

Supplementary material 3 to:

Hánová A., Bryja J., Goüy de Bellocq J., Baird S.J.E., Cuypers L., Konečný A., Mikula, O. Historical demography and climatic niches of the Natal multimammate mouse (*Mastomys natalensis*) in the Zambezian region.

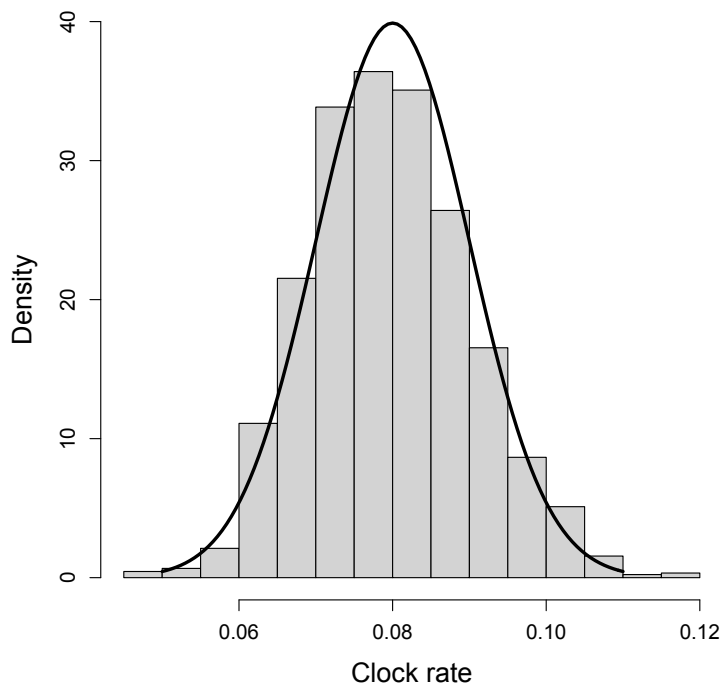
Supplementary methods. Estimation of molecular clock rates.

Molecular clock rates were estimated by re-analysis of data set from Hánová et al. (2021), which consists of 60 cytochrome *b* sequences covering the whole diversity of the genus *Mastomys*. The analysis was performed in the multispecies coalescent framework as implemented in StarBEAST 2 (Ogilvie et al. 2017). The sequences were classified into eight species: *M. angolensis*, *M. kollmannspergeri*, *M. coucha*, *M. shortridgei*, *M. erythroleucus*, *M. awashensis*, *M. huberti* and *M. natalensis*. For species tree, the same topology and node calibrations were used as in the divergence dating analysis of Hánová et al. (2021). The species tree topology was fixed to:

(angolensis,(kollmannspergeri,((coucha,shortridgei),((erythroleucus,awashensis),(huberti,natalensis)))));

which is the result of analysis of 355 nuclear loci in Hánová et al. (2021). The node calibrations (in millions of years) were log normal as follows: *M. angolensis* vs. the rest ($\mu = 1.22, \sigma = 0.10$), *M. kollmannspergeri* vs. the rest ($\mu = 0.73, \sigma = 0.11$), *M. coucha* vs. the rest ($\mu = -0.09, \sigma = 0.12$) and *M. erythroleucus* vs. *M. natalensis* ($\mu = -0.60, \sigma = 0.40$). The calibrations are in millions of years (Ma). They were taken from the divergence dating of the whole tribe Praomyini (Nicolas et al. 2021). For the species tree shape we used Yule (no extinction) prior with uninformative (broad uniform) prior on speciation rate. Constant per-branch population sizes were analytically integrated with an uninformative ($1/x$) hyperprior on the mean of population size priors. The alignment was codon position-partitioned, and every partition had its own GTR+G substitution model and its substitution rate was allowed to vary around the fixed mean. The mean clock rate was the main parameter of interest in this analysis, and it was given uniform prior with limits (0,1), i.e., proper but completely uninformative.

The clock rate prior for Bayesian skyline plot analyses in this paper was obtained by the maximum likelihood fit of normal distribution to the posterior sample of the mean clock rates, using the package MASS (Venables & Ripley 2002) for R (R Core Team 2021). Probability density corresponding to the maximum likelihood estimate ($\mu = 0.08, \sigma = 0.01$) is shown here on the background of histogram of the posterior sample:



References

- Hánová A, Konečný A, Mikula O, Bryjová A, Šumbera R, Bryja J (2021) Diversity, distribution and evolutionary history of the most studied African rodents, multimammate mice of the genus *Mastomys*: An overview after a quarter of century of using DNA sequencing. *J Zool Syst Evol Res* accepted.
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- Venables WN, Ripley BD (2002). *Modern Applied Statistics with S*. Fourth Edition. Springer, New York.