AN EXTENSION TO THE KNOWN RANGE OF THE DESERT MOUSE
PSEUDOMYS DESERTOR SOUTH INTO THE GREAT VICTORIA
DESERT, WESTERN AUSTRALIA

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THE desert mouse *Pseudomys desertor* is a medium sized rodent (15 – 30 g) which has a widespread distribution throughout the arid zone of Australia (Menkhorst and Knight 2001). It is considered locally abundant in habitats containing samphire, sedge, nitre bush or mature spinifex grasslands. A tolerance to disturbed habitat (from mining or grazing) has also been noted (Read et al. 1999). The distribution of the species once extended from the Murray-Darling through the Flinders Ranges to the Gibson and Great Sandy Deserts, to the west coast and onto Bernier Island (Read et al. 1999; Menkhorst and Knight 2001). Since European colonisation there has been a contraction of the species’ range to the central deserts (Kerle 1995; Read et al. 1999). In Western Australia, the most southerly historical or contemporary record, is from the Wajarri Nature Reserve (near Mount Keith), 370 km north of Kalgoorlie (D. Pearson pers. comm.; Western Australian Museum fauna database: http://203.30.234.168/). Recently, however, a suspected *P. desertor* was caught north-west of Queen Victoria Springs (QVS) in the Great Victoria Desert (GPS 30° 03’ 56’’S; 122° 55’ 28’’E), approximately 350 km to the south-east of its most southern known locality. The specimen had the distinctive buff-orange eye ring, size and general features of *P. desertor* described in Kerle (1995) and Menkhorst and Knight (2001). Prior to release of the specimen, an ear biopsy was obtained for DNA investigation and genomic DNA was extracted from the biopsy via a variation on the salting out procedure of Miller et al. (1988).

Molecular-based methods of species identification are well established (Baker and Palumbi 1996; Malik et al. 1997) and have been widely used with many animal species, including marsupials (Johnson et al. 2001; Alacs et al. 2003). For example, the sequencing of mitochondrial DNA (mtDNA) was recently used by Johnson et al. (2001) to identify a range extension for the purple-necked rock wallaby *Petrogale purpureicollis*. A similar approach was used for this study on *P. desertor*. We utilised a widely applied mtDNA marker for interspecific variation, the cytochrome *b* (*cyt-b*) gene (Hillis et al. 1996). A 427 bp region of *cyt-b* was amplified and sequenced as described in Alacs et al. (2003). Sequences were obtained from the QVS specimen, four known *P. desertor* individuals from Mount Keith, three other Western Australian *Pseudomys* species (*P. nanus*, *P. hermannsbergensis*, *P. chapmani*) and *Notomys alexis* to use as an outgroup (Genbank accession numbers AY176318 – AY176326). Mitochondrial sequences were aligned by eye. Phylogenetic relationships between mtDNA haplotypes were assessed by Maximum Parsimony (MP) and Neighbor-Joining (NJ) (Kimura 2P distances) using PAUP* 4.0b10 (Swofford 2002). Robustness of these analyses was tested using 1000 bootstrap replications.

The mtDNA of the QVS *Pseudomys* was consistently and strongly associated with the four *P. desertor* sequences. With both the MP and NJ analyses (Fig. 1) there was 100% bootstrap support for a monophyletic clade containing the *P. desertor* sequences plus the QVS sample. The *cyt-b* haplotype from the QVS sample was identical to the haplotype found in two of the Mt Keith *P. desertor* individuals (01-31 and 01-32, Fig. 1). Sequence divergences (as determined by Kimura 2-parameter distances) among the different haplotypes within the *P. desertor* clade (excluding the QVS sample) ranged from 0.24 – 0.72%, and the QVS haplotype diverged from the (non-identical) *P. desertor* haplotypes from 0.24 – 0.47%. Sequence divergences between the *P.


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Fig. 1. Neighbor-Joining (NJ) phylogram from 427 base-pairs of \textit{cyt-b} sequence from nine Australian rodent samples. Bootstrap values are given for NJ (above line) and Maximum Parsimony (below line). Our sample numbers are given in parentheses.

\textit{P. desertor} haplotypes and the other \textit{Pseudomys} species ranged from 10.2 – 13.1\% (and up to 13.6\% with the \textit{Notomys} sequence), the QVS haplotype diverged from the other species by 10.6 – 13.4\%. The molecular data very clearly identify the QVS specimen as a \textit{P. desertor}. This work extends the known range of \textit{P. desertor} 350 km south-east of its current range boundary.

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REFERENCES


