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:	***2015.001aM***	(to be completed by ICTV officers)

Short title: Four (4) new species in the genus *Mammarenavirus*, family *Arenaviridae*
(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 Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV:	June 15, 2015
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	***2015.001aM***	(assigned by ICTV officers)

To create 4 new species within:

Genus:	***Mammarenavirus***
Subfamily:	
Family:	***Arenaviridae***
Order:	

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)**
Gairo mammarenavirus	Gairo virus (GAIV) isolate TZ-27421	S: KJ855308 L: KJ855307
Mariental mammarenavirus	Mariental virus (MRLV) isolate N27	S: KM272987 L: KP867641
Okahandja mammarenavirus	Okahandja virus (OKAV) isolate N73	S: KM272988 L: KP867642
Wēnzhōu mammarenavirus[1]	Wēnzhōu virus (WENV) isolate Wencheng Rn-242	S: KJ909794 L: KJ909795

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

This proposal considers four published, novel mammarenaviruses for which coding complete genome sequences for both S and L segments are available and which have been isolated.

The first virus was discovered in Tanzania in Natal mastomys (*Mastomys natalensis*), and named Gairo virus (Gryseels *et al.*, 2015).

The second virus was discovered in Namibia in Namaqua micaelamys (*Micaelamys namaquensis*), and named Mariental virus (Witkowski *et al.*, 2015).

The third virus was discovered in Namibia in Namaqua micaelamys (*Micaelamys namaquensis*), and named Okahandja virus (Witkowski *et al.*, 2015).

The fourth virus was discovered in China in brown rats (*Rattus norvegicus*), Losea rats (*Rattus*

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[1] In TaxoProp 2015.001aG.v1.Diacritics it is proposed to prohibit the use of diacritics and apostrophes in taxon names. In case TaxoProp 2015.001aG.v1.Diacritics is ratified, the diacritical mark in the species name in this proposal will simply be dropped (resulting in ***Wenzhou mammarenavirus***). The Study Group may propose changing the resulting species name at a later date to correct the then incorrect orthography.

losea), oriental house rats (*Rattus tanezumi*), roof rats (*Rattus rattus*), and Asian house shrews (*Suncus murinus*) and named Wēnzhōu virus (Li *et al*., 2015).

The creation of novel species in the family *Arenaviridae* is currently based on the following species demarcation criteria established by the ICTV *Arenaviridae* Study Group (Radoshitzky *et al*. 2015):

- **an association with a specific host or group of hosts;**

  Gairo virus infects Natal mastomys, from which the mammarenaviruses Lassa, Luna, Mopeia, and Morogoro have also been isolated.

  Mariental and Okahandja viruses infect Namaqua micaelamys, from which no other arenaviruses have yet been isolated.

  Wēnzhōu virus infects brown rats, Losea rats, oriental house rats, roof rats, and Asian house shrews. Currently, no other arenaviruses are known to infect shrews.

- **presence in a defined geographical area;**

  Gairo virus was discovered in Tanzania, from where only one other arenavirus (Morogoro virus) has been isolated.

  Mariental and Okahandja viruses were discovered in Namibia, from where no arenaviruses have yet been isolated.

  Wēnzhōu virus was discovered in China, from where no arenaviruses have yet been isolated [this is the first known Asian arenavirus].

- **etiological agent (or not) of disease in humans;**

  There is no evidence for human disease caused by any of the four viruses.

- **significant differences in antigenic cross-reactivity, including lack of cross-neutralization;**

  Serological studies have not been performed with any of the four viruses.

- **significant differences in nucleotide sequence.**

  All four viruses share the arenavirus—and mammarenavirus—typical bisegmented negative strand genome organization and ambisense coding strategy.

Pairwise sequence comparison (PASC) analysis, which uses all-*vs.*-all pairwise alignments to identify logical cutoff thresholds (Bao *et al*., 2008, 2014), was performed on both complete S and L segment sequences of all four viruses and all other available coding-complete arenavirus genomes. This analysis consistently placed all four viruses into separate new species when cut-offs were chosen that bring S and L segment results into alignment and uphold the current taxonomy of other family members (chosen species cut-off: 80% for the S segment and 76% for the L segment; Radoshitzky *et al*., 2015; for results see: http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=main&action=gilist&id=448 (S segment PASC) and http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=main&action=gilist&id=446 (L segment PASC, also see Fig. 1). In this analysis, the closest relative of GAIV, MRLV, OKAV and WENV are Mobala virus (67%), Mopeia virus (50%), Merino Walk virus (62%) and Mopeia virus (57%) respectively. These results were confirmed in NP protein phylogenetic analyses (Fig. 2). The naming scheme for the two proposed species takes the form of: ***Xxx* mammarenavirus** (*Mammarenavirus*: the genus included in the family *Arenaviridae* that harbors mammalian arenaviruses; see Radoshitzky *et al*. 2015).

Accordingly, Gairo virus would become a member of the mammarenaviral species *Gairo mammarenavirus*; Mariental virus would become a member of the mammarenaviral species *Mariental mammarenavirus*; Okahandja virus would become a member of the mammarenaviral species *Okahandja mammarenavirus*; and Wēnzhōu virus would become a member of the species *Wēnzhōu mammarenavirus*.

MODULE 10: **APPENDIX**: supporting material

Figure 1. Distribution of pairwise identities among 91 complete sequences of the L segment in the *Arenaviridae* family. Regions A, B and C represent virus pairs from the same species, different species but the same genus, and different genera, respectively.

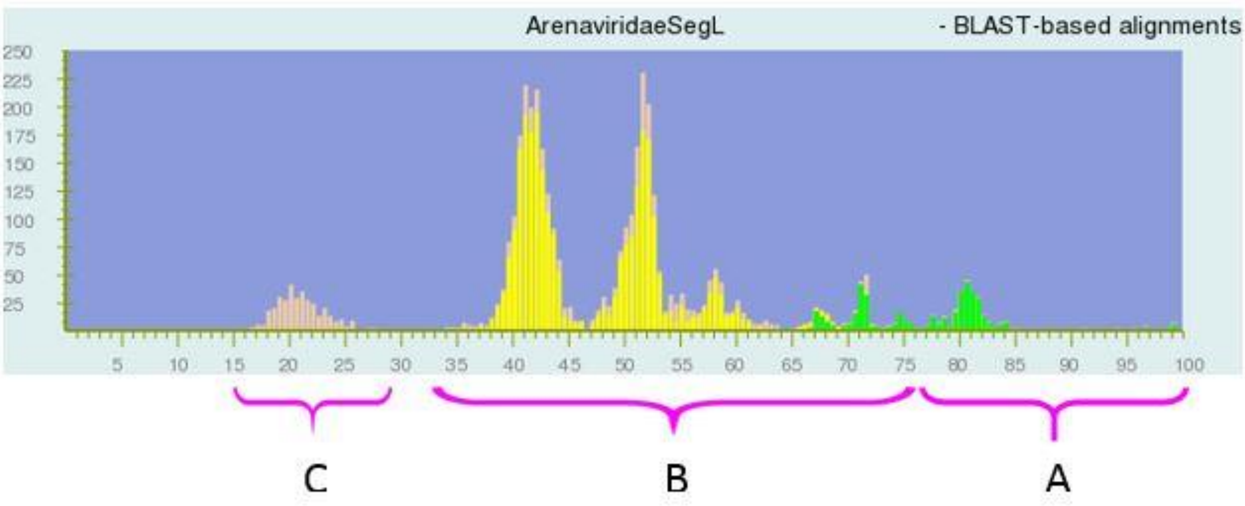
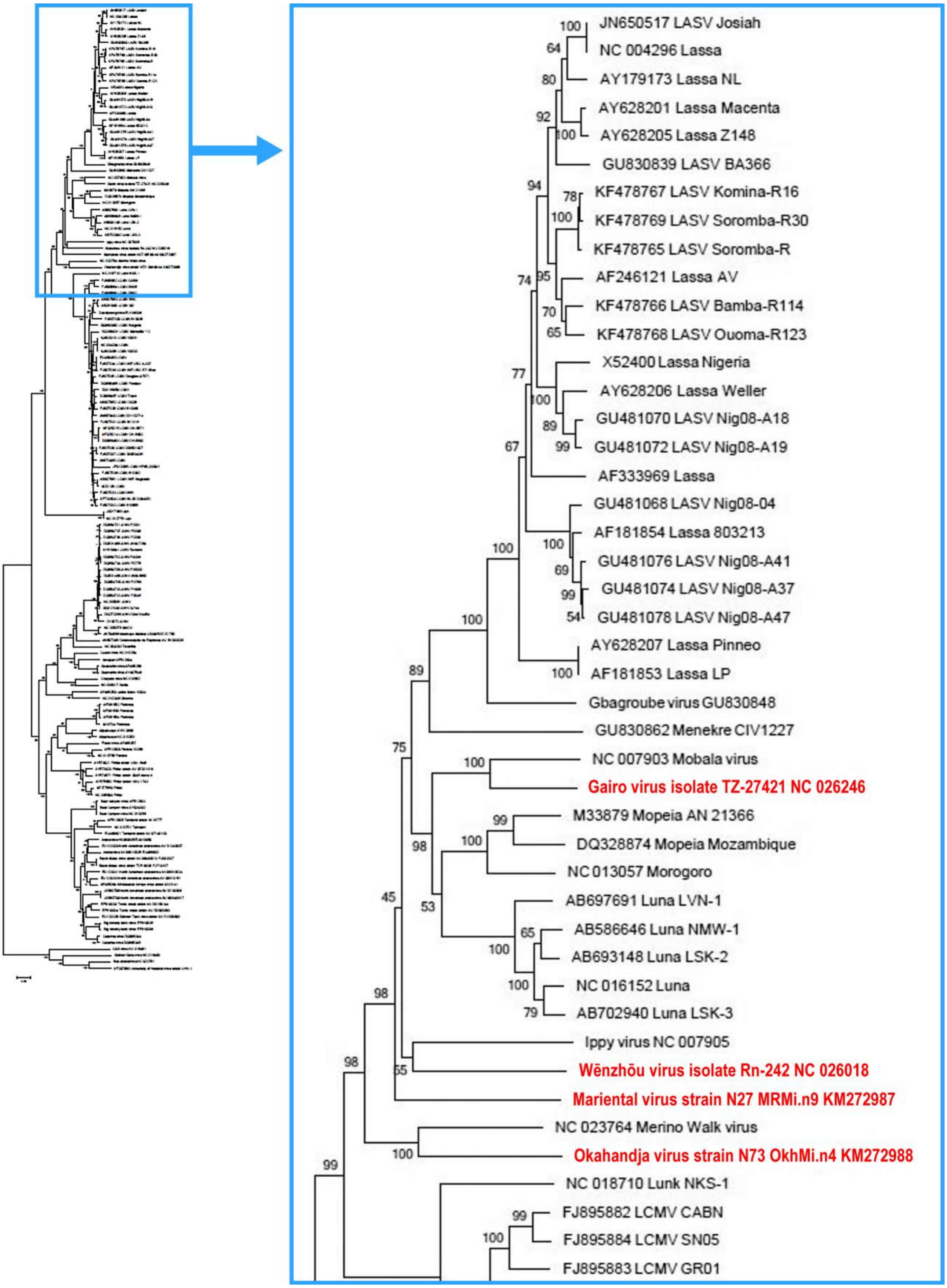


Figure 2. Phylogeny of Old World mammarenaviruses based on the analysis of complete amino acid sequences of their encoded nucleoproteins. Amino acid sequences were aligned with the ClustalW implementation in the MEGA version 6 software. The phylogenetic tree was obtained using the Neighbor Joining analysis implemented into MEGA with the pairwise distance algorithm. Support for nodes was tested by bootstrapping using 1,000 pseudoreplications.



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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.