This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.



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.

Part 1: **TITLE, AUTHORS, etc**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.003M*** | | | | (to be completed by ICTV officers) |
| **Short title: One (1) new species in the genus *Mammarenavirus* (*Arenaviridae*)** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| The discoverers of Souris virus (formerly “praomys arenavirus”):  Ng, T. F. F.  Schneider, B. S.  Gillis, A.  LeBreton, M.  Kondov, N. O.  Coffey, L.  Wolfe, N. D.  Delwart, E.  and the ICTV *Arenaviridae* Study Group:  Buchmeier, Michael J., m.buchmeier@uci.edu  Charrel, Rémi, remi.charrel@univ-amu.fr  Clegg, Christopher S., cleggjcs@yahoo.fr  de la Torre, Juan Carlos, juanct@scripps.edu  DeRisi, Joseph L., joe@derisilab.ucsf.edu  Emonet, Sébastien, sebastien.emonet@irba.fr  Gonzalez, Jean-Paul, jpgonzalez2808@gmail.com  Kuhn, Jens H., kuhnjens@mail.nih.gov  Lukashevich, Igor S., isluka01@louisville.edu  Peters, Clarence J., cj.cj.peters@gmail.com  Radoshitzky, Sheli R., sheli.r.radoshitzky.ctr@mail.mil  Romanowski, Victor, vromanowski@gmail.com  Salvato, Maria S., msalvato@ihv.umaryland.edu  Stenglein, Mark D., mark.stenglein@colostate.edu | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Jens H. Kuhn, [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | | | | | |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | **ICTV *Arenaviridae* Study Group** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

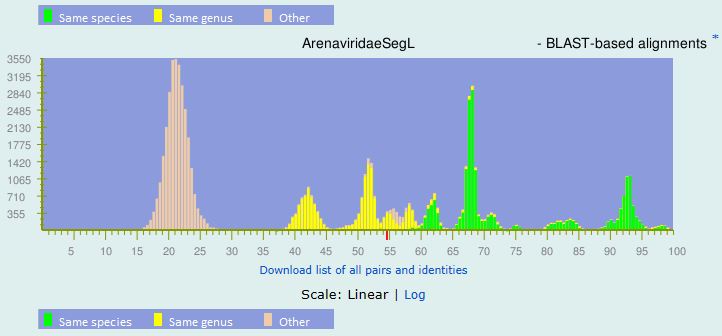
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|  |
| **Name of accompanying spreadsheet: 2017.003M.N.v1.Mammarenavirus\_sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

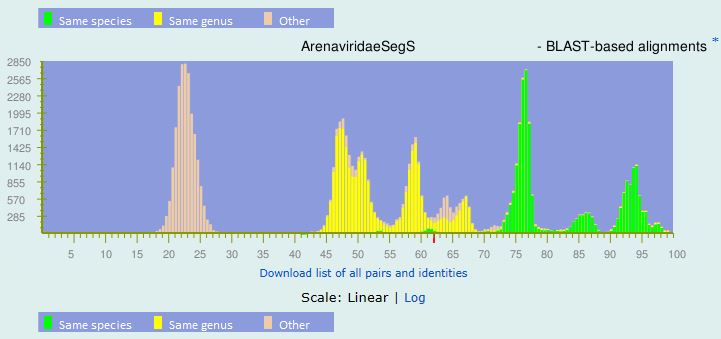
**Part 4:** **APPENDIX**: supporting material

Souris virus (SOUV) was detected in an unspecified soft-furred mouse (*Praomys* sp.) sampled in Cameroon in 2013. The virus was originally named “praomys arenavirus”.

The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (<https://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 SOUV. The closest PASC hit for the SOUV L segment is Lassa virus (*Lassa mammarenavirus*, GenBank #KM821930.1) with 54.94% pairwise identity (i.e. less than 76%), thereby justifying the creation of a novel species.



The closest PASC hit for the SOUV S segment is Lassa virus (*Lassa mammarenavirus*, GenBank KM821976.1) with 62.24% pairwise identity (i.e. less than 80%), confirming the need for a new mammarenavirus species.



| Figures 1–2. Complete mammarenavirus nucleocapsid (NP) protein sequences were aligned using MAFFT with the E-INS-I alignment strategy. Phylogenetic analysis was performed using PhyML using the Approximate Likelihood-Ratio Test (aLRT) and Dayoff substitution model. Pairwise identities were obtained using Sequence Demarcation Tool Version 1.2: |
| --- |
| **References:** |
| GenBank entries, followed by information provided by the virus discoverers. |