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:	**2011.006aV.N.v1**	(to be completed by ICTV officers)

Short title: create species named *Shimoni bat virus* in the genus *Lyssavirus*
(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:

Ivan Kuzmin (ibk3@cdc.gov) and Noel Tordo (ntordo@pasteur.fr)

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)	Rhabdoviridae Study Group

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

Supported with modifications

Date first submitted to ICTV: 08 July 2011
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	**2011.006aV**	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Lyssavirus***
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:**
Shimoni bat virus	GU170201

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

The species within the *Lyssavirus* genus are demarcated based on several criteria. These include:

1. Genetic distances, with the threshold of 80-82% nucleotide identity for the complete N gene, that provides a better quantitative resolution compared to other genes, or 80-81% nucleotide identity for concatenated coding regions of N+P+M+G+L genes. Globally, all isolates belonging to the same species have higher identity values than the threshold, except the viruses currently included in the species *Lagos bat virus*. Some authors have suggested that Lagos bat virus be subdivided into several genotypes. However, as these representatives are segregated into a monophyletic cluster in the majority of phylogenetic reconstructions, in the absence of other sufficient demarcation characters it has, to now, not been possible to subdivide Lagos bat virus, and establish several viral species for its lineages.

2. Topology and consistency of phylogenetic trees, obtained with various evolutionary models.

3. Antigenic patterns in reactions with anti-nucleocapsid monoclonal antibodies (preceded by serologic cross-reactivity and definition of lyssavirus serotypes, using polyclonal antisera).

4. Whenever available, additional characters, such as ecological properties, host and geographic range, pathological features are recruited.

Phylogenetic and serological relationship correlate, which contributes to the delineation of two major phylogroups within the genus *Lyssavirus*. Phylogroup I includes Rabies virus (RABV), Duvenhage virus (DUVV), European bat lyssaviruses, type 1 and 2 (EBLV-1 and 2), Australian bat lyssavirus (ABLV), Aravan virus (ARAV), Khujand virus (KHUV) and Irkut virus (IRKV). Phylogroup II includes Lagos bat virus (LBV) and Mokola virus (MOKV). In addition, West Caucasian bat virus (WCBV) cannot be included into any of these phylogroups, based on the criteria above. There is a significant serological cross-neutralization within phylogroups, but very limited cross-neutralization has been detected between phylogroups.

Based on these criteria, Shimoni bat virus cannot be included in any of the existing species but should be considered a distinct species.

Shimoni bat virus (SHIBV) was isolated from the Commerson's leaf-nosed bat (*Hipposideros commersoni*) in Kenya in 2009. It is pathogenic to laboratory mice and hamsters via intracranial and intramuscular inoculation routes, causing acute progressive fatal encephalitis (rabies). Genome organization and sequence relationships of SHIBV are consistent with its classification as a lyssavirus. The genome (GenBank accession No. GU170201) is a negative-sense, single-stranded RNA, 12045 nt in length, that contains 5 genes arranged in the order 3'-N-P-M-G-L-5'.

Demarcation from other lyssavirus species:

1. SHIBV demonstrates 78.8% of nucleotide identity for the N gene, and 75.1% identity for the concatenated sequences of N+P+M+G+L genes, to the most similar isolates of LBV (Annex; Tables 1 and 2).

2. In all phylogenetic constructions, except those for the G gene, SHIBV is placed within Phylogroup II, either between LBV and MOKV, or ancestrally to these viruses, without significant support for joining to either of these species (Annex; Figure 1). The only exception is G gene, where SHIBV is confidently (but still ancestrally) joined to LBV, with 99% bootstrap support.

3. Antigenic patterns in reactions with anti-nucleocapsid monoclonal antibodies distinguish SHIBV from other lyssaviruses (Annex; Table 3). Chimeric rabies vaccine, that coded for glycoprotein of LBV, did not protect laboratory animals from challenge with SHIBV.

4. The SHIBV (isolated from insectivorous Commerson's leaf-nosed bat *H. commersoni*) demonstrates phylogenetic relatedness to LBV, that circulates in fruit bats of the family *Pteropodidae* (including Egyptian fruit bats, *Rousettus aegyptiacus*, which sympatrically roost in the cave with Commerson's leaf-nosed bats from which SHIBV was isolated). Thus, Commerson's leaf-nosed bats could be the reservoir hosts for SHIBV, or SHIBV could have occurred from a spill-over infection from Egyptian fruit bats. A serological survey demonstrated partial cross-reactivity between SHIBV and LBV, which is commonly observed within lyssavirus phylogroups. However, Commerson's leaf-nosed bats demonstrated greater seroprevalence and greater virus-neutralizing titers to SHIBV than to LBV (mean difference 1.16 $\log_{10}$ (95% CI: 0.94-1.40; $p<0.001$). The opposite pattern was observed for sera of Egyptian fruit bats, showing greater seroprevalence and virus-neutralizing titers to LBV than to SHIBV (mean titer difference 1.06 $\log_{10}$ (95% CI: 0.83-1.30; $p<0.001$) (Annex; Figure 2). Moreover, the seroprevalence of Commerson's leaf-nosed bats to SHIBV was similar in the cave where these bats roosted sympatrically with Egyptian fruit bats bats, and in a distant cave, where no Egyptian fruit bats were present.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bourhy H., B. Kissi, H. Badrane, N. Tordo, 1993. Molecular diversity of the Lyssavirus genus. Virology 194, 70-81.

Badrane H., C. Bahloul, P. Perrin, N. Tordo, 2001. Evidence of two lyssavirus phylogroups with distinct pathogenicity and immunogenicity, J. Virol. 75, 3268-3276.

Kuzmin, I.V., Hughes, G.J., Botvinkin, A.D., Orciari, L.A., Rupprecht, C.E., 2005. Phylogenetic relationships of Irkut and West Caucasian bat viruses within the Lyssavirus genus and suggested quantitative criteria based on the N gene sequence for lyssavirus genotype definition. Virus Res. 111, 28-43.

Markotter, W., Kuzmin, I., Rupprecht, C.E., Nel, L.H., 2008. Phylogeny of Lagos bat virus: challenges for lyssavirus taxonomy. Virus Res. 135(1), 10-21.

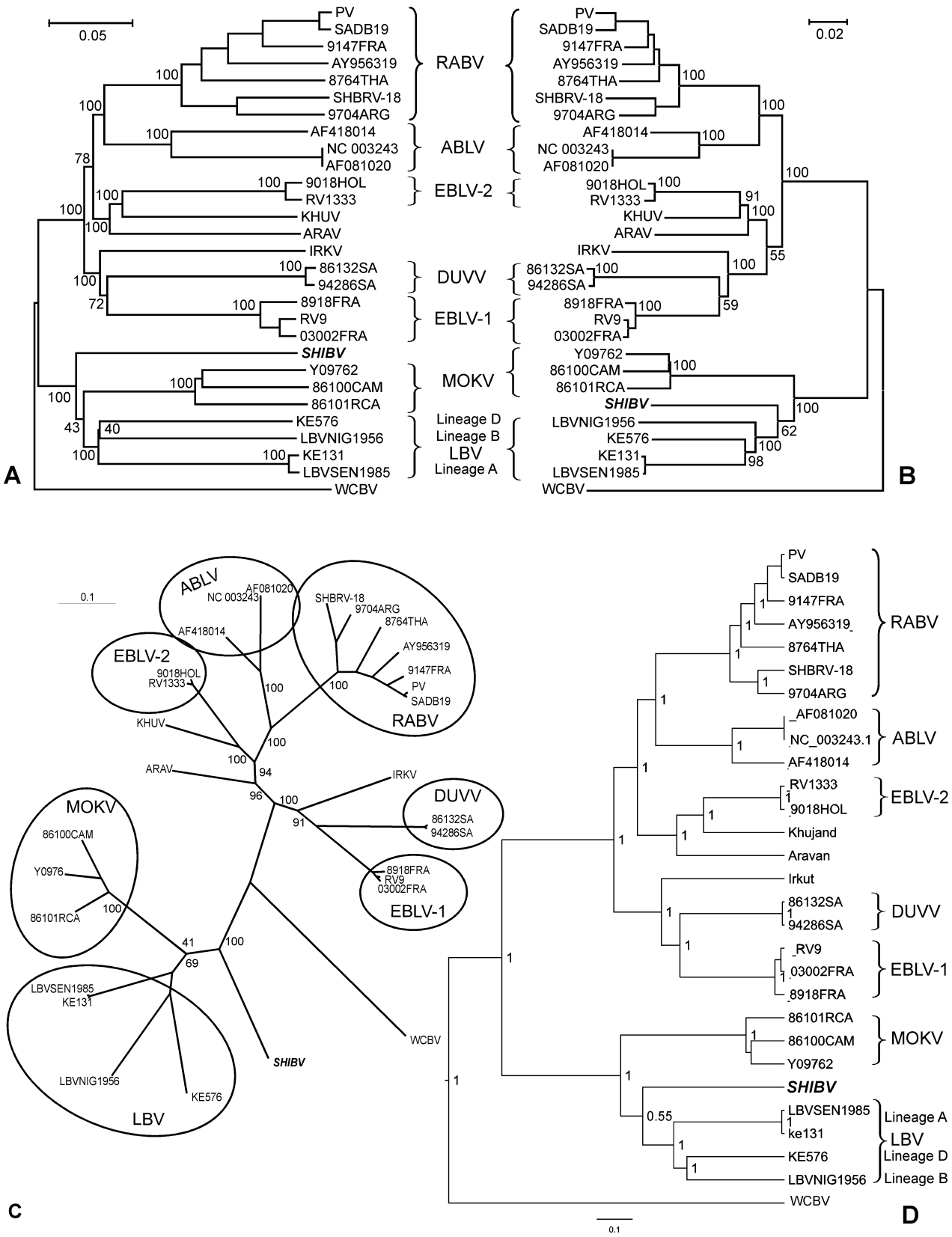
Delmas, O., Holmes, E.C., Talbi, C., Larrous, F., Dacheux, L., Bouchier, C., Bourhy, H., 2008. Genomic diversity and evolution of the lyssaviruses. PloS One. 3(4), e2057.

Kuzmin I.V., Mayer A.E., Niezgoda M., Markotter W., Agwanda B., Breiman R.F., Rupprect C.E., 2010. Shimoni bat virus, a new representative of *Lyssavirus* genus. Virus Res. 149: 197-210.

Kuzmin I.V., Turmelle A.S., Agwanda B., Markotter W., Niezgoda M., Breiman R.F., Rupprecht C.E. 2011. Commerson's leaf-nosed bat (*Hipposideros commersoni*) is the likely reservoir of Shimoni bat virus. Vector Borne and Zoonotic Dis (in press).

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.



Annex. Figure 1. Phylogenetic reconstructions of the *Lyssavirus* genus based on the concatenated sequences of the N+P+M+G+L genes. A: neighbor-joining, nucleotides; B: neighbor-joining, amino acids; C: maximum likelihood, nucleotides; D: Bayesian, nucleotides.

Table1
Identity values (%) of the N genes and deduced nucleoprotein sequences of lyssaviruses.

Species	RABV	LBV	MOKV	DUVV	EBLV1	EBLV2	ABLV	ARAV	KHUV	IRKV	WCBV	SHIBV
RABV	*93.7–100.0*[a] 82.3–99.9	*81.1–85.3*	*76.4–82.8*	*87.3–88.4*	*87.1–88.8*	*86.2–89.8*	*89.1–92.8*	*88.9–90.4*	*89.6–91.1*	*85.7–87.5*	*80.5–81.2*	*85.1–86.2*
LBV	72.0–75.1	*92.8–100.0* 79.4–99.7	*88.4–91.7*	*85.3–87.5*	*83.1–86.4*	*79.1–82.7*	*81.3–85.3*	*84.6–88.2*	*81.3–84.8*	*84.2–87.1*	*82.4–84.2*	*90.8–93.2*
MOKV	69.4–73.7	75.5 –78.7	*98.2–98.8* 88.1–88.5	*84.2–84.7*	*82.9–84.0*	*79.1–80.9*	*82.4–84.0*	*84.6–85.7*	*81.5–82.6*	*84.4–85.3*	*82.0–82.8*	*89.1–89.5*
DUVV	70.1–75.3	73.0 –75.3	71.9 –73.6	*100.099.1*	*92.6–93.2*	*85.3–86.2*	*88.4–89.5*	*91.3*	*88.9*	*90.0*	*84.2*	*87.1*
EBLV1	70.4–76.2	73.4 –75.9	71.9 –73.1	79.0 –79.8	*99.1–100.0* 95.4–98.4	*86.9–88.0*	*88.0–90.0*	*91.7–92.0*	*89.5–90.2*	*92.0–92.6*	*82.0–82.4*	*86.4–86.6*
EBLV2	70.9–75.5	71.8 –73.7	70.7 –72.7	75.6 –75.9	76.1 –76.8	*98.6 97.5*	*86.4–87.8*	*88.2–88.6*	*90.2–91.1*	*86.2–86.6*	*80.2–80.9*	*80.0–80.7*
ABLV	72.4–78.9	72.8 –75.4	71.9 –73.3	76.0 –77.0	76.7 –77.4	74.5 –76.2	95.5–100.0 83.8–99.9	*91.1–92.4*	*90.4–92.2*	*87.7*	*81.3*–82.6	84.4–*85.5*
ARAV	73.2–76.8	74.2 –75.8	74.0 –74.9	77.6 –77.9	77.8 –78.2	76.6	76.5 –76.6		*92.6*	*90.6*	*83.5*	*86.8*
KHUV	75.3–76.5	71.9 –74.0	70.4 –71.0	75.6 –75.8	77.0 –77.6	79.0 –79.5	75.8 –78.1	79.0		*88.0*	*81.1*	*84.2*
IRKV	73.4–75.1	73.1 –75.1	73.3 –74.3	77.5 –77.8	78.2 –78.5	76.9 –77.3	75.2 –76.0	76.2	76.1		*83.1*	*86.4*
WCBV	72.2–74.2	73.9 –75.2	72.8 –73.2	73.3 –73.7	72.2 –72.8	72.1 –72.4	73.1	73.1	70.5	72.1		*83.5*
SHIBV	71.9–74.8	77.4 –78.8	76.2 –77.1	74.7 –74.9	73.3 –73.9	72.6 –73.2	72.5 –74.6	75.1	73.9	75.3	74.0	

[a] Above the dash and in the upper-right triangle—mino acid identities (in italics); below the dash and in the lower-left triangle—nucleotide identiti es (in bold). When only one sequence of a certain species was available for comparison, there is no value.

Table2
Identity values (%) of the aligned concatenated N + P + M + G + L genes and deduced protein sequences of lyssaviruses.

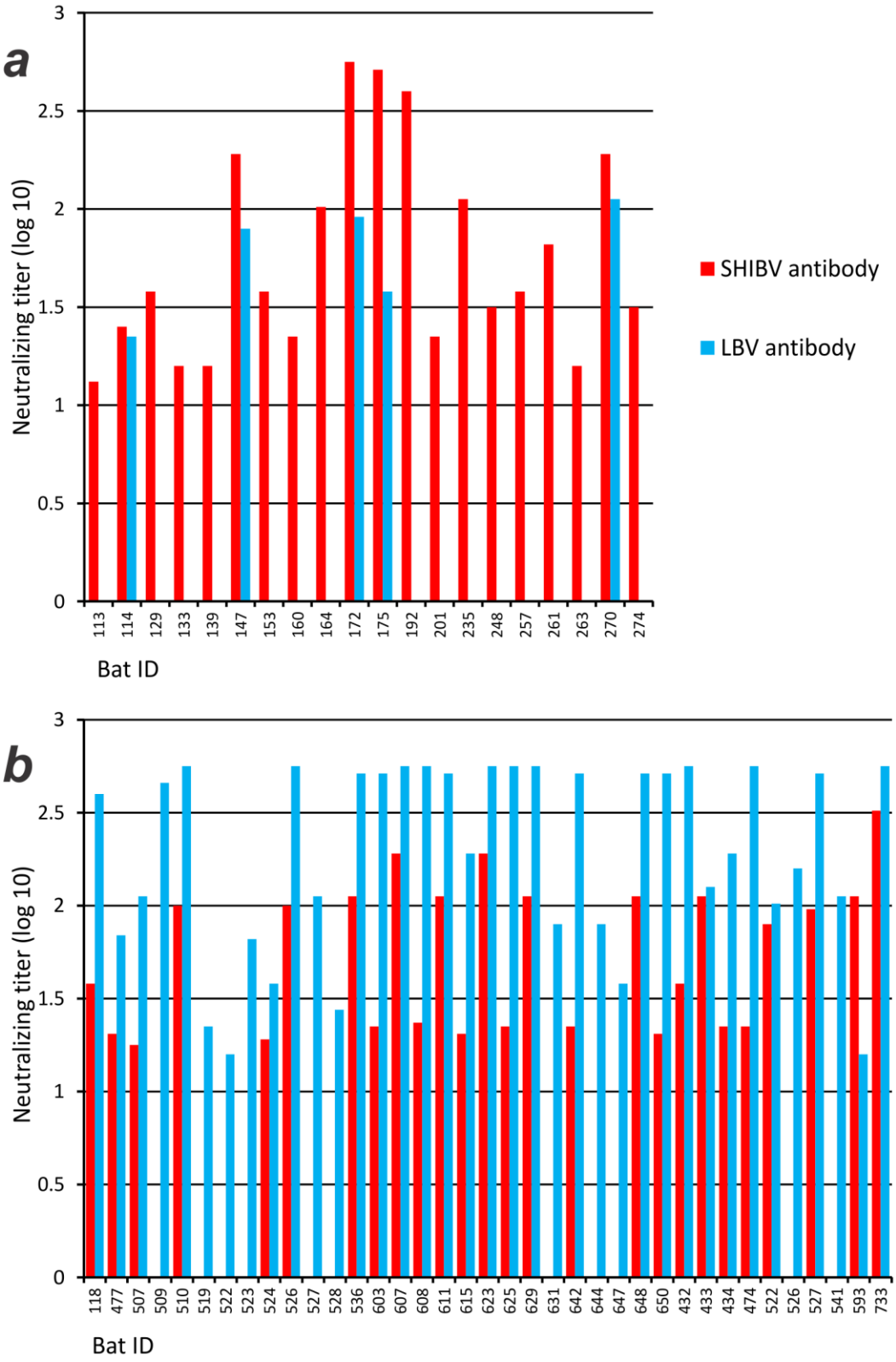
Species	RABV	LBV	MOKV	DUVV	EBLV1	EBLV2	ABLV	ARAV	KHUV	IRKV	WCBV	SHIBV
RABV	*91.2–100.0*[a] 81.6–98.2	*73.1–75.0*	*72.5–74.0*	*79.5–81.0*	*81.2–82.7*	*82.5–84.5*	*83.2–86.9*	*83.1–84.5*	*83.9–85.3*	*80.5–82.0*	*68.8–69.8*	*74.3–75.4*
LBV	66.6–68.1	*87.6–99.7* 76.1–98.8	*83.3–85.6*	*73.9–74.7*	*75.1–76.0*	*74.0–75.5*	*73.4–75.3*	*75.4–76.2*	*74.6–75.8*	*75.6–76.0*	*70.6–71.4*	*85.6–86.3*
MOKV	66.9–67.8	73.2 –74.2	*95.3* 86.5–87.4	*73.0–73.3*	*74.4–74.7*	*73.6–74.0*	*72.6–74.3*	*74.1–74.5*	*74.1*	*75.2*	*70.2–70.6*	*81.7–82.1*
DUVV	70.8–71.7	67.3 –68.0	67.0 –67.5	*99.3* 89.9	*87.5–87.8*	*82.6–83.0*	*80.0–81.9*	*84.6*	*83.8*	*85.1–85.4*	*69.9*	*74.4*
EBLV1	71.6–72.4	68.0 –68.7	67.3 –67.8	75.9 –76.1	*98.7–99.4* 95.5–98.1	*85.3–85.7*	*81.8–84.0*	*87.7–88.0*	*86.5*	*89.0*	*70.6*	*76.1*
EBLV2	72.3–73.7	67.2 –68.2	67.5 –68.0	73.2	74.2	*99.1* 98.0	*84.7–87.0*	*89.3*	*90.8*	*84.5*	*70.3*	*74.4*
ABLV	73.0–74.6	66.9 –68.8	66.5 –67.7	73.9 –75.5	72.3 –73.5	73.9 –75.5	*92.7–100.0* 82.7–99.9	*84.8–87.1*	*85.8–88.6*	*82.0–83.3*	*69.9–70.8*	*74.5–75.6*
ARAV	72.5–73.2	68.2 –68.6	67.7 –68.1	73.7 –75.0	75.3	76.8	73.7 –75.0		*90.7*	*86.3*	*70.8*	*75.5*
KHUV	72.9–73.8	67.5 –68.1	67.2	74.5 –75.8	74.6	78.7	74.5 –75.8	77.5		*85.6*	*70.6*	*75.5*
IRKV	71.3–72.3	67.9 –68.7	67.8 –68.3	71.6 –72.8	76.4	73.7	71.6 –72.8	74.1	74.3		*70.6*	*75.9*
WCBV	64.7–65.5	65.8	65.2 –65.6	65.2	65.5	65.5	65.2	65.7	65.4	65.5		*71.2*
SHIBV	67.0–67.6	73.8 –75.1	71.9 –72.2	67.1 –68.0	68.1	68.1	67.1 –68.0	68.5	67.9	68.5	66.4	

[a] Above the dash and in the upper-right triangle—amino acid identities (in italics); below the dash and in the lower-left triangle—nucleotide identit ies (in bold). When only one sequence of a certain species was available for comparison, there is no value.

Table3
Antigenic patterns of SHIBV compared to other lyssaviruses by a panel of N-MAbs.

Isolate	N-MAbs																			
	C1 (3-1)	C2 (8-2)	C3 (11-1)	C4 (15-2)	C5 (22-3)	C6 (23-4)	C7 (24-1)	C8 (24-10)	C9 (52-1)	C10 (52-2)	C11 (61-1)	C12 (62-4)	C13 (71-2)	C15 (97-3)	C16 (97-11)	C17 (141-1)	C18 (143-1)	C19 (146-3)	C20 (164-2)	422-5
SHIBV		+	+	+	+				+	+						+				+
LBV (LBVNIG1956)			+		+				+	+						+				+
LBV (LBVSA1982)			+		+				+	+						+				+
LBV (LBVAFR1999)			+		+				+	+						+				+
LBV (KE131)			+		+				+	+						+				+
LBV (KE576)			+		+		+		+	+						+				+
MOKV		+	+		+				+	+						+				+
RABV (CVS)	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
RABV (Fox, Europe) [a]	+	+	+	+	+	+		+	+	+	+		+	+	+	+		+	+	
EBLV1 [a]	+		+		+	+		+	+	+						+			+	
EBLV2 [a]	+		+		+			+	+	+			+			+	+	+		
DUVV [a]			+		+	+		+	+	+	+					+				+
ARAV [b]			+		+	+		+	+	+						+		+		
KHUV [b]	+				+	+										+		+	+	
IRKV [b]	+		+		+	+		+	+	+						+				
WCBV [b]		+			+		+		+		+	+	+							

[a] Patterns obtained from Smith (1989) .
[b] Patterns obtained from Botvinkin et al. (2003)



Annex. Figure 2. Antibody titers against LBV and SHIBV in Commerson's leaf-nosed bats (a) and Egyptian fruit bats (b) during the serologic survey in Kenya, 2009-2010.