

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

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| **Code assigned:** | **2021.007M** |  |
| **Short title:** Create one new species (*Mammarenavirus kwanzaense*) in genus *Mammarenavirus* (*Bunyavirales*: *Arenaviridae*) | | |
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**Authors and email addresses**

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| Těšíková J, Krásová J, Goüy de Bellocq J | jana.tesikova@gmail.com; krasova@ivb.cz; joellegouy@gmail.com |

**Authors’ institutional addresses**

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| Institute of Vertebrate Biology of the Czech Academy of Sciences, Brno, Czech Republic. |

**Corresponding author**

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| Těšíková J (jana.tesikova@gmail.com) |

**List the ICTV Study Group 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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| None. |

**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 |

**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | May 28, 2021 |
| Date of this revision (if different to above) | September 13, 2021 |

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

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| * Text of proposal is a bit confusing –not clear where partial sequences were derived from or how they add to the determination of a new species.   Response: moved these parts into brackets and labeled them “additional information” below the PASC criteria.   * criteria for demarcation are not clearly laid out--return for clarification and explicit inclusion of criteria for demarcation prior to reconsideration   Response: paragraph added: “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. PASC cut-off values chosen for classifying arenaviruses within the same species are >80% and >76% nucleotide sequence identity in the S and L segments, respectively.”   * Read the EC-distributed guidance on species naming document, confirm that proposed species names adhere to the guidance, and confirm that you would like to keep the proposed species names as originally proposed.   Response: Read, confirmed, and confirmed. |

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

**Name of accompanying Excel module**

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| 2021.007M.R.Mammarenavirus\_1nsp\_Kwanza |

**Abstract**

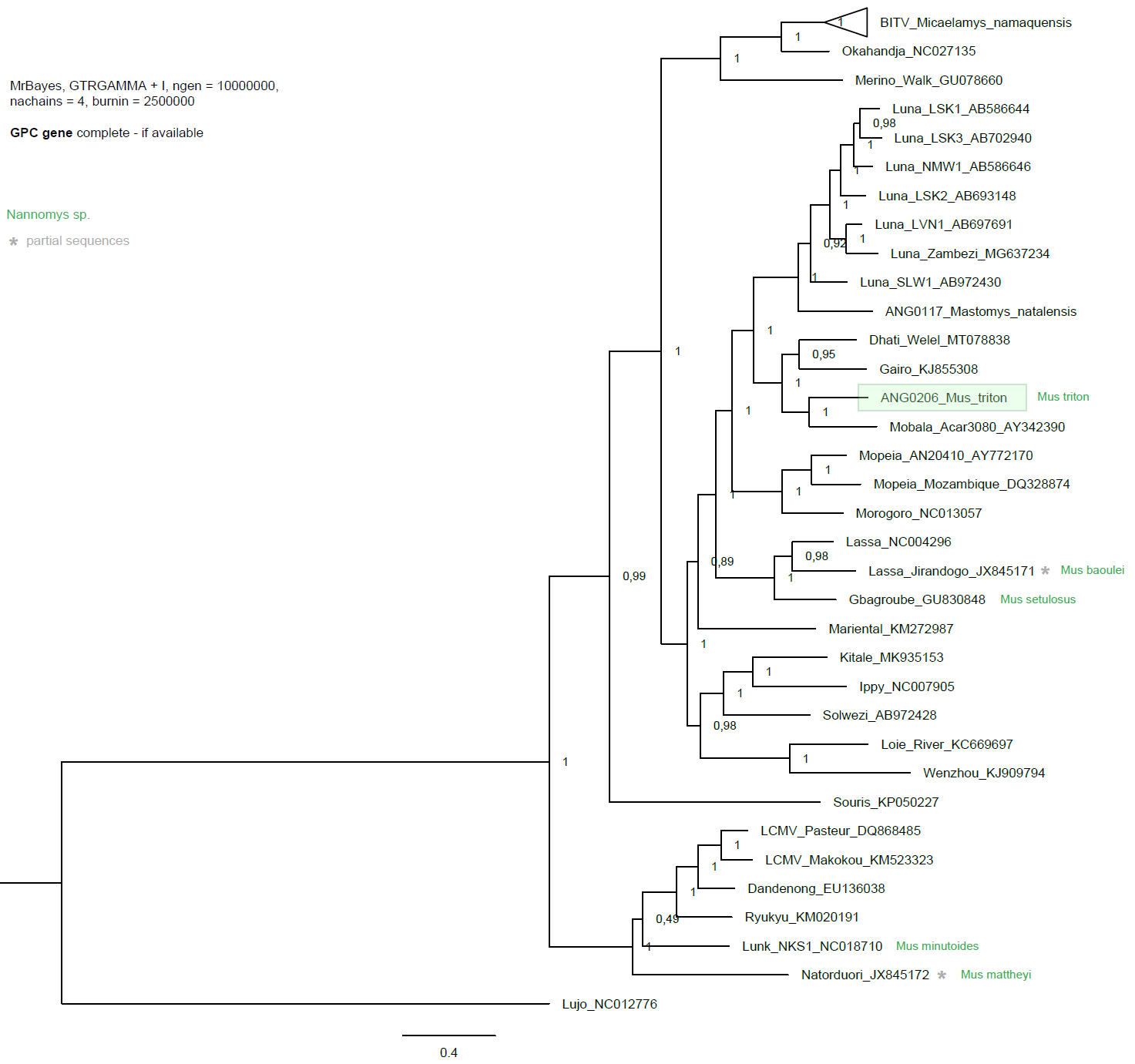
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| Kwanza virus (KWAV) was detected in a gray-bellied mouse (*Mus triton* (Thomas, 1909)) sampled in Angola in 2017, and its coding-complete genome was characterised in Těšíková *et al.* 2021.  KWAV fulfils the ICTV criteria (Radoshitzky *et al.* 2019) to be considered a member of a new *Mammarenavirus* species (see below). Therefore, we propose the establishment of a novel mammarenavirus species named *Mammarenavirus kwanzaense*, named after KWAV, which in turn was named after Cuanza Sul Province (Kwanza Kombuelo Volupale in Ubundu), Angola. |

**Text of proposal**

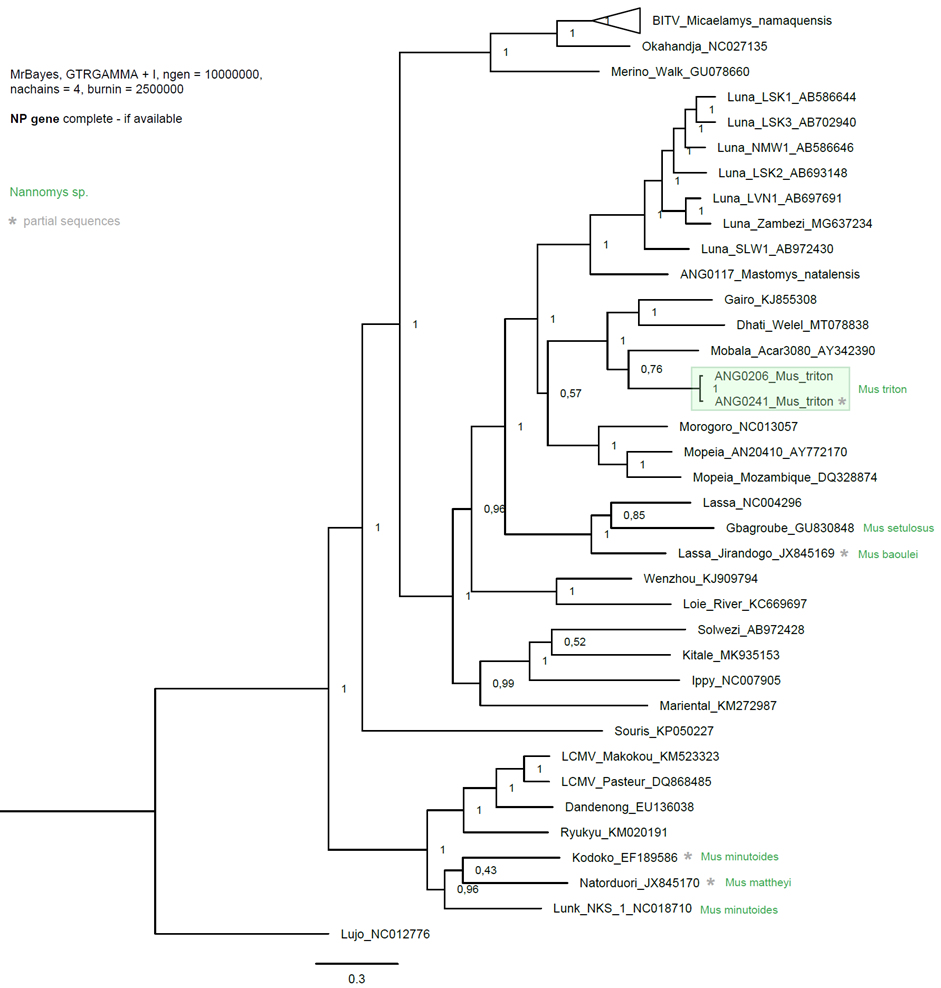
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| --- | --- |
| |  | | --- | | The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) for the assessment of novel arenaviruses. PASC cut-off values chosen for classifying arenaviruses within the same species are >80% and >76% nucleotide sequence identity in the S and L segments, respectively. PASC generated the closest hit for KWAV as MOBV: 74.45% and 67.47% nucleotide sequence identity in the genomic S and L segments, respectively (Figure 2).  [Additional information: Besides the coding-complete genome sequence of KWAV strain ANG0206 (GenBank #MZ065540-41), we obtained *L* (GenBank #MZ065514) and *NP* (#MZ065527) gene fragment sequences of sample ANG0241. In the phylogeny, KWAV settled in a cluster of mobala-like mammarenaviruses, where it forms a sister lineage of mobala virus (MOBV), with various support of 0.76 to 1 depending on the gene (Figure 1). Sequence comparison results of KWAV with the most related virus (MOBV) are: 69.7% (*Z*), 69.5% (*L*), 75.2% (*GP*) and 76.7% (*NP*) at the nucleotide sequence level and 62.6% (Z), 74.3% (L), and 88% (NP) identities at the amino acid sequence level. The GPC protein is most closely related to that of the unclassified Dhati Welel virus found in natal mastomys (*Mastomys natalensis* (Smith, 1934)) in Ethiopia (85.7%; Table 1)] | |

**Supporting evidence**

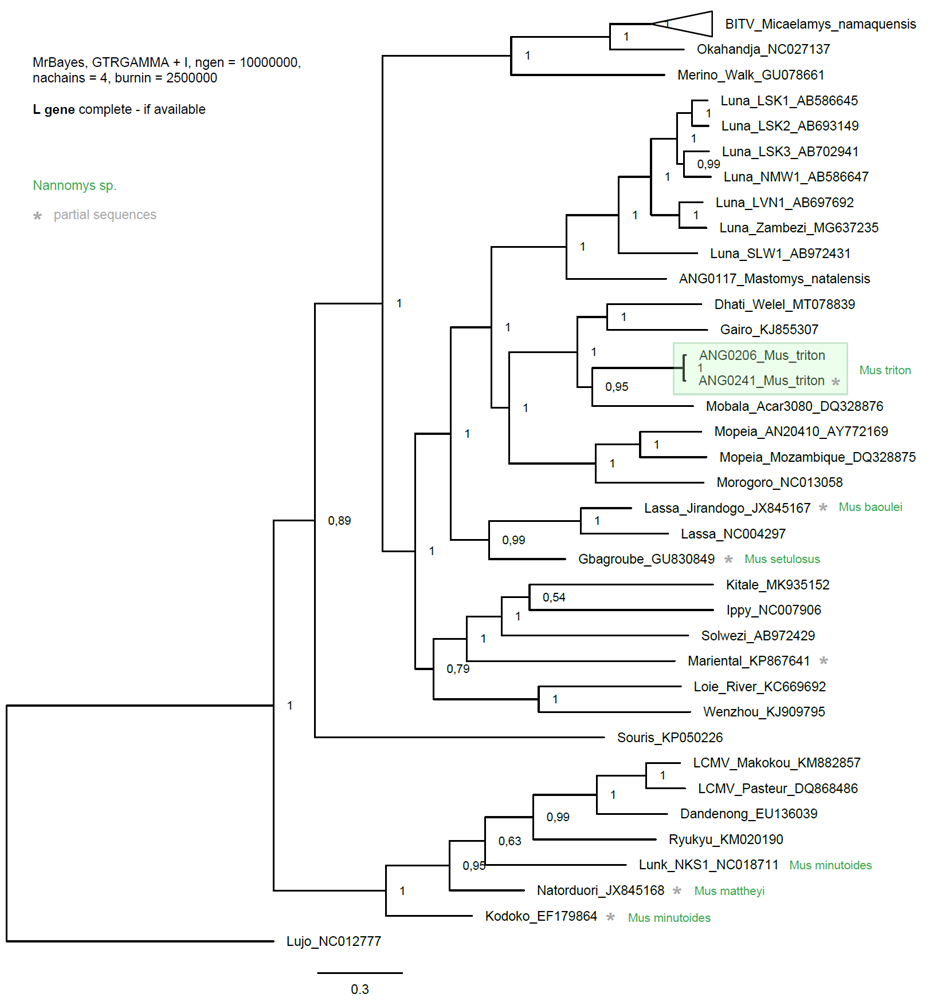
**Figure 1** Bayesian phylogenetic trees based on nucleotide sequences of *GPC* **(a)**, *NP* **(b)** and *L* **(c)** genes of selected Old World mammarenaviruses, with Lujo virus as an outgroup. Posterior probabilities (PP) are used to assess branch support. Partial sequences are labeled with asterisks. Kwanza virus (KWAV) is highlighted in green.

 **(a)** *GP* gene

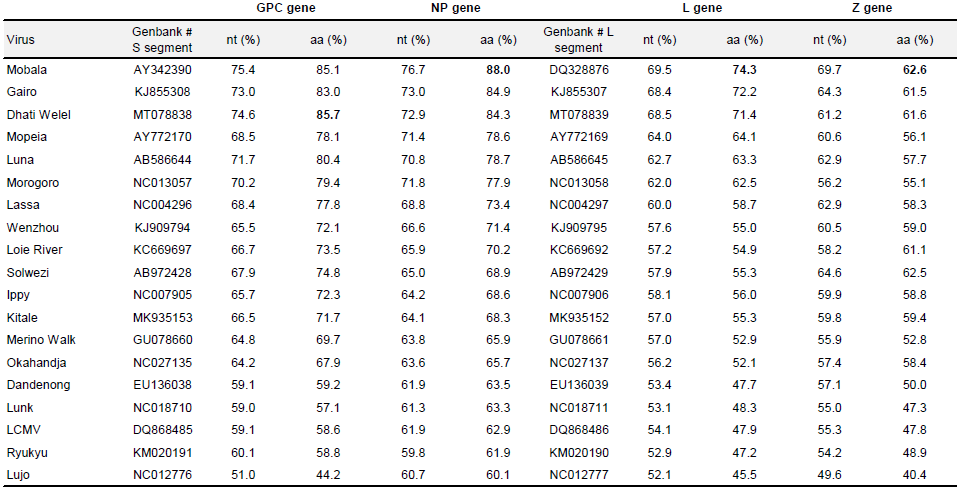
**(b)** *NP* gene



**(c)** *L* gene

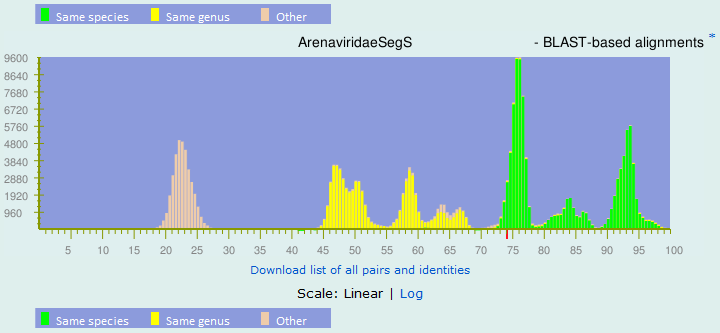
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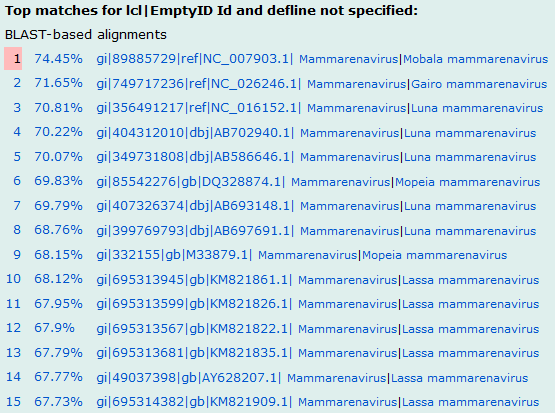
**Table 1** Nucleotide sequence and amino acid identity comparison of ANG0206 (Kwanza virus) and other Old World mammarenaviruses.

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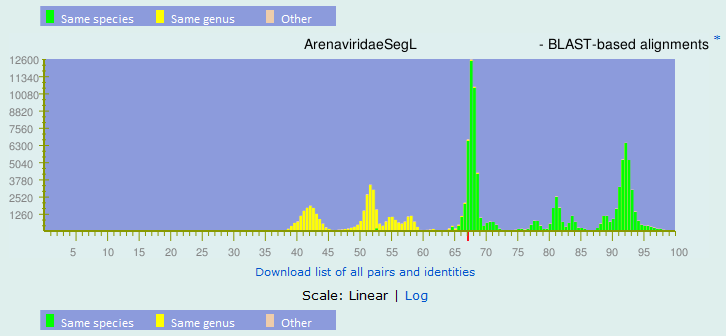
**Figure 2** PASC analyses.

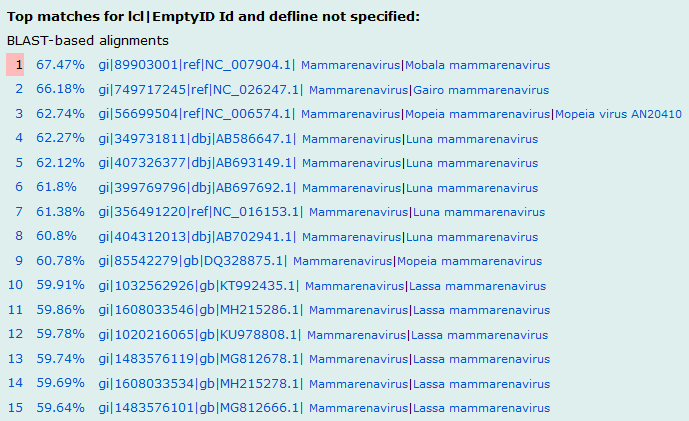
1. S segment

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1. L segment

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**References**

1. Těšíková, J.; Krásová, J.; Goüy de Bellocq, J. Multiple Mammarenaviruses Circulating in Angolan Rodents. *Viruses* 2021, 13, 982. https://doi.org/10.3390/ v13060982
2. Radoshitzky, S.R.; Buchmeier, M.J.; Charrel, R.N.; Clegg, J.C.S.; Gonzalez, J.J.; Günther, S.; Hepojoki, J.; Kuhn, J.H.; Lukashevich, I.S.; Romanowski, V.; Salvato, M.S.; Sironi, M.; Stenglein, M.D.; de la Torre, J.C. & Ictv Report Consortium. ICTV Virus Taxonomy Profile: *Arenaviridae*. *J Gen Virol* 2019, 100, 1200-1201. doi: 10.1099/jgv.0.001280 PMID: 31192784