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:	***2016.014aM***	(to be completed by ICTV officers)

Short title: One (1) new species in the genus *Mammarenavirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Kim Blasdell, kblasdell@hotmail.co.uk
Veasna Duong, dveasna@pasteur-kh.org
Marc Eloit, marc.eloit@pasteur.fr
Fabrice Chretien, fabrice.chretien@pasteur.fr
Sowath Ly, lsowath@pasteur-kh.org
Vibol Hul, vibol_hul@yahoo.com
Vincent Deubel, deubelvincent@gmail.com
Serge Morand, serge.morand@univ-montp2.fr
Philippe Buchy, buchyphilippe@hotmail.com / Philippe.x.buchy@GSK.com

Corresponding author with e-mail address:

Philippe Buchy, buchyphilippe@hotmail.com / Philippe.x.buchy@GSK.com

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 *Arenaviridae* Study Group

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

Date first submitted to ICTV:	July 18, 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	***2016.014aM***	(assigned by ICTV officers)

To create new species within:

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.

Genus:	***Mammarenavirus***
Subfamily:	**N/A**
Family:	***Arenaviridae***
Order:	**N/A**

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Loei River mammarenavirus	Loei River virus (LORV) isolate R5074	KC669698 (S segment) KC669693 (L segment)

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 11

Ten rodents from three agricultural-associated species were found to be infected with a novel virus, Loei River virus (LORV), in Loei, Thailand: six Savile's bandicoot rats, three greater bandicoot rats and one Indomalayan niviventer (Blasdell *et al*.). LORV is the first mammarenavirus to be detected in *Bandicota* rodents and, alongside the Cardamones variant of Wēnzhōu virus (WENV, species *Wenzhou mammarenavirus*), the first to be detected in this geographic region.

The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool for the assessment of novel arenaviruses (Radoshitzky *et al*.). Cut-off values chosen for classifying arenaviruses belonging to the same species using this tool are >80% and >76% nucleotide sequence identity in the S and L segments respectively. We therefore performed PASC on LORV: all samples were found most closely related to Wēnzhōu virus: 70.3–70.6% identity for the S segment and 62.7–63.1% identity for the L segment.

Deduced amino acid (aa) and nt sequences from two LORV isolates (R4937 and R5074) were compared to those of other representative mammarenaviruses (Blasdell *et al*.). An aa sequence divergence of >25% for the nucleoprotein (NP) was found between the Loei River isolates and mammarenaviruses of all currently established species.

MODULE 11: **APPENDIX**: supporting material

References:

Blasdell KR, Duong V, Eloit M, Chretien F, Ly S, Hul V, Deubel V, Morand S, Buchy P. 2016. Evidence of human infection by a new mammarenavirus endemic to Southeastern Asia. Elife **5**:e13135.

Radoshitzky SR, Bào Y, Buchmeier MJ, Charrel RN, Clawson AN, Clegg CS, DeRisi JL, Emonet S, Gonzalez J-P, Kuhn JH, Lukashevich IS, Peters CJ, Romanowski V, Salvato MS, Stenglein MD, de la Torre JC. 2015. Past, present, and future of arenavirus taxonomy. Arch Virol **160:**1851–1874.

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.

Animals tested for arenavirus RNA by animal (species) and site, with number of positives shown in bold (Blasdell *et al*.)

Animal (species)	**Thailand**			**Lao PDR**		**Cambodia**		**Total**
	Buriram	**Loei**	**Nan**	**Luang Prabang**	**Pakse**	**Mondulkiri**	**Veal Renh**	
Greater bandicoot rat (*Bandicota indica*)	0	12/**3**	17	1	1	0	0	31/**3**
Savile's bandicoot rat (*Bandicota savilei*)	2	21/**6**	0	0	1	11	0	35/**4**
Berdmore's berylmys (*Berylmys berdmorei*)	0	3	0	0	0	0	6	9
Bower's berylmys (*Berylmys bowersi*)	0	11	0	1	0	0	0	12
Indomalayan pencil-tailed tree mouse (*Chiropodomys gliriodes*)	0	1	0	0	0	0	0	1
Asian gray shrew (*Crocidura attenuata*)	0	1	0	0	0	0	0	1
Edward's leopoldamys (*Leopoldamys edwardsi*)	0	2	0	0	0	0	0	2
Indomalayan leopoldamys (*Leopoldamys sabanus*)	0	2	0	0	0	0	0	2
Indomalayan maxomys (*Maxomys surifer*)	0	9	0	0	0	2	11	22
Ryukyu mouse (*Mus caroli*)	4	9	0	0	0	0	0	13
Fawn-colored mouse (*Mus cervicolor*)	2	17	1	2	0	0	0	22
Cook's mouse (*Mus cookii*)	0	8	0	1	0	0	0	14

Details of rodent samples positive for arenavirus infection by screening RT-PCR (Blasdell *et al*.)

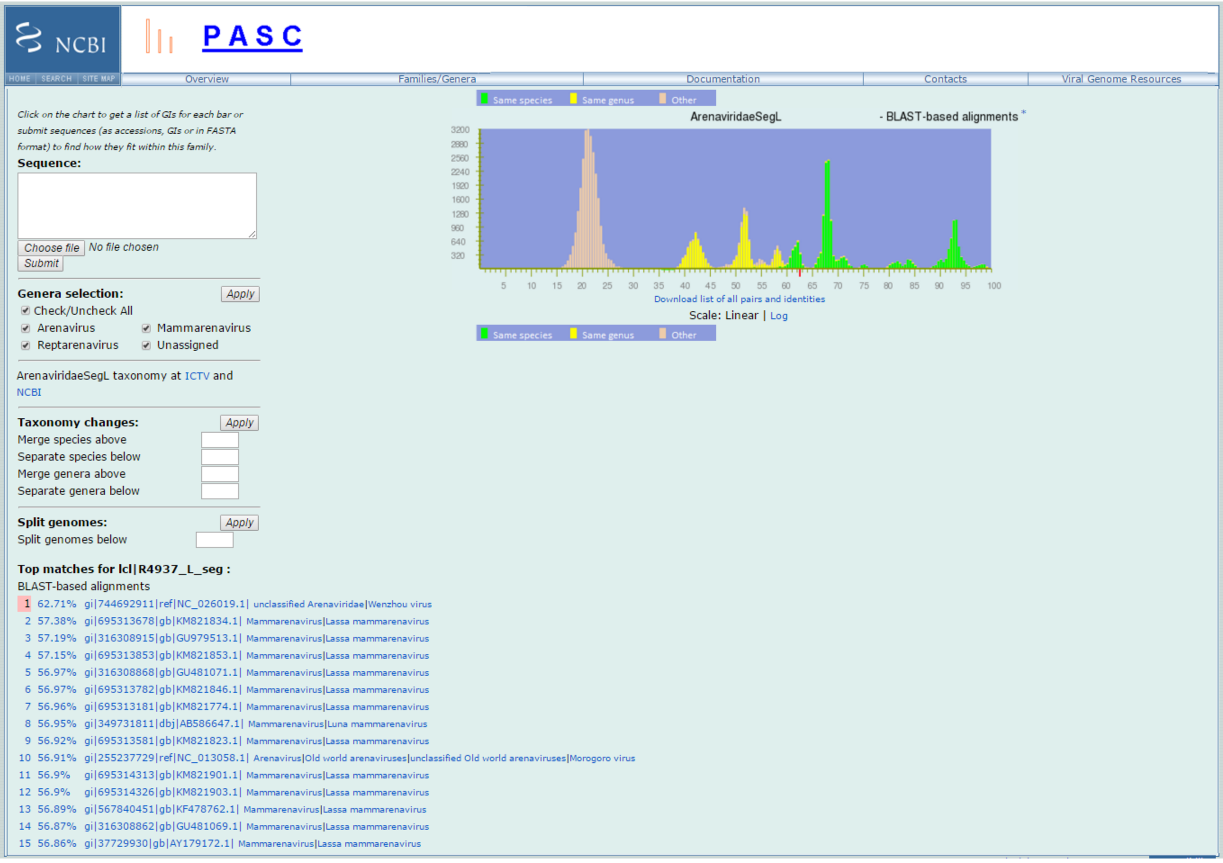
ID	Animal (species)	Date caught	Habitat type	Trapping site	Country
C0210	Brown rat (*Rattus norvegicus*)	26/11/2008	Isolated settlement alongside canal	Veal Renh	Cambodia
C0232	Pacific rat (*Rattus exulans*)	27/11/2008	Isolated settlement		
C0253	Pacific rat (*Rattus exulans*)	28/11/2008	Village		
C0283	Pacific rat (*Rattus exulans*)	29/11/2008	Village		
C0605	Brown rat (*Rattus norvegicus*)	09/07/2009	Hunter, unknown		
C0617	Brown rat (*Rattus norvegicus*)	09/07/2009	Village		
C0621	Pacific rat (*Rattus exulans*)	09/07/2009	Village		
C0623	Pacific rat (*Rattus exulans*)	09/07/2009	Village		
C0639	Pacific rat (*Rattus exulans*)	10/07/2009	Village		
C0649	Pacific rat (*Rattus exulans*)	10/07/2009	Village		
C0650	Pacific rat (*Rattus exulans*)	10/07/2009	Village		
C0651	Pacific rat (*Rattus exulans*)	10/07/2009	Village		
C0661	Pacific rat (*Rattus exulans*)	11/07/2009	Village		
C0663	Pacific rat (*Rattus exulans*)	11/07/2009	Village		
C0667	Brown rat (*Rattus norvegicus*)	11/07/2009	Village		
C0671	Pacific rat (*Rattus exulans*)	11/07/2009	Village		
C0680	Pacific rat (*Rattus exulans*)	11/07/2009	Village		
R4831	Great bandicoot rat (*Bandicota indica*)	12/02/2008	Lowland soybean plantation	Loei	Thailand
R4866	Savile's bandicoot rat (*Bandicota savilei*)	13/02/2008	Lowland soybean plantation		
R4868	Savile's bandicoot rat (*Bandicota savilei*)	13/02/2008	Lowland soybean plantation		
R4919	Savile's bandicoot rat (*Bandicota savilei*)	14/02/2008	Lowland soybean plantation		
R4937	Great bandicoot rat (*Bandicota indica*)	15/02/2008	Hunter, unknown		
R4961	Savile's bandicoot rat (*Bandicota savilei*)	16/02/2008	Hunter, unknown		
R4977	Great bandicoot rat (*Bandicota indica*)	16/02/2008	Hunter, unknown		
R4990	Savile's bandicoot rat (*Bandicota savilei*)	16/02/2008	Hunter, unknown		
R5074	Savile's bandicoot rat (*Bandicota savilei*)	18/02/2008	Lowland soybean plantation		
R5167	Indomalayan niviventer (*Niviventer fulvescens*)	20/02/2008	Hunter, unknown		

Nucleotide and amino acid sequence identities (%) between Cambodian (Cardamones variant of Wēnzhōu virus) and Thai isolates (Loei River virus) and selected other mammarenaviruses (Blasdell *et al*.)

Isolates	**Segment or ORF**	**nt / aa**	**Cambodian isolates**	**Thai isolates**	**Wenzhou**	**Lassa**	**Ippy**	**Mopeia**	**LCMV**	**Junin**	**Luna**	**Morogoro**
Cambodian isolates	L segment	nt	98.9	69.2-69.4	87.5-88.6	55.8-56.4	57.7-57.8	60.8	56.9	50.2-50.4	61.1-61.4	60.9-61.0
	L ORF	nt	99.3	67.3-67.5	88.0-89.0	59.7-60.6	60.4-60.5	59.2-59.4	55.6	50.6-50.9	59.6-60.9	59.6
		aa	99.6	69.2-69.4	92.2-94.8	55.5-56-4	57.7-57.8	56.6-57.1	48.5	37.9-38.0	55.8-55.9	55.6
	Z ORF	nt	99.5	73.4-74.5	837.-87.9	66.8-67.4	63.6	62.5	57.6-58.2	54.9-55.4	69.0-70.1	64.7-65.2
		Aa	98.8	79.2	89.4-93.9	70.1-75.3	70.1	64.9	59.4	40.3	63.6-64.9	61.0
	S segment	nt	99.5	71.7-72.1	87.5-89.8	61.7-68.1	66.6-66.8	66.6-67.0	61.6-61.8	54.6-54.8	67.6-68.2	66.7-66.9
	NP ORF	nt	99.3	73.1-74.4	86.6-90.0	67.1-68.2	68.3-68.4	67.6-67.9	62.9-63.2	55.1-55.6	69.0-70.3	68.7
		aa	99.8	82.9-84.2	87.3-96.5	72.2-73.8	74.4-74.6	73.5-73.8	64.0	51.9-52.5	73.3-74.0	74.0-74.6
	GPC	nt	99.7	69.1-70.0	88.6-89.7	67.3-68.6	64.7-65.7	65.3-65.7	61.2-61.4	53.4-53.6	66.3-66.6	49.9-65.2
		aa	99.8	79.5-81.1	95.5-96.4	74.2-76.2	69.5-71.3	71.5-72.8	57.2-57.5	48.2-43.0	72.6-74.4	73.1-74.4
Thai virus	L segment	nt	68-68.1	94.6	66.6-67.5	60.7-61.8	61.3-61.5	61.1-61.4	57.1	50.2-50.5	60.7-61.4	61.4-61.5
	L ORF	nt	67.3-67.5	95.1	67.9-68.8	59.6-59.9	59.9-60.4	61.6-62.1	55.7-56.2	49.9-50.8	60.4-61.6	59.9-60.2
		aa	69.2-69.4	96.7	69.6-70.7	55.7-56.4	56.5	56.6-57.1	49.0-49.4	37.1-37.5	55.9-56.3	56.5-56.7
	Z ORF	nt	73.4-74.5	95.4	69.4-75.0	65.2-66.8	64.1-65.8	69.0-69.6	58.7-59.2	54.3-56.0	65.8-72.8	66.3-66.8
		aa	79.2	98.5	73.1-74.6	67.5-71.4	68.8	70.1	58.4	42.9-44.2	70.1-71.4	66.2
	S segment	nt	71.7-72.1	94.4	71.0-72.2	65.8-67.3	66.1-66.8	66.2-67	61.7-62.6	53.9-55.0	65.2-68.1	66.1-67.9
	NP ORF	nt	73.1-74.4	94.6	72.2-74.1	65.2-67.8	66.6-67.3	66.9-67.7	62.4-63.2	54.1-54.4	66.1-68.0	67.3-68.9
		aa	82.9-84.2	98.1	78.3-87.2	73.3-74.6	72.0-72.9	73.8-74.4	64.2-64.6	49.9-51.0	72.0-73.5	74-75.5
	GPC	nt	69.1-70	94.1	69.2-69.9	66.0-67.6	65.0-66.1	66.4-67	61.5-62.6	53.9-56.0	65.8-69.2	66.1-67.5
		aa	79.5-81.1	97.5	80.1-81.1	73.5-75.7	71.5-72.4	71.0-74.2	59.7-61.0	43.0-43.9	74.2-74.8	73.1-75.9

PASC analysis

R4937: L segment



Click on the chart to get a list of GIs for each bar or submit sequences (as accessions, GIs or in FASTA format) to find how they fit within this family.

Sequence:

Choose file No file chosen

Submit

Genera selection: Apply

☑ Check/Uncheck All

☑ Arenavirus ☑ Mammarenavirus

☑ Reptarenavirus ☑ Unassigned

ArenaviridaeSegL taxonomy at ICTV and NCBI

Taxonomy changes: Apply

Merge species above

Separate species below

Merge genera above

Separate genera below

Split genomes: Apply

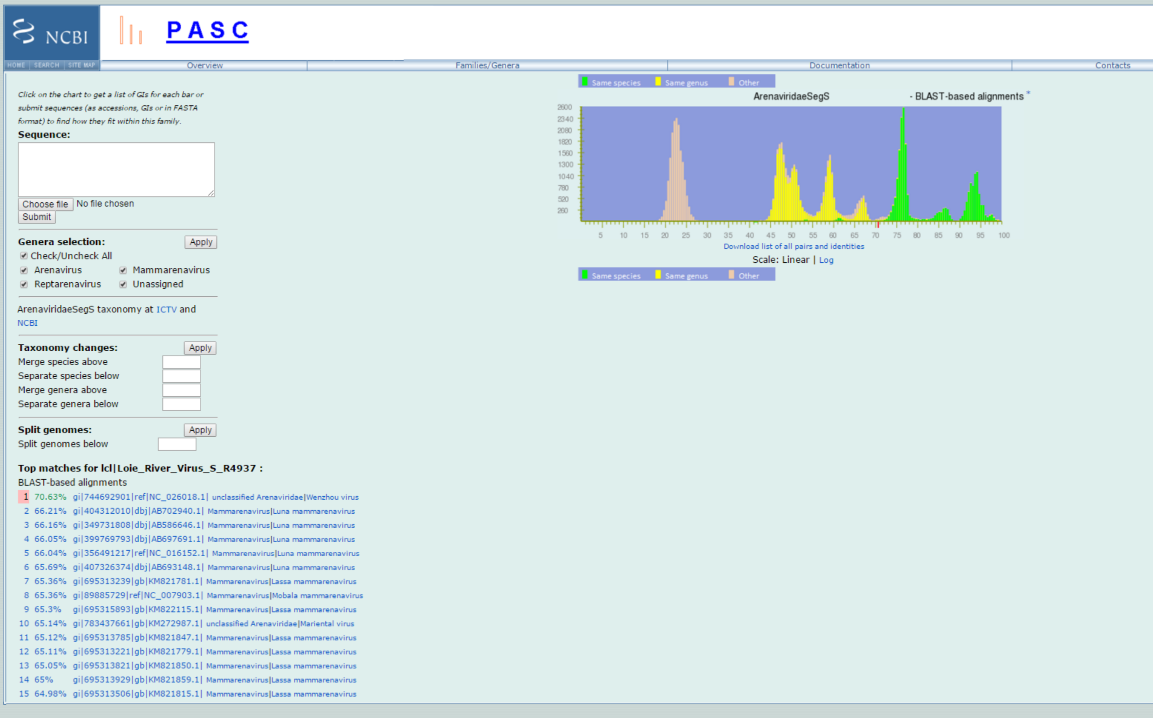
Split genomes below

Top matches for lcl|R4937_L_seg :

BLAST-based alignments

1 62.71% gi|744692911|ref|NC_026019.1| unclassified Arenaviridae|Wenzhou virus
2 57.38% gi|695313678|gb|KM821834.1| Mammarenavirus|Lassa mammarenavirus
3 57.19% gi|316308915|gb|GU979513.1| Mammarenavirus|Lassa mammarenavirus
4 57.15% gi|695313853|gb|KM821853.1| Mammarenavirus|Lassa mammarenavirus
5 56.97% gi|316308868|gb|GU481071.1| Mammarenavirus|Lassa mammarenavirus
6 56.97% gi|695313782|gb|KM821846.1| Mammarenavirus|Lassa mammarenavirus
7 56.96% gi|695313181|gb|KM821774.1| Mammarenavirus|Lassa mammarenavirus
8 56.95% gi|349731811|dbj|AB586647.1| Mammarenavirus|Luna mammarenavirus
9 56.92% gi|695313581|gb|KM821823.1| Mammarenavirus|Lassa mammarenavirus
10 56.91% gi|255237729|ref|NC_013058.1| Arenavirus|Old world arenaviruses|unclassified Old world arenaviruses|Morogoro virus
11 56.9% gi|695314313|gb|KM821901.1| Mammarenavirus|Lassa mammarenavirus
12 56.9% gi|695314326|gb|KM821903.1| Mammarenavirus|Lassa mammarenavirus
13 56.89% gi|567840451|gb|KF478762.1| Mammarenavirus|Lassa mammarenavirus
14 56.87% gi|316308862|gb|GU481069.1| Mammarenavirus|Lassa mammarenavirus
15 56.86% gi|37729930|gb|AY179172.1| Mammarenavirus|Lassa mammarenavirus

R4937: S segment



Click on the chart to get a list of GIs for each bar or submit sequences (as accessions, GIs or in FASTA format) to find how they fit within this family.

Sequence:

Choose file No file chosen

Submit

Genera selection: Apply

☑ Check/Uncheck All

☑ Arenavirus ☑ Mammarenavirus

☑ Reptarenavirus ☑ Unassigned

ArenaviridaeSegS taxonomy at ICTV and NCBI

Taxonomy changes: Apply

Merge species above

Separate species below

Merge genera above

Separate genera below

Split genomes: Apply

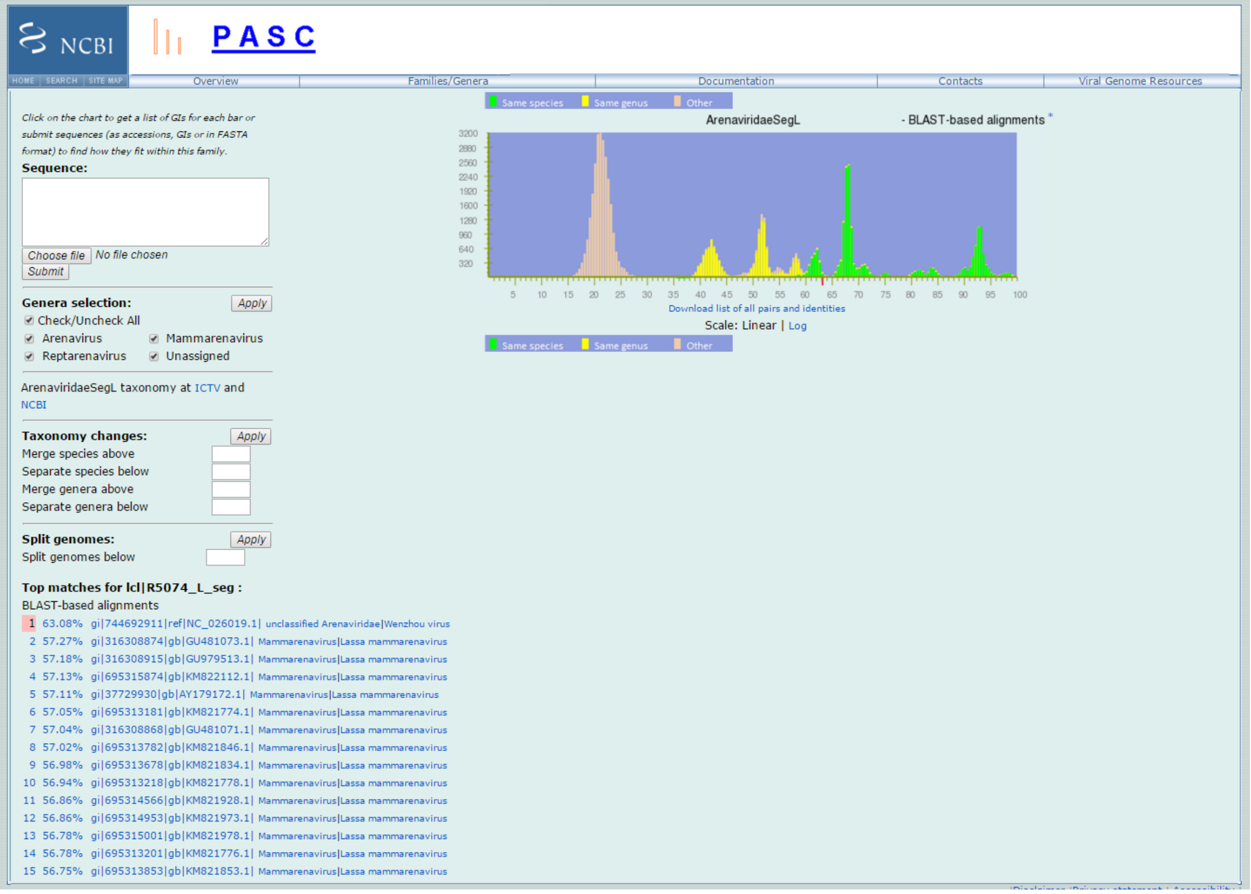
Split genomes below

Top matches for lcl|Loie_River_Virus_S_R4937 :

BLAST-based alignments

1 70.63% gi|744692901|ref|NC_026018.1| unclassified Arenaviridae|Wenzhou virus
2 66.21% gi|404312010|dbj|AB702940.1| Mammarenavirus|Luna mammarenavirus
3 66.16% gi|349731808|dbj|AB586646.1| Mammarenavirus|Luna mammarenavirus
4 66.05% gi|399769793|dbj|AB697691.1| Mammarenavirus|Luna mammarenavirus
5 66.04% gi|356491217|ref|NC_016152.1| Mammarenavirus|Luna mammarenavirus
6 65.69% gi|407326374|dbj|AB693148.1| Mammarenavirus|Luna mammarenavirus
7 65.36% gi|695313239|gb|KM821781.1| Mammarenavirus|Lassa mammarenavirus
8 65.36% gi|89885729|ref|NC_007903.1| Mammarenavirus|Mobala mammarenavirus
9 65.3% gi|695315893|gb|KM822115.1| Mammarenavirus|Lassa mammarenavirus
10 65.14% gi|783437661|gb|KM272987.1| unclassified Arenaviridae|Mariental virus
11 65.12% gi|695313785|gb|KM821847.1| Mammarenavirus|Lassa mammarenavirus
12 65.11% gi|695313221|gb|KM821779.1| Mammarenavirus|Lassa mammarenavirus
13 65.05% gi|695313821|gb|KM821850.1| Mammarenavirus|Lassa mammarenavirus
14 65% gi|695313929|gb|KM821859.1| Mammarenavirus|Lassa mammarenavirus
15 64.98% gi|695313506|gb|KM821815.1| Mammarenavirus|Lassa mammarenavirus

R5074: L segment



Click on the chart to get a list of GIs for each bar or submit sequences (as accessions, GIs or in FASTA format) to find how they fit within this family.

Sequence:

Genera selection:

☑ Check/Uncheck All

☑ Arenavirus ☑ Mammarenavirus

☑ Reptarenavirus ☑ Unassigned

ArenaviridaeSegL taxonomy at ICTV and NCBI

Taxonomy changes:

Merge species above

Separate species below

Merge genera above

Separate genera below

Split genomes:

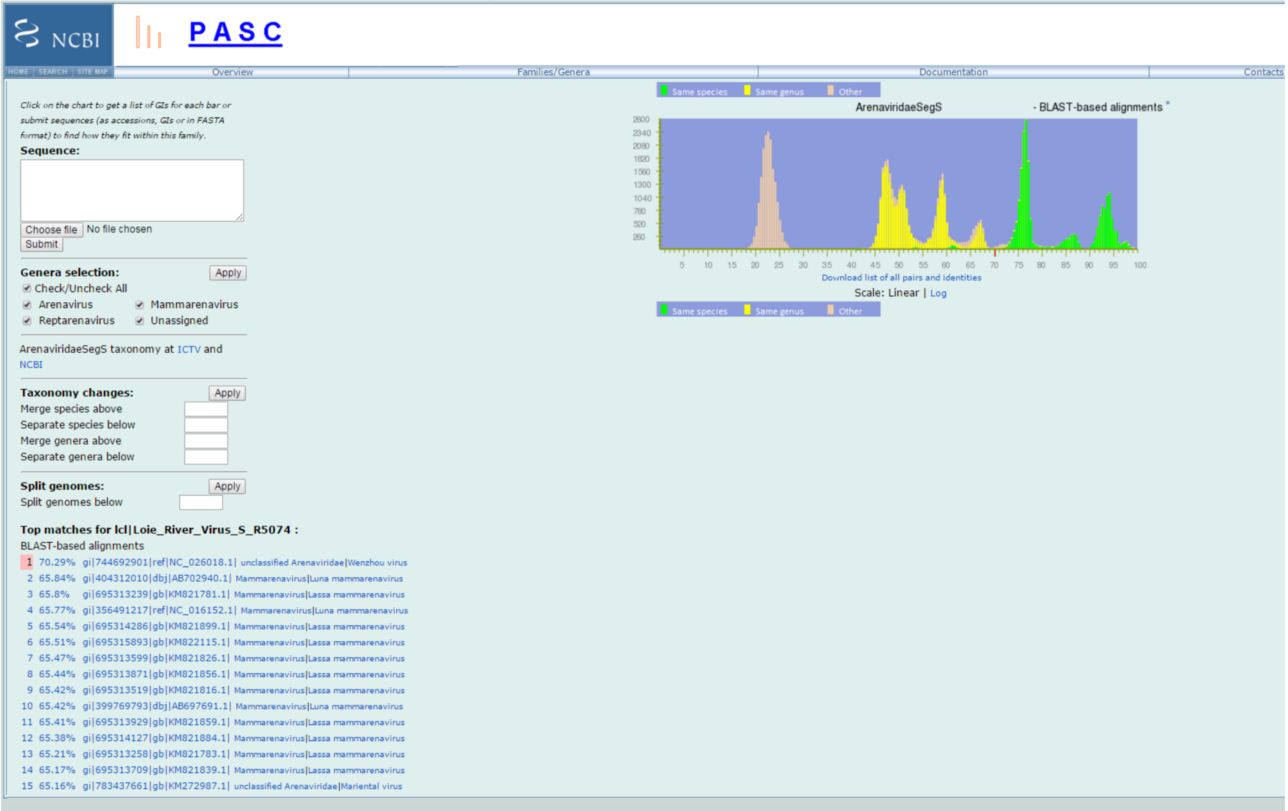
Split genomes below

Top matches for lcl|R5074_L_seg :

BLAST-based alignments

1	63.08%	gi|744692911|ref|NC_026019.1|	unclassified Arenaviridae|Wenzhou virus
2	57.27%	gi|316308874|gb|GU481073.1|	Mammarenavirus|Lassa mammarenavirus
3	57.18%	gi|316308915|gb|GU979513.1|	Mammarenavirus|Lassa mammarenavirus
4	57.13%	gi|695315874|gb|KM822112.1|	Mammarenavirus|Lassa mammarenavirus
5	57.11%	gi|37729930|gb|AY179172.1|	Mammarenavirus|Lassa mammarenavirus
6	57.05%	gi|695313181|gb|KM821774.1|	Mammarenavirus|Lassa mammarenavirus
7	57.04%	gi|316308868|gb|GU481071.1|	Mammarenavirus|Lassa mammarenavirus
8	57.02%	gi|695313782|gb|KM821846.1|	Mammarenavirus|Lassa mammarenavirus
9	56.98%	gi|695313678|gb|KM821834.1|	Mammarenavirus|Lassa mammarenavirus
10	56.94%	gi|695313218|gb|KM821778.1|	Mammarenavirus|Lassa mammarenavirus
11	56.86%	gi|695314566|gb|KM821928.1|	Mammarenavirus|Lassa mammarenavirus
12	56.86%	gi|695314953|gb|KM821973.1|	Mammarenavirus|Lassa mammarenavirus
13	56.78%	gi|695315001|gb|KM821978.1|	Mammarenavirus|Lassa mammarenavirus
14	56.78%	gi|695313201|gb|KM821776.1|	Mammarenavirus|Lassa mammarenavirus
15	56.75%	gi|695313853|gb|KM821853.1|	Mammarenavirus|Lassa mammarenavirus

R5074: S segment



Click on the chart to get a list of GIs for each bar or submit sequences (as accessions, GIs or in FASTA format) to find how they fit within this family.

Sequence:

Genera selection:

☑ Check/Uncheck All

☑ Arenavirus ☑ Mammarenavirus

☑ Reptarenavirus ☑ Unassigned

ArenaviridaeSegS taxonomy at ICTV and NCBI

Taxonomy changes:

Merge species above

Separate species below

Merge genera above

Separate genera below

Split genomes:

Split genomes below

Top matches for lcl|Loie_River_Virus_S_R5074 :

BLAST-based alignments

1	70.29%	gi|744692901|ref|NC_026018.1|	unclassified Arenaviridae|Wenzhou virus
2	65.84%	gi|404312010|dbj|AB702940.1|	Mammarenavirus|Luna mammarenavirus
3	65.8%	gi|695313239|gb|KM821781.1|	Mammarenavirus|Lassa mammarenavirus
4	65.77%	gi|356491217|ref|NC_016152.1|	Mammarenavirus|Luna mammarenavirus
5	65.54%	gi|695314286|gb|KM821899.1|	Mammarenavirus|Lassa mammarenavirus
6	65.51%	gi|695315893|gb|KM822115.1|	Mammarenavirus|Lassa mammarenavirus
7	65.47%	gi|695313599|gb|KM821826.1|	Mammarenavirus|Lassa mammarenavirus
8	65.44%	gi|695313871|gb|KM821856.1|	Mammarenavirus|Lassa mammarenavirus
9	65.42%	gi|695313519|gb|KM821816.1|	Mammarenavirus|Lassa mammarenavirus
10	65.42%	gi|399769793|dbj|AB697691.1|	Mammarenavirus|Luna mammarenavirus
11	65.41%	gi|695313929|gb|KM821859.1|	Mammarenavirus|Lassa mammarenavirus
12	65.38%	gi|695314127|gb|KM821884.1|	Mammarenavirus|Lassa mammarenavirus
13	65.21%	gi|695313258|gb|KM821783.1|	Mammarenavirus|Lassa mammarenavirus
14	65.17%	gi|695313709|gb|KM821839.1|	Mammarenavirus|Lassa mammarenavirus
15	65.16%	gi|783437661|gb|KM272987.1|	unclassified Arenaviridae|Mariental virus

Summary of PASC analysis

Sample ID	Country of origin	PASC: S segment		PASC: L segment	
		Sequence identity (%)	Closest virus	Sequence identity (%)	Closest virus
C0617	Cambodia	88.80	Wēnzhōu virus	86.27	Wēnzhōu virus
C0649	Cambodia	88.51	Wēnzhōu virus	85.98	Wēnzhōu virus
R4937	Thailand	70.63	Wēnzhōu virus	62.71	Wēnzhōu virus
R5074	Thailand	70.29	Wēnzhōu virus	63.08	Wēnzhōu virus

Figure 1: Maximum likelihood phylogenetic tree of novel mammarenavirus isolates and other representative mammarenaviruses for a, the complete ORF of L gene with sequences from rodents only, b, partial L sequences including sequences from rodents and patients. Cambodian strains detected in rodent (triangle), human (square), and Thai strains detected in rodent (circle) are in bold. Clade A, B, and C are three evolutionary lineages of New World mammarenaviruses within the Tacaribe complex. A/Rec denotes the recombinant clade including the three Northern American viruses (Blasdell *et al.*). The virus names are abbreviated according to Study Group recommendations as published by Radoshitzky *et al*.

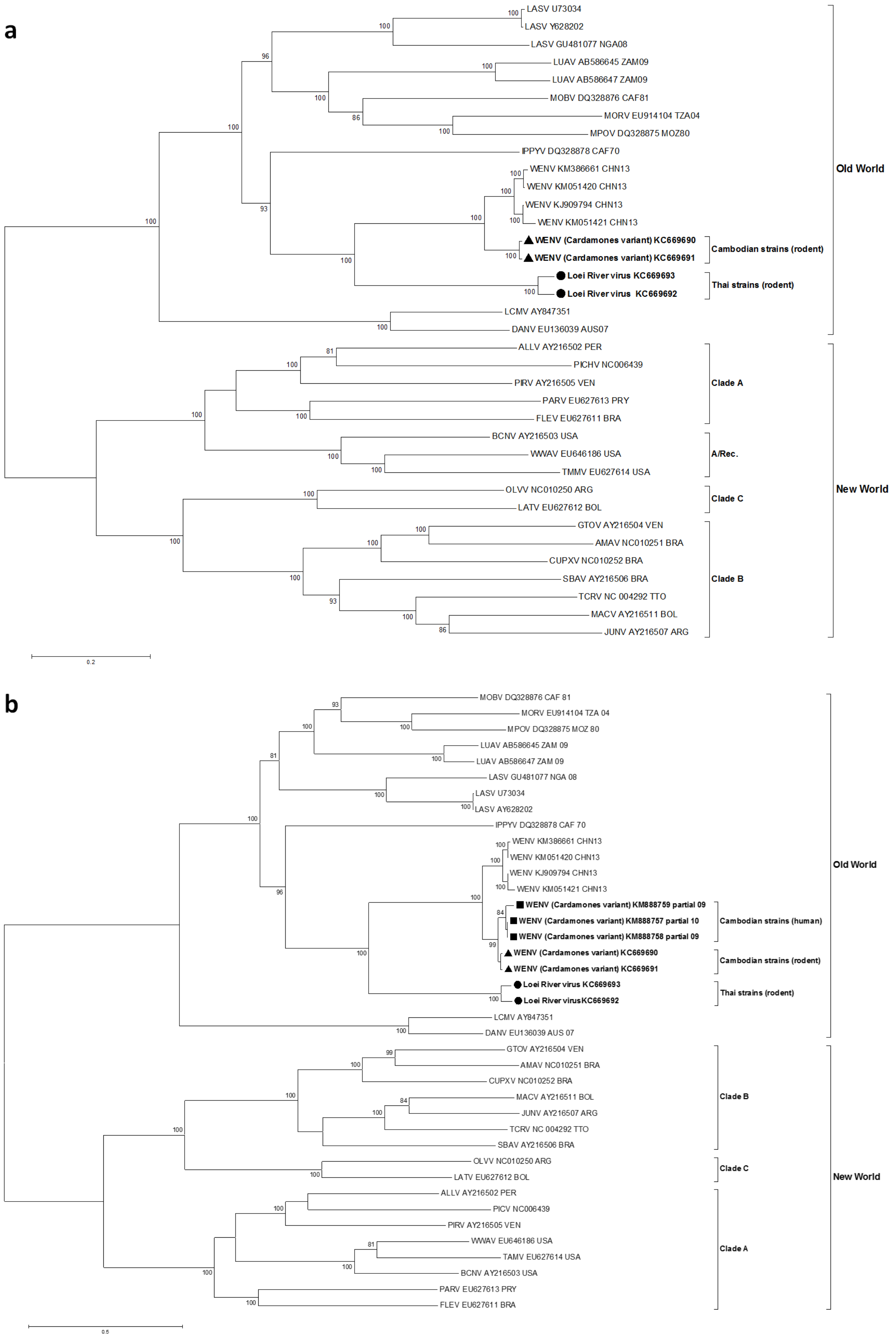
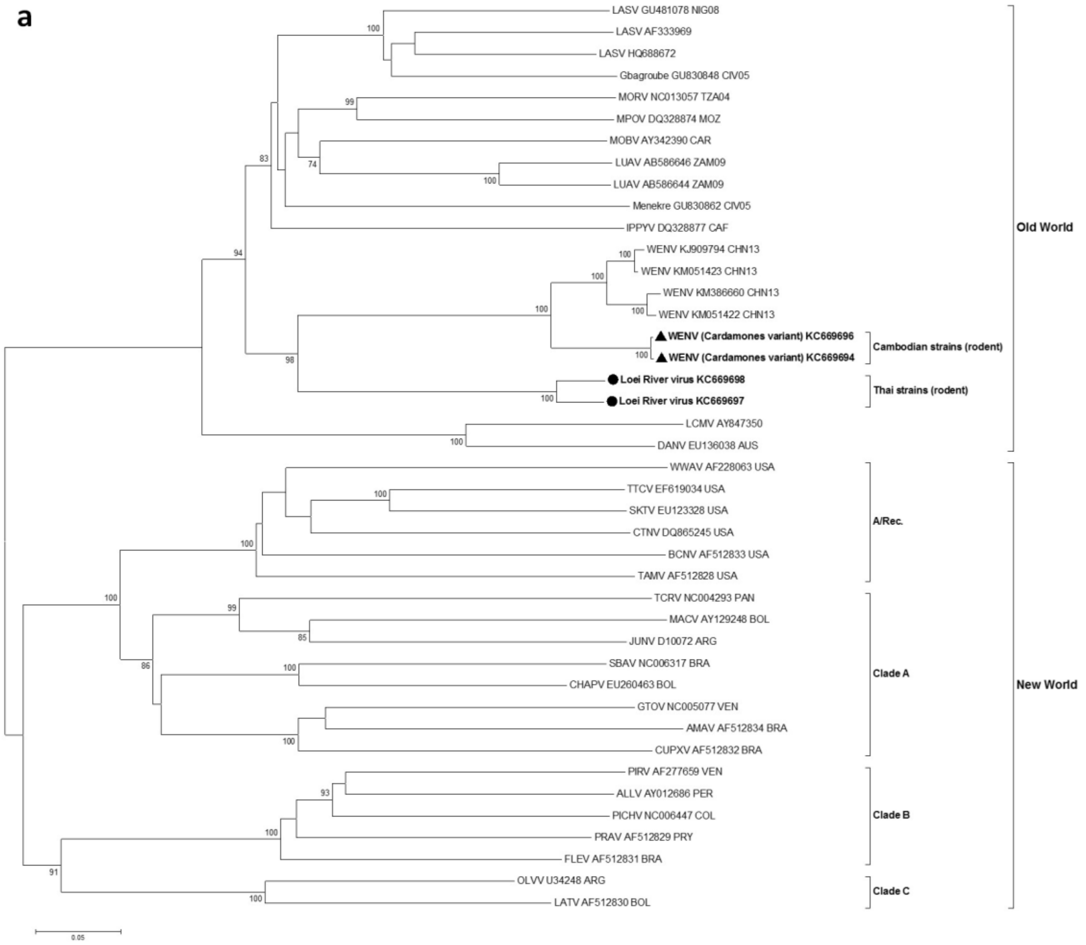
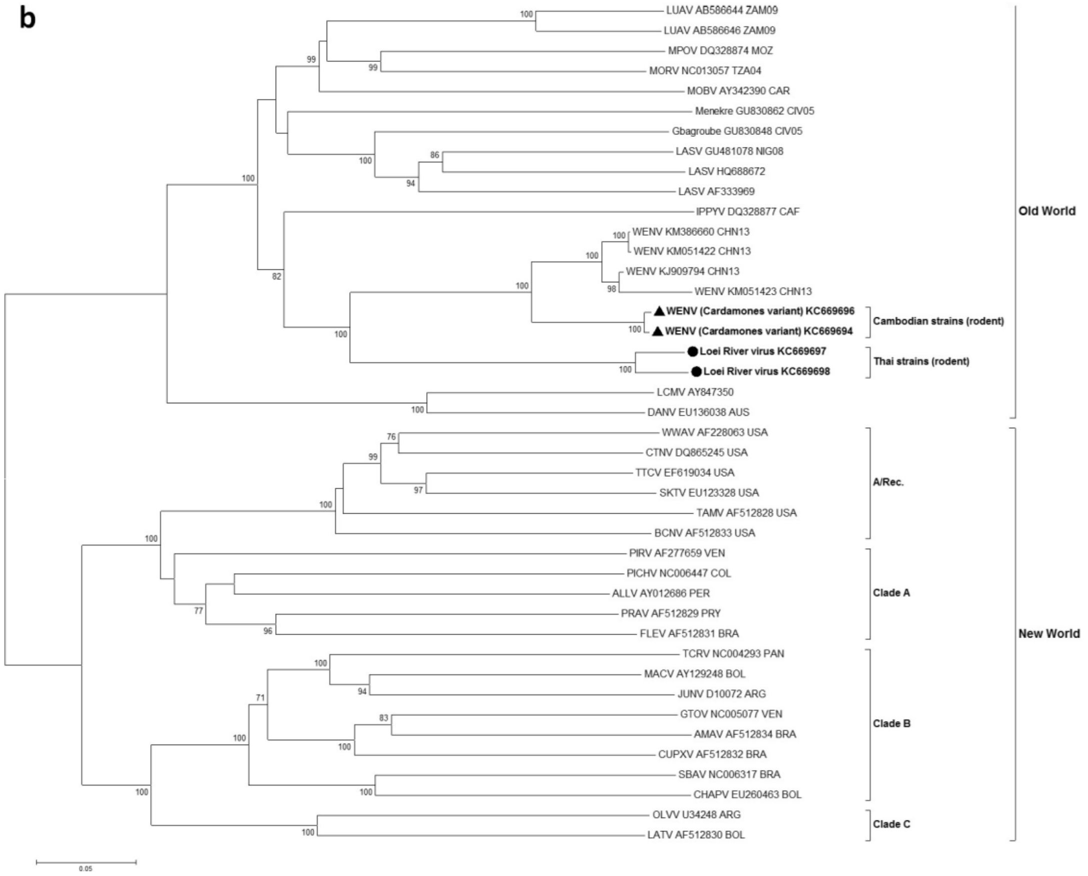

a
LASV U73034
LASV Y628202
LASV GU481077 NGA08
LUAV AB586645 ZAM09
LUAV AB586647 ZAM09
MOBV DQ328876 CAF81
MORV EU914104 TZA04
MPOV DQ328875 MOZ80
IPPYV DQ328878 CAF70
WENV KM386661 CHN13
WENV KM051420 CHN13
WENV KJ909794 CHN13
WENV KM051421 CHN13
▲ WENV (Cardamones variant) KC669690
▲ WENV (Cardamones variant) KC669691
● Loei River virus KC669693
● Loei River virus KC669692
LCMV AY847351
DANV EU136039 AUS07
ALLV AY216502 PER
PICHV NC006439
PIRV AY216505 VEN
PARV EU627613 PRY
FLEV EU627611 BRA
BCNV AY216503 USA
WWAV EU646186 USA
TMMV EU627614 USA
OLVV NC010250 ARG
LATV EU627612 BOL
GTOV AY216504 VEN
AMAV NC010251 BRA
CUPXV NC010252 BRA
SBAV AY216506 BRA
TCRV NC 004292 TTO
MACV AY216511 BOL
JUNV AY216507 ARG
Cambodian strains (rodent)
Thai strains (rodent)
Old World
Clade A
A/Rec.
Clade C
Clade B
New World
0.2
b
MOBV DQ328876 CAF 81
MORV EU914104 TZA 04
MPOV DQ328875 MOZ 80
LUAV AB586645 ZAM 09
LUAV AB586647 ZAM 09
LASV GU481077 NGA 08
LASV U73034
LASV AY628202
IPPYV DQ328878 CAF 70
WENV KM386661 CHN13
WENV KM051420 CHN13
WENV KJ909794 CHN13
WENV KM051421 CHN13
■ WENV (Cardamones variant) KM888759 partial 09
■ WENV (Cardamones variant) KM888757 partial 10
■ WENV (Cardamones variant) KM888758 partial 09
▲ WENV (Cardamones variant) KC669690
▲ WENV (Cardamones variant) KC669691
● Loei River virus KC669693
● Loei River virusKC669692
LCMV AY847351
DANV EU136039 AUS 07
GTOV AY216504 VEN
AMAV NC010251 BRA
CUPXV NC010252 BRA
MACV AY216511 BOL
JUNV AY216507 ARG
TCRV NC 004292 TTO
SBAV AY216506 BRA
OLVV NC010250 ARG
LATV EU627612 BOL
ALLV AY216502 PER
PICV NC006439
PIRV AY216505 VEN
WWAV EU646186 USA
TAMV EU627614 USA
BCNV AY216503 USA
PARV EU627613 PRY
FLEV EU627611 BRA
Cambodian strains (human)
Cambodian strains (rodent)
Thai strains (rodent)
Old World
Clade B
Clade C
Clade A
New World
0.5

Figure 2: Maximum likelihood phylogenetic tree of novel mammarenavirus isolates and other representative mammarenaviruses for a, the complete ORF of GPC gene and b, complete ORF of NP gene. Cambodian strains (triangle) and Thai strains (circle) detected in rodents are in bold. Clade A, B, and C are three evolutionary lineages of New World mammarenaviruses within the Tacaribe complex. A/Rec denotes the recombinant clade including Northern American viruses (Blasdell et al.). The virus names are abbreviated according to Study Group recommendations as published by Radoshitzky *et al*.

a


LASV GU481078 NIG08
100
LASV AF333969
LASV HQ688672
Gbagroube GU830848 CIV05
99
MORV NC013057 TZA04
MPOV DQ328874 MOZ
MOBV AY342390 CAR
83
74
LUAV AB586646 ZAM09
100
LUAV AB586644 ZAM09
Menekre GU830862 CIV05
IPPYV DQ328877 CAF
Old World
94
100
WENV KJ909794 CHN13
100
WENV KM051423 CHN13
WENV KM386660 CHN13
100
WENV KM051422 CHN13
100
▲ WENV (Cardamones variant) KC669696
Cambodian strains (rodent)
100
▲ WENV (Cardamones variant) KC669694
98
● Loei River virus KC669698
Thai strains (rodent)
100
● Loei River virus KC669697
LCMV AY847350
100
DANV EU136038 AUS
WWAV AF228063 USA
100
TTCV EF619034 USA
SKTV EU123328 USA
A/Rec.
CTNV DQ865245 USA
100
BCNV AF512833 USA
TAMV AF512828 USA
100
TCRV NC004293 PAN
99
MACV AY129248 BOL
85
JUNV D10072 ARG
86
100
SBAV NC006317 BRA
Clade A
CHAPV EU260463 BOL
New World
GTOV NC005077 VEN
AMAV AF512834 BRA
100
CUPXV AF512832 BRA
PIRV AF277659 VEN
93
ALLV AY012686 PER
PICHV NC006447 COL
Clade B
100
PRAV AF512829 PRY
FLEV AF512831 BRA
91
OLVV U34248 ARG
Clade C
100
LATV AF512830 BOL
0.05

b


100
LUAV AB586644 ZAM09
LUAV AB586646 ZAM09
99
MPOV DQ328874 MOZ
99
MORV NC013057 TZA04
MOBV AY342390 CAR
Menekre GU830862 CIV05
Gbagroube GU830848 CIV05
100
86
LASV GU481078 NIG08
100
LASV HQ688672
94
LASV AF333969
IPPYV DQ328877 CAF
Old World
100
WENV KM386660 CHN13
100
WENV KM051422 CHN13
82
WENV KJ909794 CHN13
100
98
WENV KM051423 CHN13
▲ WENV (Cardamones variant) KC669696
Cambodian strains (rodent)
100
▲ WENV (Cardamones variant) KC669694
100
● Loei River virus KC669697
Thai strains (rodent)
100
● Loei River virus KC669698
LCMV AY847350
100
DANV EU136038 AUS
76
WWAV AF228063 USA
99
CTNV DQ865245 USA
TTCV EF619034 USA
A/Rec.
97
SKTV EU123328 USA
100
TAMV AF512828 USA
BCNV AF512833 USA
100
PIRV AF277659 VEN
PICHV NC006447 COL
ALLV AY012686 PER
Clade A
77
PRAV AF512829 PRY
96
FLEV AF512831 BRA
New World
100
TCRV NC004293 PAN
MACV AY129248 BOL
94
JUNV D10072 ARG
71
83
GTOV NC005077 VEN
100
AMAV AF512834 BRA
Clade B
100
CUPXV AF512832 BRA
SBAV NC006317 BRA
100
100
CHAPV EU260463 BOL
OLVV U34248 ARG
Clade C
100
LATV AF512830 BOL
0.05