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:** | ***2016.019aM*** | (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**<br>(modules 1 and 11 are required) | **2** ☒ **3** ☐ **4** ☐ **5** ☐<br>**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 *Arenaviridae* Study Group |

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

The proposal has the full support of the *Arenaviridae* SG. 1 member did not respond

| | |
|---|---|
| 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 | ***2016.019aM*** | (assigned by ICTV officers) |

**To create 1 new species within:**

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

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)** |
|---|---|---|
| *Solwezi mammarenavirus* | Solwezi virus (SOLV)<br>13ZR68 | AB972428 (S segment)<br>AB972429 (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

SOLV was detected in a rodent (*Grammomys* sp.) sampled in Solwezi, Zambia, and isolated from grammomys kidney tissue homogenate in Vero E6 cells.

The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) 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 SOLV. The closest PASC hit for the SOLV L segment is Ippy virus (*Ippy mammarenavirus*, RefSeq #NC_007906.1) with 58.95% pairwise identity (i.e. less than 76%), thereby justifying the creation of a novel species. The closest PASC hit for the SOLV S segment is Ippy virus with 67.59% pairwise identity (i.e. less than 80%), confirming the need for a new mammarenavirus species.

In addition, the creation of a new mammarenavirus species is justified by a pairwise identity comparison of the SOLV NP protein with the nucleoproteins (NPs) of other mammarenaviruses (see Table in Appendix).

## MODULE 11: **APPENDIX**: supporting material

| | **Percent identity of mammarenavirus nucleoproteins (NPs)** | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | AB586644_LUNV_LSK-1 | - | | | | | | | | | | | | | | |
| 2 | AB693148_LUNV_LSK-2 | 95.44 | - | | | | | | | | | | | | | |
| 3 | AB586646_LUNV_NAM-1 | 96.32 | 96.84 | - | | | | | | | | | | | | |
| 4 | AB972430_LULV_SLW-1[1] | 92.46 | 92.63 | 92.63 | - | | | | | | | | | | | |
| 5 | NC013057_MORV | 81.23 | 80.7 | 80.35 | 80.88 | - | | | | | | | | | | |
| 6 | NC006575_MOPV | 80.88 | 80 | 80.18 | 80.88 | 87.89 | - | | | | | | | | | |
| 7 | NC07903_MOBV | 78.07 | 76.67 | 77.19 | 75.79 | 78.77 | 78.25 | - | | | | | | | | |
| 8 | HQ688672_LASV_Josiah | 73.33 | 73.51 | 74.21 | 74.21 | 74.04 | 73.86 | 72.63 | - | | | | | | | |
| 9 | AB972428_SOLV | 70 | 70.53 | 70.35 | 71.05 | 68.95 | 68.95 | 67.72 | 70.53 | - | | | | | | |
| 10 | NC007905_IPPYV | 70.88 | 71.58 | 70.7 | 71.23 | 70.35 | 70.35 | 70.18 | 69.12 | 74.04 | - | | | | | |
| 11 | GU078660_MNWV | 66.49 | 67.37 | 67.19 | 67.54 | 67.89 | 67.72 | 65.38 | 67.14 | 67.61 | 67.37 | - | | | | |
| 12 | AY847350_LCMVarm | 63.57 | 63.57 | 63.22 | 64.62 | 63.75 | 63.4 | 62.28 | 60.77 | 63.68 | 62.7 | 64.66 | - | | | |
| 13 | NC018710_LNKV_NKS | 63.05 | 63.05 | 63.57 | 63.75 | 63.05 | 62.52 | 62.11 | 60.77 | 61.58 | 62.87 | 64.49 | 82.26 | - | | |
| 14 | FJ952384_LUJV | 58.42 | 58.07 | 58.07 | 58.42 | 56.14 | 55.79 | 57.12 | 58.17 | 56.87 | 55.96 | 56.86 | 57.77 | 58.66 | - | |
| 15 | NC_005081_JUNV | 49.39 | 48.7 | 49.04 | 48.52 | 49.22 | 48.7 | 47.74 | 48.43 | 47.56 | 48.17 | 49.38 | 48.78 | 48.78 | 46.63 | - |

IPPYV, Ippy virus; JUNV, Junín virus; LASV, Lassa virus; LCMV, lymphocytic choriomeningitis virus; LNKV, Lunk virus; LUJV, Lujo virus; LUNV, Luna virus; MNWV, Merino Walk virus; MOBV, Mobala virus; MOPV, Mopeia virus; MORV, Morogoro virus; SOLV, Solwezi virus.

[1] This virus, Luli virus (LULV), was discovered during the same study that uncovered SOLV. Although PASC analysis suggests the necessity of a novel species for LULV based on L segment analysis (whereas S segment analysis has borderline results), NP pairwise identity comparison (above), and phylogenetic analyses do not. It is therefore the opinion of the authors of this proposal and the members of the ICTV *Arenaviridae* Study Group that LULV ought to be classified in the already existing species “*Luna mammarenavirus*” together with Luna virus (LUNV).

## References:

| GenBank entries, followed by information provided by the contributors. |
|---|

## 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.