

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2021.006M** |  |
| **Short title:** Create one new species (*Mammarenavirus bituense*) in the genus *Mammarenavirus* (*Bunyavirales*: *Arenaviridae*) | | |
|  | | |

**Authors and email addresses**

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

**Authors’ institutional addresses**

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

**Corresponding author**

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

**List the ICTV Study Group that have seen this proposal**

|  |
| --- |
| ICTV *Arenaviridae* Study Group |

**ICTV study group comments and response of proposer**

|  |
| --- |
| None. |

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

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

**Submission dates**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
| * 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**

|  |
| --- |
| 2021.006M.R.Mammarenavirus\_1nsp\_Bitu |

**Abstract**

|  |
| --- |
| Bitu virus (BITV) was detected in a Namaqua micaelamys (*Micaelamys namaquensis* (A. Smith, 1834)) sampled in Angola in 2017. Its complete genome was characterised in Těšíková *et al.* 2021.  BITV 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 bituense* after “Bitu”, a portmanteau of Bibala (Namibe Province) and Tundavala (Huíla Province) in Angola, where the virus was discovered. |

**Text of proposal**

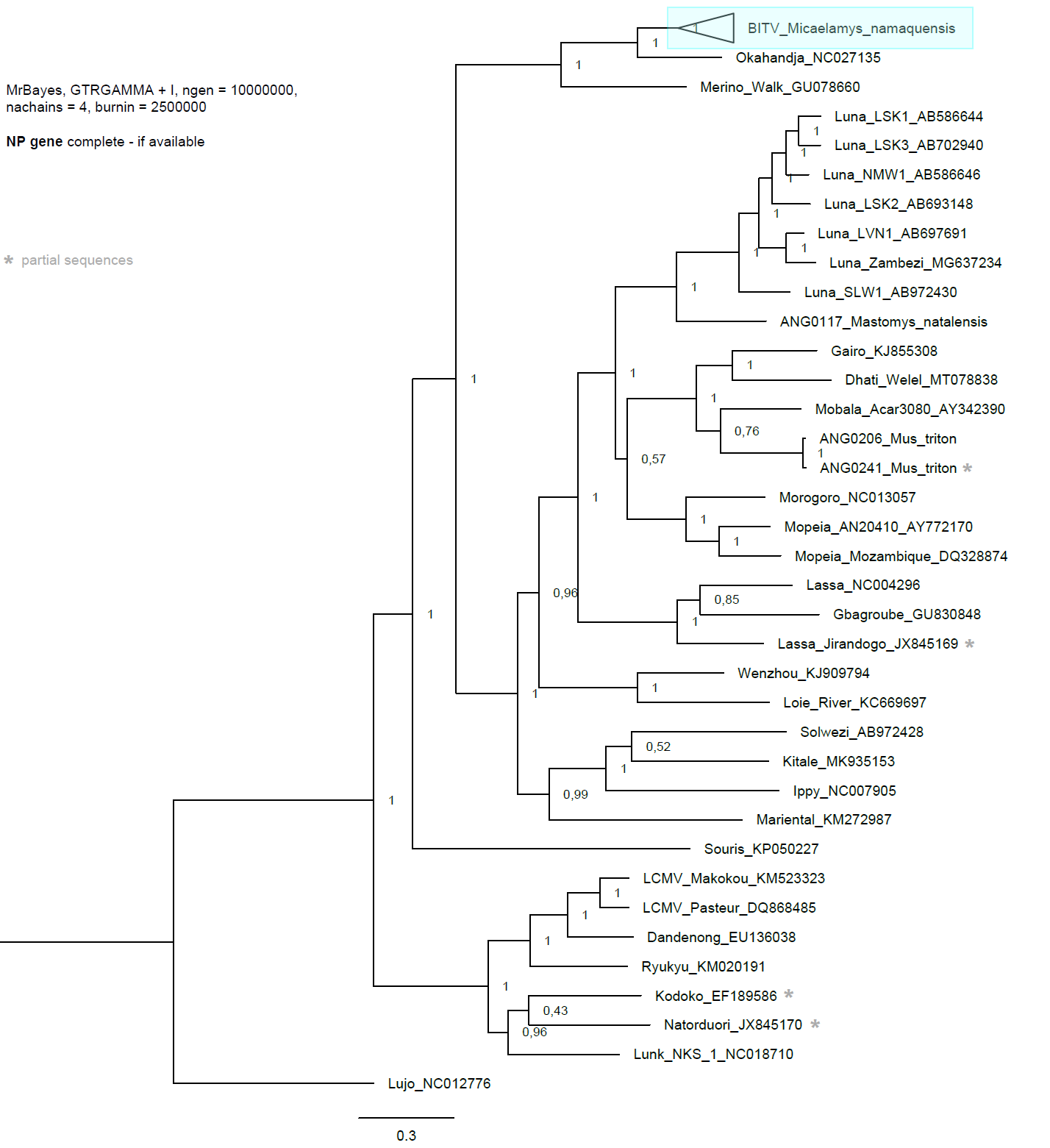
|  |  |
| --- | --- |
| |  | | --- | | The ICTV *Arenaviridae* Study Group has recommended the use of the PAirwise Sequence Comparison (PASC) tool (https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview) for the assessment of novel arenaviruses. PASC cut-off values chosen for classifying arenaviruses within the same species are >80% and >76% nucleotide sequence identity in the S and L segments, respectively. The closest relative of ANG0052 (75.1% in S and 71.56% in L segment) as well as ANG0070 (76.1% and 71.7%) was OKAV (the first analysis is displayed in Figure 2). All phylogenetic trees grouped BITV sequences into one highly supported clade (PP = 1) in which three sequences from Tundavala Province (partial ANG0017-18 and complete ANG0052) form a sister lineage to all sequences from Bibala (PP = 1), with the remaining Tundavala sequences (including complete ANG0070) forming a third cluster sister to the two previous (PP = 1) (Figure 3).  Although BITV shares the same putative host with OKAV from Namibia, the Angolan clade of *M. namaquensis* has recently been defined as a divergent phylogeographic taxon (MOTU 2 in Krásová *et al.* 2021), potentially a distinct cryptic species from all other *M. namaquensis* inhabiting the South African region, including those from Namibia (Russo *et al.* 2010). Thereby, the association with a specific host species criterion is also met for this new virus.  [Additional information In addition to the complete genome sequences of BITV strain ANG0052 (GenBank #MZ065536-37) and ANG0070 (GenBank #MZ065538-39), we obtained 11 unique partial sequences of the *L* gene (GenBank #MZ065503-13), 12 of the *NP* gene (GenBank #MZ065515-26) and eight of the *GP* gene (GenBank #MZ065528-35). The phylogenetic position, similar for all three genes, grouped BITV with Okahandja (OKAV) with high support (PP = 1, Figure 1). *p*-distance analysis provided sufficiently low identity in amino acid sequence of the *NP* gene, 85.9% for ANG0052 and 87.2% for ANG0070 with OKAV (Table 1)] | |

**Supporting evidence**

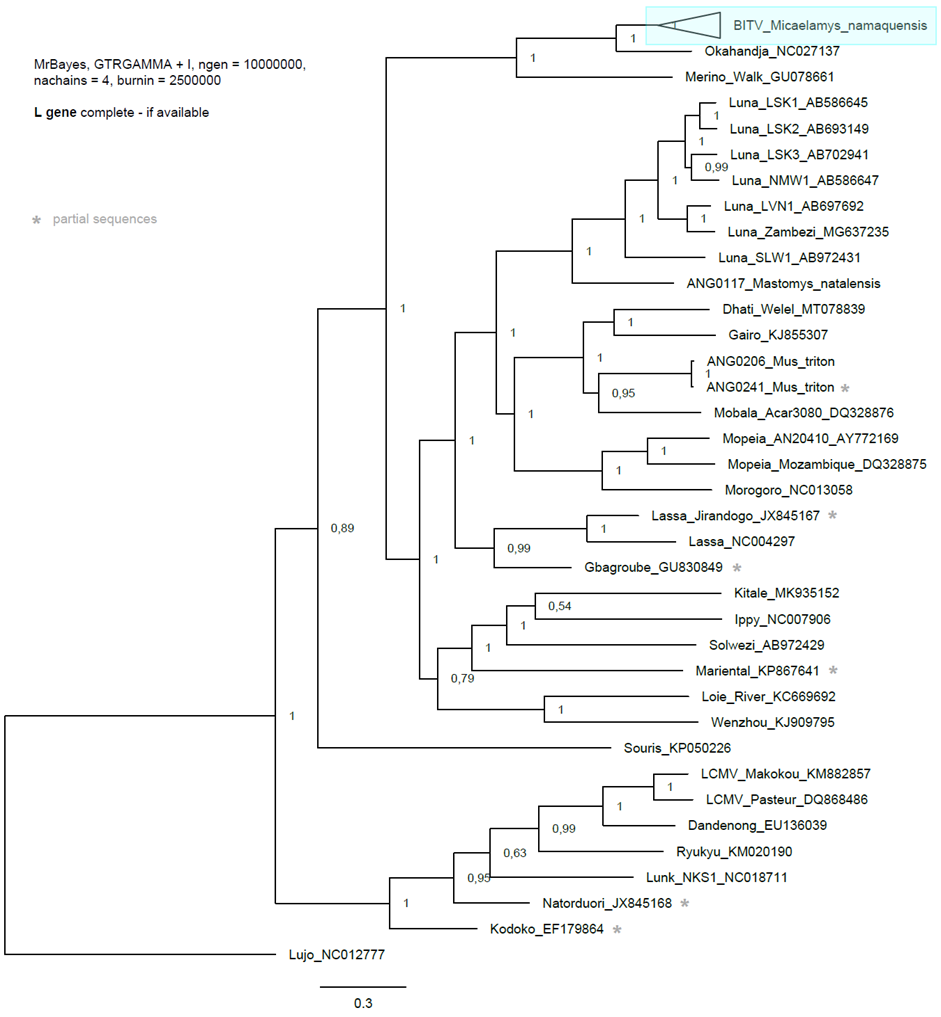
**Figure 1** Bayesian phylogenetic trees based on nucleotide sequences of *GPC* **(a)**, *NP* **(b)** and *L* **(c)** genes of selected Old World mammarenaviruses, with Lujo virus as an outgroup. Posterior probabilities (PP) are used to assess branch support. Partial sequences are labeled with asterisks. Bitu virus (BITV) is highlighted in blue. Part of the BITV phylogeny has been collapsed for clarity but is provided in Figure 3.

** (a)** *GP* gene

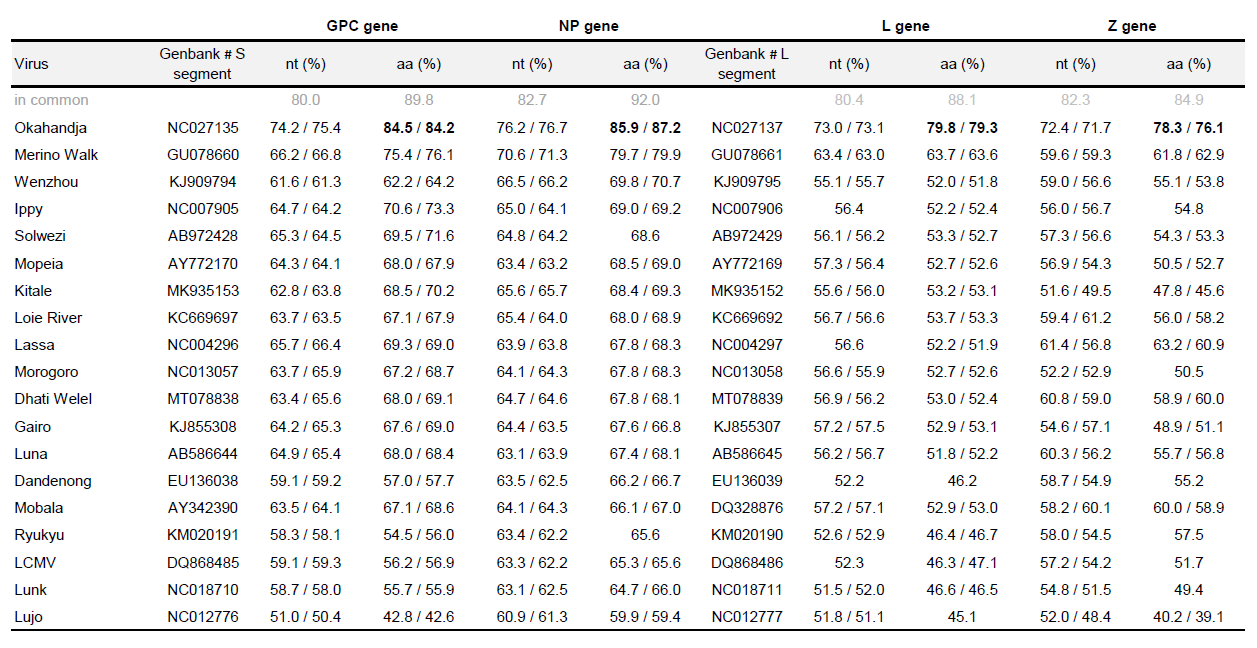
****

 **(b)** NP gene

**(c)** *L* gene

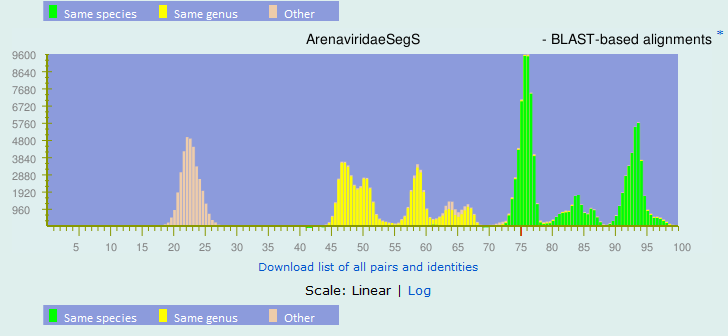
****

**Table 1** Nucleotide sequence and amino acid identity comparison of ANG0052 / ANG0070 (Bitu virus) and other Old World mammarenaviruses.

****

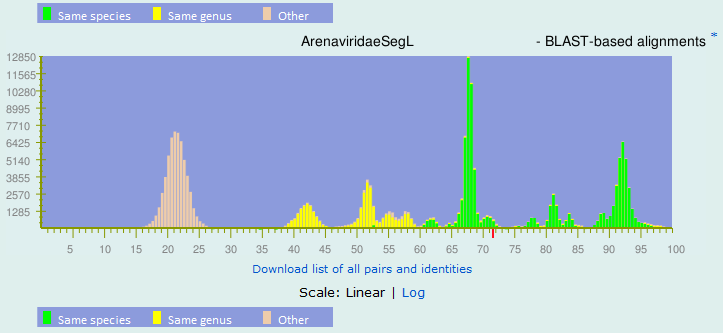
**Figure 2** PASC analyses.

1. S segment

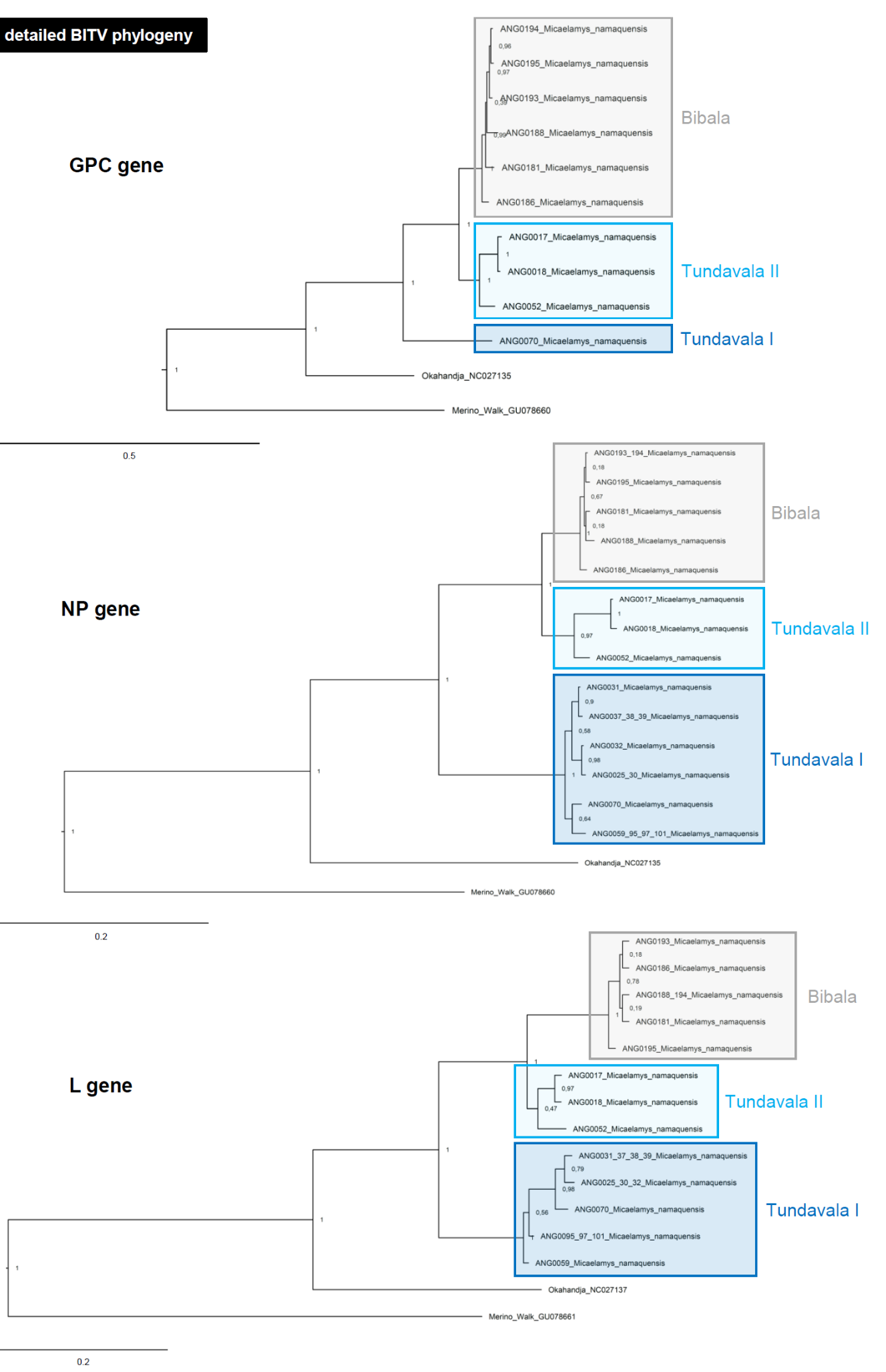
****

****

1. L segment

****

****

**Figure 3** BITV phylogeny in detail.

**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
3. Krásová, J.; Mikula, O.; Bryja, J.; Baptista, N.L.; António, T.; Aghová, T.; Šumbera, R. Biogeography of Angolan rodents: The first glimpse based on phylogenetic evidence. *Divers Distrib* 2021. under review
4. Russo, I.-R.M.; Chimimba, C.T.; Bloomer, P. Bioregion heterogeneity correlates with extensive mitochondrial DNA diversity in the Namaqua rock mouse, *Micaelamys namaquensis* (Rodentia: Muridae) from southern Africa - Evidence for a species complex. *BMC Evol Biol* 2010, 10, 307. doi: 10.1186/1471-2148-10-307 PMID: 20942924