

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

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| **Code assigned:** | ***2023.013M*** |  |
| **Short title:** Create one new species in genus *Mammarenavirus* (*Bunyavirales*: *Arenaviridae*) |
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**Author(s) and email address(es)**

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**Author(s) institutional address(es) (optional)**

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**Corresponding author**

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| Cuypers LN |

**List the ICTV Study Group(s) that have seen this proposal**

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| ICTV *Arenaviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| ICTV *Arenaviridae* Study Group | 13 | 0 | 0 |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| N/A | N/A | N/A |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | June 23, 2023 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

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| N/A |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2023.013M.N.v1.Mammarenavirus\_1nsp |

**Abstract**

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| We propose the establishment of one new species in arenavirid genus *Mammarenavirus* to accommodate Mafiga virus discovered in single-striped lemniscomys in Tanzania. |

**Text of proposal**

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| A distinct mammarenavirus was detected in single-striped lemniscomys (murid *Lemniscomys rosalia* (Thomas, 1904) first in Mafiga, Morogoro and then in Komtema, Tanga, in Tanzania (Goüy de Bellocq et al. (2010); Cuypers et al. (2022)). Metagenomic sequencing revealed a complete, single S segment, but two complete, distinct L segments. The TZ29841 L segments are 87% identical to each other and 82-83% identical to the ‘*Lemniscomys*/F4-8/TZA/2008’ fragment, indicating they all belong to the same mammarenavirus species. This virus, named Mafiga virus (MAFV), is hosted by single-striped lemniscomys, not known to host any other mammarenavirus (demarcation criterion: association of the virus with a distinct main host or group of sympatric hosts). PAirwise Sequence Comparison (PASC) analysis (https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi) reveals that the TZ29841 segments share 70% nucleotide sequence identity for S (demarcation criterion: < 80%) and 61% for both L segments (demarcation criterion: <76%) with Solwezi virus. NP amino acid sequence identity shared with Solwezi virus is 79% (demarcation criterion: < 88%). MAFV therefore meets the ICTV requirements to be assigned to a new mammarenavirus species. |

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**Supporting evidence**

**Figure 1 (adapted from Figure 2 from Cuypers et al., 2022)**: *L*, *NP*, and *GPC* gene phylogenetic trees. The trees were inferred with MrBayes v3.2.7a with codon partitioning and a GTR+G nucleotide substitution model. In two independent runs four chains ran for 10,000,000 generations with a burn-in of 25%. Average standard deviations of split frequencies were examined for convergence, as were parameter effective sample sizes and trace patterns in Tracer ([https://beast.community/tracer](https://protect2.fireeye.com/v1/url?k=31323334-501d0a38-31357b2d-454441504e31-1ca0d0a4b0d49483&q=1&e=1499d573-f201-4626-8e31-73da61160726&u=https%3A%2F%2Fbeast.community%2Ftracer)). Trees were visualized in FigTree (<http://tree.bio.ed.ac.uk/software/figtree/>). The scale bars indicate 0.5 nt substitutions per site. Numbers at the nodes represent posterior probability.

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**Figure 2 (adapted from S2 from Cuypers et al., 2022):** PASC figures. PASC (PAirwise Sequence Alignment) webtool histogram of pre-computed pairwise identities of known arenavirus sequences. The best hit for the three Mafiga virus segments was Solwezi virus (S: NC\_038367/AB972428; L: NC\_038366/AB972429), those pairwise identities are marked by a red stripe on the x-axis.

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**S**

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**L1**

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**L2**

**References**

Cuypers LN, Čížková D, Goüy de Bellocq J (2022) Co-infection of mammarenaviruses in a wild mouse, Tanzania. *Virus Evol.* 8, veac065. doi: 10.1093/ve/veac065

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Radoshitzky SR, Buchmeier MJ, Charrel RN, Clegg JCS, Gonzalez JJ, Günther S, Hepojoki J, Kuhn JH, Lukashevich IS, Romanowski V, Salvato MS, Sironi M, Stenglein MD, de la Torre JC & ICTV Report Consortium (2019) ICTV Virus Taxonomy Profile: *Arenaviridae*. *J Gen Virol* 100, 1200-1201. doi: 10.1099/jgv.0.001280 PMID: 31192784