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:** | ***2012.004aV*** | (to be completed by ICTV officers) |

**Short title:** Create species named *Luna virus* in the genus *Arenavirus*, family *Arenaviridae*
(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) | **Arenaviridae SG**<br>**contact (SG chair): juanct@scripps.edu** |

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

| | |
|---|---|
| Date first submitted to ICTV: | 2011/10/06 |
| Date of this revision (if different to above): | 25th October 2012 (SGS) |

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 | ***2012.004aV*** | (assigned by ICTV officers) |

**To create new species within:**

| | |
|---|---|
| Genus: | ***Arenavirus*** |
| 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.

| **And name the new species:** | **GenBank sequence accession number(s) of reference isolate:** |
|---|---|
| *Luna virus* | AB586644 - LUNV; LSK-1 strain; S segment<br>AB586645 - LUNV; LSK-1; 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 9

Members of an arenavirus species:
- share a specific host in the same species or genus,
- share a similar geographic distribution,
- are / are not an agent of disease in humans,
- share antigenic cross-reactivity,
- show a divergence of no more than 12% in the nucleoprotein (NP) amino acid sequence.

Luna viruses were identified in an investigation of arenavirus at Lusaka and Namwala in Zambia. The virus was isolated from kidney tissues in *Mastomys natalensis* and named Luna virus (LUNV) based on its geographic origins from Lusaka and Namwala in Zambia. Luna virus should be classified as a new species in the genus *Arenavirus* based on:

1) The host reservoir of Luna virus is *Mastomys natalensis*.
2) Genetically similar non-pathogenic Lassa virus-related arenaviruses are identified in the neighbor countries, DRC, Tanzania and South Africa, but not in Zambia.
3) Having more than 19% divergence of its deduced NP amino acid sequence when compared to other known arenavirus species.
4) Having 41% divergence of its deduced NP amino acid sequence when compared to the known Zambian arenavirus, Lujo virus.

Antigenic cross-reactivity of Luna virus is unknown.

## MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

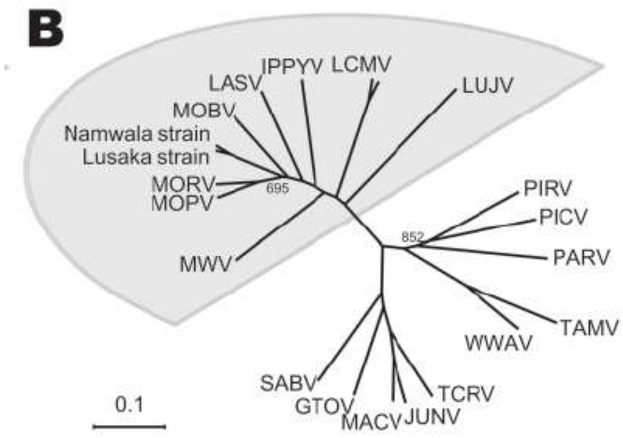
**References:**

Ishii, A., Y. Thomas, L. Monnga, I. Nakamura, A. Ohnuma, B. M. Hang'ombe, A. Takada, A. Mweene, H. Sawa (2011) Novel Arenavirus, Zambia. Emerg. Inf. Dis. 17(10) http://dx.doi.org/10.3201/eid1710.10452

**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.

Phylogenetic analysis of Luna protein sequences (this one is for NP protein) indicating that Mopeia and Mobala are nearest related viruses



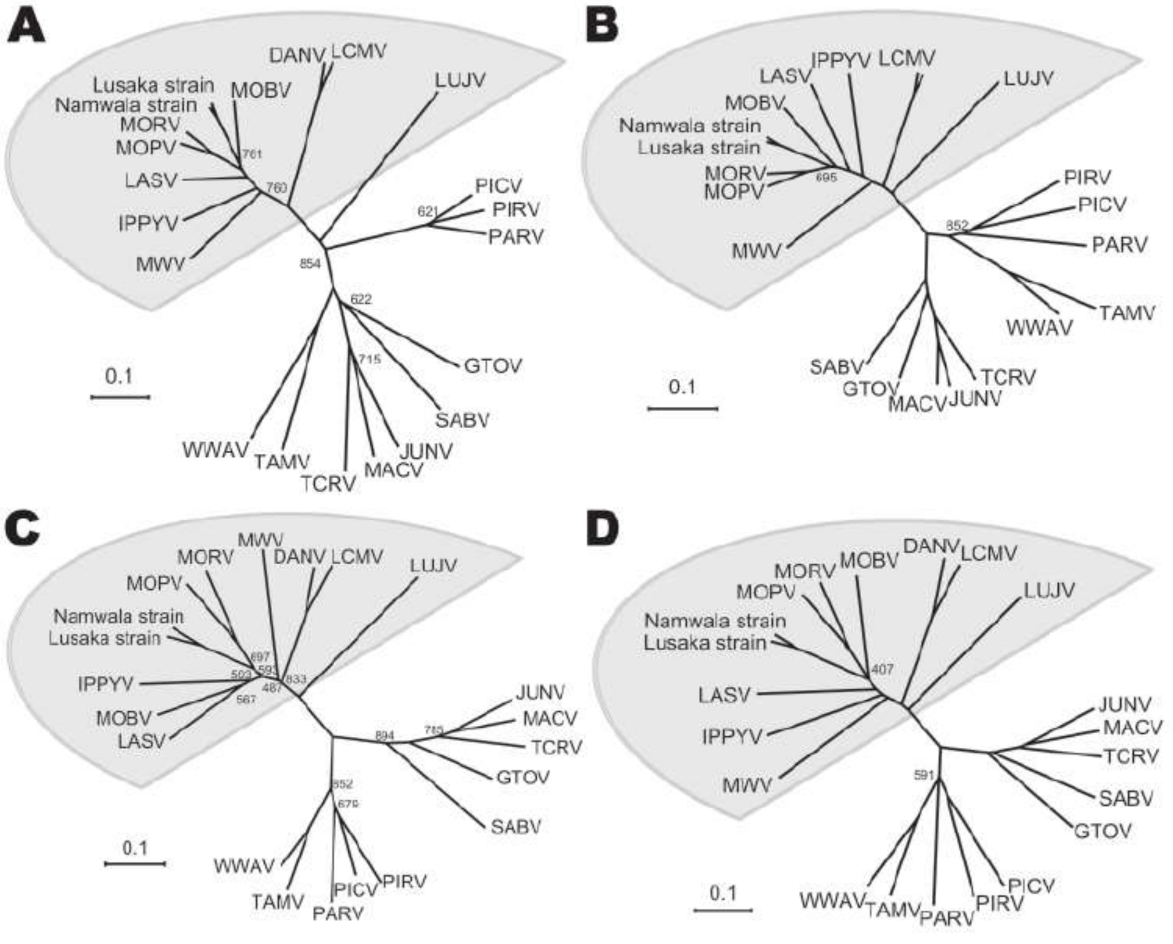


Figure 1. Phylogenetic analysis of Luna virus proteins based on the amino acid sequence, Zambia, 2009. Phylogenetic tree of A) glycoprotein precursor, B) nucleoprotein (NP), C) Z protein, and D) L protein. Bootstrap values are indicated in the trees (<900). Data from which amino acid sequences used for phylogenetic analyses were deduced are provided online (www.cdc.gov/EID/content/17/10/10-1452-F1.htm). Scales bars indicate amino acid substitutions per site.

At the request of the EC, the above figure was revised to indicate species, not isolates, include the method of phylogenetic analysis and to state that the shaded area represents Old World Arenaviruses (OWA). I (SGS) have inserted the revised figure below.

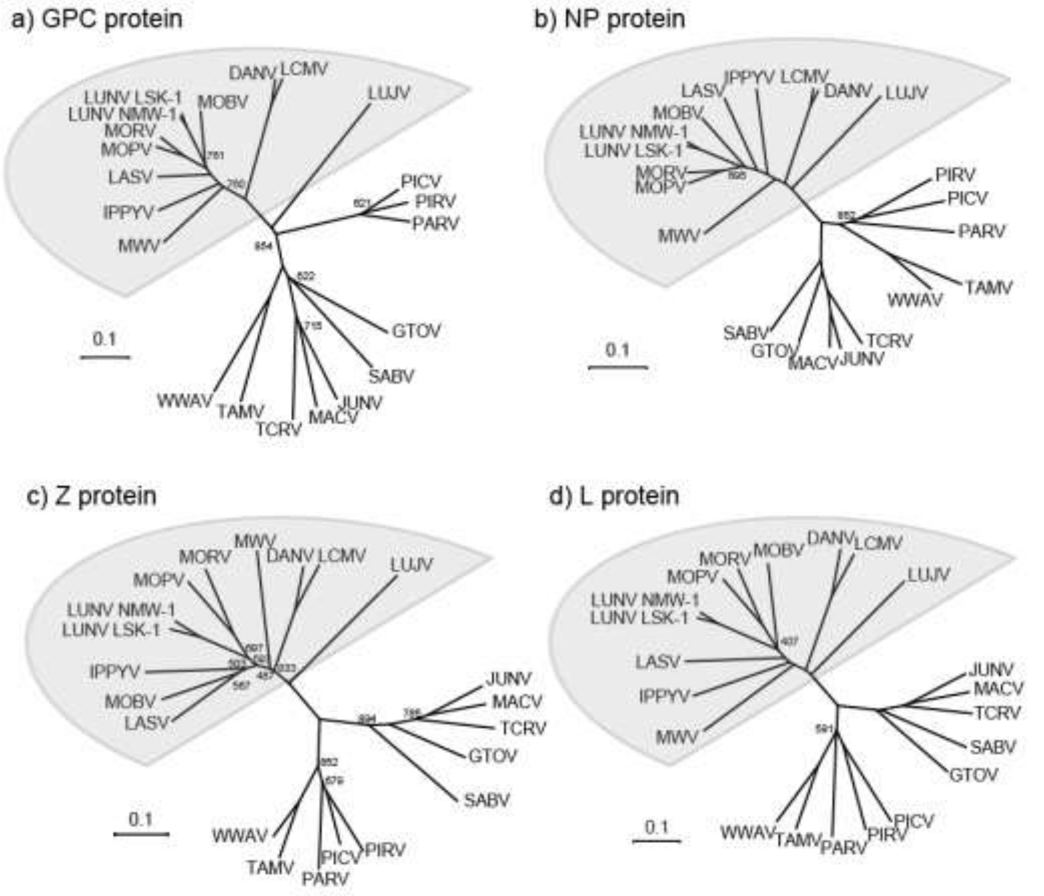


Figure. Phylogenetic analysis of Luna virus based on the amino acid sequence.
Phylogenetic trees of (a) glycoprotein precursor (GPC), (b) nucleoprotein (NP), (c) Z, and (d) L proteins were inferred by Neighbor-joining method. Bootstrap values are indicated in the trees (<900) and OWAs were indicated by the gray-shaded area. The amino acid sequences used for phylogenetic analyses were deduced from the data below:
(S and L segment): DANV (Dandenong virus: [EU136038] and [EU136039]), IPPYV (Ippy virus: [NC_007905] and [NC_007906]), LASV (Lassa virus: [NC_004296] and [NC_004297]), LUJV (Lujo virus: [FJ952384] and [FJ952385]), LUNV LSK-1 (Luna virus LSK-1:[AB586644] and [AB586645]), LUNV NMW-1 (Luna virus NMW-1:[AB586646] and [AB5866457]), LCMV (Lymphocytic choriomeningitis virus: [EU480450] and [EU480453]), MWV (Merino Walk virus: [GU078660] and [GU078661]), MOBV (Mobala virus: [NC_007903] and [NC_007904]), MOPV (Mopeia virus: [NC_006575] and [NC_006574]), MORV (Morogoro virus: [NC_013057] and [NC_013058]), GTOV (Guanarito virus: [AY129247] and [AY358024]), JUNV (Junin virus: [AY746353] and [AY746354]), MACV (Machupo virus: [AY624355] and [AY624354]), PARV (Parana virus: [AF512829] and [NC_010761]), PICV (Pichinde virus: [EF529746] and [EF529747]), PIRV (Pirital virus: [EU542420] and [NC_005897]), SABV (Sabia virus: [NC_006317] and [NC_006313]), TCRV (Tacaribe virus: [NC_004293] and [NC_004292]), TAMV (Tamiami virus: [NC_010701] and [NC_010702]), and WWAV (Whitewater Arroyo virus: [NC_010700] and [NC_0107003]).