

**Patterns and processes underlying  
genetic diversity in the Namaqua rock  
mouse *Micaelamys namaquensis* Smith,  
1834 (Rodentia: Muridae) from  
southern Africa**

**By**

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**Submitted in partial fulfilment of the requirements for the degree Philosophiae  
Doctor in the Faculty of Natural and Agricultural Sciences**

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Co-supervisor: Prof. C.T. Chimimba**

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### **Declaration**

I, the undersigned, hereby declare that this thesis, which I hereby submit for the degree Philosophiae Doctor at the University of Pretoria, is my own work and has not previously been submitted by me for a degree at this or any other tertiary institution.

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## SUMMARY

African rock rats of the genera *Aethomys* Thomas, 1915 and *Micaelamys* Ellerman, 1941, are endemic to East, Central and southern Africa but extend marginally into West Africa. In the past 16 subspecies have been described in the Namaqua rock mouse *M. namaquensis* Smith, 1834. Recent morphometric and morphological patterns of intraspecific variation suggested the recognition of only four subspecies: *M. n. namaquensis*, *M. n. alborarius*, *M. n. monticularis* and *M. n. lehocla*, of which the distributions appeared to coincide with the major phytogeographical zones of southern Africa. In the present study earlier analyses of mitochondrial DNA (mtDNA) cytochrome *b* (cyt *b*) gene variation were extended. Taken together these results show that *M. namaquensis* represents a polytypic species complex but with much more diversity than detected using morphology. Phylogenetic and phylogeographic analyses revealed 14 genetically distinct lineages of which several show strong geographic association with particular vegetation biomes or bioregions. The distributional ranges of eight of these lineages showed some correspondence with the type localities of previously described subspecies of *M. namaquensis*. Some clades displayed considerable within-lineage variation indicating possible fine-scale population structuring, while others showed very little differentiation. Divergence times between lineages varied between 7.26 MYA and 2.70 MYA, corresponding to a Late Miocene to Pliocene radiation. Cytochrome *b* sequences alone do not fully resolve the evolutionary relationships among the lineages and the phylogenetic analysis was thus supplemented with nuclear Recombination Activating Gene 1 (RAG1) sequences. This gene was successfully sequenced for 11 of the identified lineages. Independent analyses of the two genes were not congruent possibly as a result of incomplete lineage sorting of the nuclear gene. The combined dataset yielded good support for six of the lineages. Finally, a more detailed phylogeographic analysis was conducted among ten localities of the Eastern Kalahari Bushveld lineage based on mitochondrial cyt *b* sequences to elucidate processes underlying diversification in this species complex. A genetic pattern of phylogenetic continuity with a lack of spatial separation was observed. The mismatch distribution analysis suggests that the lineage has expanded its population size and the geographical expansion may have followed environmental changes in the recent past. Estimates of female gene flow indicate connectivity among localities but not to the extent expected for a panmictic population. Instead a combination of a stepping-stone model and metapopulation dynamics may be applicable to this lineage. Examination of

type material of described subspecies is needed to resolve the identity of the unique lineages which will allow us to better understand the phylogeography and mode of speciation in *M. namaquensis*. In addition, localities of sympatry (lineages in sympatry) should also be studied in more detail in order to help resolve the current taxonomic uncertainties within *M. namaquensis*. Future research should therefore include a multidisciplinary approach, such as cytogenetics, morphology and more gene regions.



*For my sister, Rethana Russo*

*Thank you for your support, encouragement and  
unconditional love*

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