	ABLV	96-1256	*Lyssavirus*	*Australian bat lyssavirus*	11918	AF081020
Bokeloh bat lyssavirus	BBLV	21961	Lyssavirus	*Bokeloh bat lyssavirus*	11900	JF311903
European bat lyssavirus 2	EBLV2	RV1333	*Lyssavirus*	*European bat lyssavirus 2*	11930	EF157977
Khujand virus	KHUV		*Lyssavirus*	*Khujand lyssavirus*	11903	EF614261
Aravan virus	ARAV		*Lyssavirus*	*Aravan lyssavirus*	11918	EF614259
Duvenhage virus	DUVV	86132SA	*Lyssavirus*	*Duvenhage lyssavirus*	11976	EU293119
European bat lyssavirus 1	EBLV1	RV9	*Lyssavirus*	*European bat lyssavirus 1*	11966	EF157976
Irkut virus	IRKV	J426	*Lyssavirus*	*Irkut lyssavirus*	11980	EF614260
Ozernoe virus	OZEV	OI56	not classified		11980	FJ905105
North Creek virus #	NORCV	954	not classified		partial	KF360973
Riverside virus	RISV	Drava-1	not classified		11713	KU248085
Beaumont virus	BEAUV	6	not classified		partial	KF310911
Culex tritaeniorhynchus rhabdovirus	CTRV	GHK	not classified		11190	LC026102
Merida virus	MERDV	Mex-07	not classified		11798	KU194360
Shayang fly virus 2	SFV2	SYY1-8	not classified		12291+	KM817635
Wuhan fly virus 2	WFV2	SYY1-3	not classified		12247+	KM817646
Wuhan house fly virus 1	WHFV1	SYY2-4	not classified		12651+	KM817648
Drosophila melanogaster sigmavirus	DMelSV	HAP23	*Sigmavirus*	*Drosophila melanogaster sigmavirus*	12390+	GQ375258
Drosophila obscura sigmavirus	DObSV	10A	*Sigmavirus*	*Drosophila obscura sigmavirus*	12676+	NC022580
Pararge aegeria rhabdovirus	PAeRV		not classified		13062	KR822826
Fikirini virus	FKRV	KEN352	not classified		11139+	KC676792
Kolente virus	KOLEV	DakArK7292	not classified		11120	KC984953
Oita virus	OITAV	296-1972	not classified		11355+	KM204998
Kumasi rhabdovirus	KRV	M35	not classified		11072	KJ179955
Wuhan louse fly virus 5	WLFV5	BFJSC-5	not classified		11103+	KM817654
Mount Elgon bat virus	MEBV	BP846	not classified		10941+	KM205026
Kern Canyon virus	KCV	M03790	not classified		11528+	KM204992
Le Dantec virus	LDV	DakHD763	not classified		11450+	KM205006
Yongjia tick virus 2	YTV2	YJ1-2	not classified		10833	KM817662
Nkolbisson virus	NKOV	YM 31-65	not classified		10942+	KM205017
Nishimuro virus	NISV		not classified		10881+	AB609604
Barur virus	BARV	6235	not classified		10853+	KM204983
Fukuoka virus	FUKV	FUK-11	not classified		10863	KM205001
Keuraliba virus	KEUV	DakAnD5314	not classified		11457+	KM205021
hybrid snakehead virus	HSV	C1207	not classified		11545	KC519324
Siniperca chuatsi rhabdovirus	SCRV		not classified		11545	DQ399789
dolphin rhabdovirus	DRV	pxV1	not classified		11141	KF958252
eel virus European X	EVEX	153311	*Perhabdovirus*	*Anguillid perhabdovirus*	11806	FN557213
perch rhabdovirus	PRV	J424	*Perhabdovirus*	*Perch perhabdovirus*	11487+	JX679246
Scophthalmus maximus rhabdovirus	SMRV		not classified		11492	HQ003891
pike fry rhabdovirus	PFRV	F4	*Sprivivirus*	*Pike fry sprivivirus*	11097	FJ872827
spring viremia of carp virus	SVCV	VR-1390	*Sprivivirus*	*Carp sprivivirus*	11019	AJ318079
Malpais Spring virus	MSPV	85-488NM	not classified		11019	KC412247
Chandipura virus	CHNV	CIN0451	*Vesiculovirus*	*Chandipura vesiculovirus*	11120	GU212856
Isfahan virus	ISFV	91026-167	*Vesiculovirus*	*Isfahan vesiculovirus*	11088	AJ810084

Perinet virus	PERV	DakArMg802	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	*Curiovirus**	*Itacaiunas curiovirus*	12536+	KM204984
Iriri virus	IRIRV	BeAr408005	*Curiovirus**	*Iriri curiovirus*	13070	KM204995
Curionopolis virus	CURV	BeAr440009	*Curiovirus**	*Curionopolis curiovirus*	13170	KM204994
Rochambeau virus	RBUV	CaAr16102	*Curiovirus**	*Rochambeau curiovirus*	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.	*Flanders virus*	13038	KM205002
Hart Park virus	HPV	AR7C	not classified		13104	KM205011
Mosqueiro virus	MQOV	BeAr185559	not classified		12957	KM205014
Landjia virus	LJAV	DakAnB769d	not classified		13695+	KM205010
Manitoba virus	MANV	Mn936-77	not classified		13784+	KM205008
Gray Lodge virus	GLOV	BFN3187	not classified		12403	KM205022
Marco virus	MCOV	BeAn40290	not classified		13294+	KM205005
Joinjakaka virus	JOIV	AusMK7937	not classified		13155	KM205016
Ngaingan virus	NGAV	MRM14556	unassigned sp.	*Ngaingan virus*	15764	NC013955
La Joya virus	LJV	J-134	not classified		15721	KM204986
Wongabel virus	WONV	CS264	unassigned sp.	*Wongabel virus*	13196	NC011639
Ord River virus	ORV	OR1023	not classified		13189+	KM205025
Parry Creek virus	PCV	OR189	not classified		13205+	KM204988
Bivens Arm virus	BAV	UF-10	not classified		13288+	KM205019
Tibrogargan virus	TIBV	CS132	*Tibrovirus*	*Tibrogargan tibrovirus*	13298	GQ294472
Sweetwater Branch virus	SWBV	UF-11	not classified		13141+	KM204997
Coastal Plains virus	CPV	DPP53	*Tibrovirus*	*Coastal Plains tibrovirus*	13203	GQ294473
Ekpoma-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	*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.