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:** | ***2017.002M*** | | | | (to be completed by ICTV officers) |
| **Short title: Create one new species, *Ryukyu mammarenavirus*, in the genus *Mammarenavirus*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| The discoverers of Ryukyu virus (formerly “rat arenavirus 1”):  Jin, Qi, [zdsys@vip.sina.com](mailto:zdsys@vip.sina.com)  Wu, Zhiqiang, [wuzq2009@ipbcams.ac.cn](mailto:wuzq2009@ipbcams.ac.cn)  Yang, Li, [barbie\_yl@163.com](mailto:barbie_yl@163.com)  Du, Jiang, [dujiang@ipbcams.ac.cn](mailto:dujiang@ipbcams.ac.cn)  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): | | | |  | |

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

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

|  |
| --- |
| Ryukyu virus (RYKV) was detected and its genome directly sequenced from an anal swab sample obtained from a Ryukyu mouse (*Mus (Mus) caroli*) sampled in Yúnnán Province, China, in 2013. The virus was originally named “rat arenavirus 1”.  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 RYKV. The closest PASC hit for the RYKV L segment is lymphocytic choriomeningitis virus (*Lymphocytic choriomeningitis mammarenavirus*, GenBank #DQ868488.1) with 66.27% pairwise identity (i.e. less than 76%), thereby justifying the creation of a novel species.  The closest PASC hit for the RYKV S segment is lymphocytic choriomeningitis virus (*Lymphocytic choriomeningitis mammarenavirus*, GenBank #AB627952.1|) with 76.03% pairwise identity (i.e. less than 80%), confirming the need for a new mammarenavirus species.  Phylogenetic trees based on the L protein **(A)**, the nucleoprotein (NP) **(B)**, and the glycoprotein (GPC) **(C)** of Ryukyu virus YN2013 (S: KM020191, L: KM020190) and previously reported arenaviruses. MEGA6.0 was used to align the deduced amino acid sequences using the MUSCLE package and default parameters. The best substitution model was then evaluated using the Model Selection package. We used maximum-likelihood to process the phylogenetic analyses with 1,000 bootstrap replicates. |
| **Name of accompanying spreadsheet: 2017.002M.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

| additional material in support of this proposal |
| --- |
| **References:** |
| GenBank entries, followed by information provided by the virus discoverers. |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |