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:	***2010.009aV***	(to be completed by ICTV officers)

Short title: create species named Moussa virus in the family Rhabdoviridae
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

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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)	I. Kuzmin, C. Calisher, R Dietzgen

ICTV-EC or Study Group comments and response of the proposer:

suppported.

Date first submitted to ICTV: 09/02/2010
Date of this revision (if different to above):

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	***2010.009aV***	(assigned by ICTV officers)

To create one new species within:

Genus:	**unassigned**
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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Moussa virus	FJ985748 and FJ985749

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

Electron microscopy shows that the prototype virus of the species, Moussa virus (MOUV) has the distinctive morphology of rhabdoviruses (Figure 1), combined with a 11.5 kb genome with rhabdoviral organization (Figure 2). This justifies the placement of the virus in the family *Rhabdoviridae* in the order *Mononegavirales*. However, sequence comparisons and phylogenetic analyses do not associate MOUV with one of the recognized species or genera of this family (Table 1, Figure 3).

The MOUV genome has five non-overlapping ORF, separated by 2-3 bp intergenic regions that show distant relationships to rhabdoviral N, G, and L genes, while ORF2 and ORF3 have no significant similarity to sequences deposited in GenBank. Sequence similarity to other rhabdoviruses is <50% at amino acid level (<35% identity) for individual ORFs (Table 1). Phylogenetic analyses of L gene sequence indicates distant relationships to Tupaia virus, a species in the family not assigned to a genus, and to the unclassified Tibrogargan virus (Figure 3). Sequences for two MOUV strains are deposited under GenBank accession numbers FJ985748 and FJ985749.

MOUV was isolated from pools of *Culex decens* and *Culex* spp. mosquitoes collected in Côte d'Ivoire, Africa, in February-June of 2004 at locations within or adjacent to Taï National Park. The virus is propagated continuously in C6/36 cells, but inoculation of Vero, BHK, PSEK, 293, A549, Hep2, or primary chicken fibroblasts did not indicate a productive infection.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Quan et al. (2010) 'Moussa virus: A new member of the Rhabdoviridae family isolated from Culex decens mosquitoes in Côte d'Ivoire'. Virus Res. 147:17-24.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

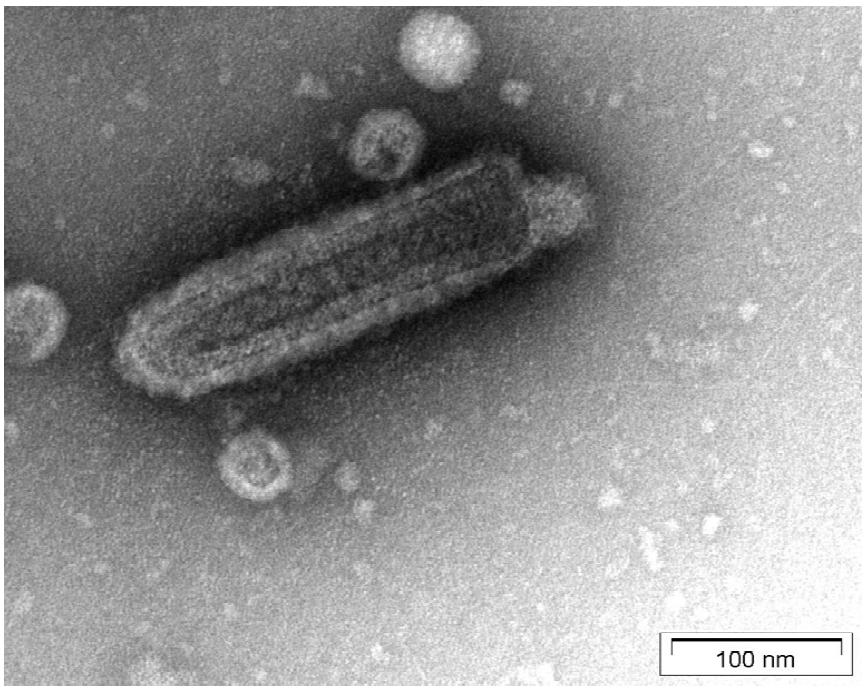

Figure 1. Morphology of MOUV (from Quan et al. (2010) Virus Res. 147: 17-24).

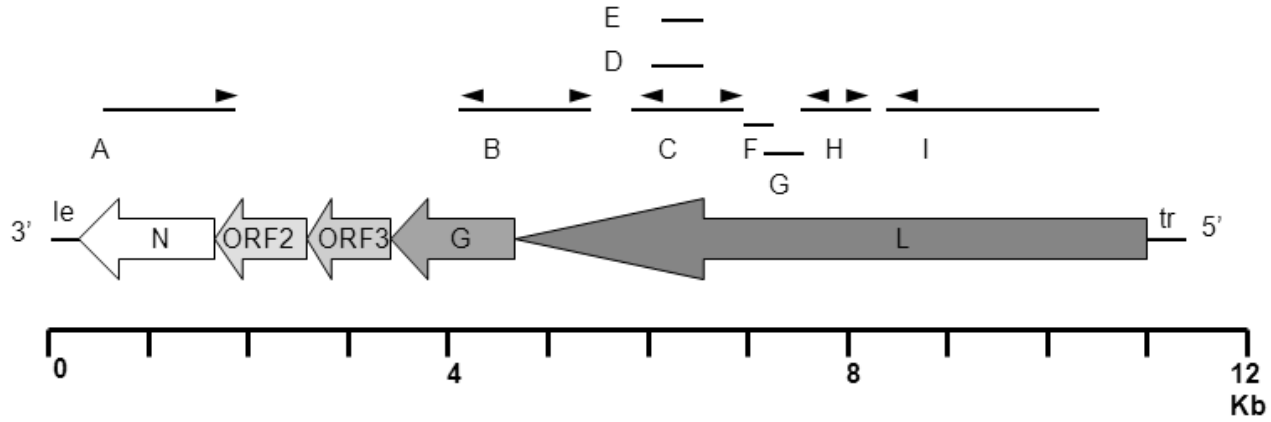

Figure 2. Schematic of genome organization of MOUV. Arrows represent the five open reading frames (ORF) of the 11,526 nt single strand, negative sense genome (from Quan et al. (2010) Virus Res. 147: 17-24).

Table 1. Sequence identity (I) and similarity (S) between MOUV (isolate D24) and other rhabdoviruses (from Quan et al. (2010) Virus Res. 147: 17-24).
***** Highest values for each gene are shown in bold

Virus	**Genus**	**N**		**[a]ORF2**		**[b]ORF3**		**G**		**L**	
		I	**S**	**I**	**S**	**I**	**S**	**I**	**S**	**I**	**S**
SYNV	*Nucleorhabdovirus*	16.1	26.1	12	21	15.4	22.7	13.8	21.3	17.4	27.7
LNYV	*Cytorhabdovirus*	15.3	25	14	20.7	16.5	22.2	12.7	19.8	18	29.5
IHNV	*Novirhabdovirus*	15.7	23.3	15.3	24.1	13.4	21.7	**23.2**	**36**	18.5	31.1
BEFV	*Ephemerovirus*	20.3	36.2	16.2	23.3	15.3	23.6	14.3	25.6	29.7	45.8
ABLV	*Lyssavirus*	22.1	36.9	16.2	26.8	15.3	22.6	22	33.1	29.5	46.3
EBV-1	*Lyssavirus*	20.6	34.7	15.6	27.9	16.8	28	19.5	30.4	29.4	46
EBV-2	*Lyssavirus*	17.6	31.8	15.8	24.6	13.8	19.2	21.7	36.1	29.2	46
MOKV	*Lyssavirus*	20.6	36	19.2	28.8	15.1	25.6	20.1	33.4	28.6	44.9
RABV	*Lyssavirus*	21	35.4	14	23.1	10.4	17.8	20.8	32.9	29.5	47
VSIV	*Vesiculovirus*	**23.5** *	40.2	17.8	29	14.4	24.3	22.9	35.5	**32.6**	**48.3**
COCV	*Vesiculovirus*	21.8	**42.2**	17.8	27.3	17.7	32.3	20.9	35.6	31.4	46.4
CHPV	*Vesiculovirus*	22.5	38.1	17.4	27.7	16.6	29.6	19.9	32.7	31.1	47.4
ISFV	*Vesiculovirus*	17.9	32.9	19.3	29.7	16.8	26.4	20.4	31.8	30	45.7
TUPV	unassigned	23	38	12.9	18.8	14.3	25.4	20.7	33	31.4	47.3
FLAV	unassigned	20.4	34.3	19.6	28.8	19	30.3	18.1	32.1	30.5	46.6
WONV	unassigned	22.6	36.4	**20.9**	**30.1**	**20.7**	**35**	20.3	33.3	30	46.8

[a]ORF2: genomic position of P
[b]ORF3: genomic position of M

ABLV : Australian bat lyssavirus; **BEFV** : Bovine ephemeral fever virus; **CHPV** : Chandipura virus ; **COCV** : Cocal virus ; **EBLV-1**: European bat lyssavirus 1; **EBLV-2**: European bat lyssavirus 2; ; **FLAV**: Flanders virus; **IHNV** : Infectious hematopoietic necrosis virus; **ISFV** : Isfahan virus; **LNYV** : Lettuce necrotic yellows virus; **MOKV** : Mokola virus; **RABV** : Rabies virus ; **SYNV** : Sonchus yellow net virus; **TUPV** : Tupaia rhabdovirus; **VSIV** : Vesicular stomatitis Indiana virus; **WONV** : Wongabel virus

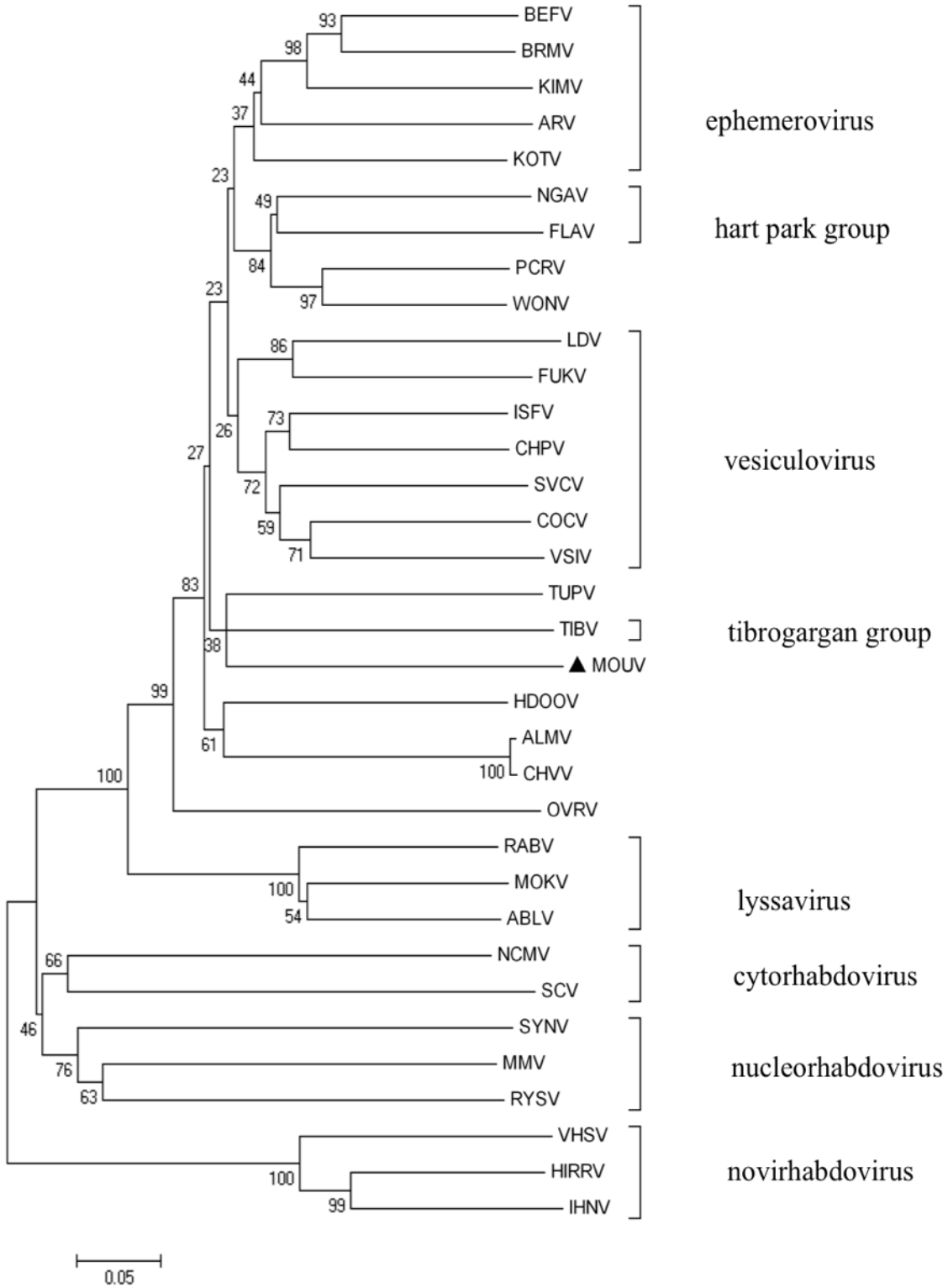

Figure 4. Phylogenetic analysis of partial L protein sequence (aa 560-700) (from Quan et al. (2010) Virus Res. 147: 17-24).

ABLV : Australian bat lyssavirus; **ALMV:** Almpiwar virus**; ARV:** Adelaide River virus; **BEFV**: Bovine ephemeral fever virus; **BRMV:** Berrimah virus**; CHPV** : Chandipura virus ; **CHVV:** Charleville virus; **COCV** : Cocal virus; **FLAV**: Flanders virus; **FUKV :** Fukuoka virus **;** **HDOOV:** Humpty Doo virus; **HIRRV:** Hirame rhabdovirus; **IHNV** : Infectious hematopoietic necrosis virus; **ISFV** : Isfahan virus; **KIMV:** Kimberley virus**; KOTV:** Kotonkon virus; **LDV**: Le

Dantec virus; **MMV**: Maize mosaic virus; **MOKV** : Mokola virus; **MOUV**: Moussa virus; **NCMV:** Northern cereal mosaic virus; **NGAV**: Ngaingan virus; **OVRV:** Oak-vale virus; **PCRV:** Parry Creek virus**; RABV** : Rabies virus ; **RYSV:** Rice yellow; stunt virus; **SCV**: Spring viremia of carp virus**; SVCV:** Spring viremia of carp virus; **SYNV** : Sonchus yellow net virus; **TIBV:** Tibrogarganvirus **TUPV** : Tupaia rhabdovirus; **VHSV:** Viral hemorrhagic septicemia virus; **VSIV** : Vesicular stomatitis Indiana virus; **WONV** : Wongabel virus