



# A southern range extension for *Sminthopsis macroura* in Western Australia, at Eucla

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## ABSTRACT

The stripe-faced dunnart (*Sminthopsis macroura*) is one of the most widespread dasyurids in Australia, occurring mostly in semiarid and arid habitats. It is not known to inhabit coastal regions of southern Australia, and no records have previously been recorded from latitudes greater than 28.5°S in Western Australia. Following the capture of an individual south of the known species range provisionally identified based on external morphology as *S. macroura*, we used DNA and craniodental morphology to corroborate the specimen's identification, providing a record of the species at Eucla, Western Australia. This represents a large range extension for *S. macroura* of 630 km from the nearest confirmed records of the species in Western Australia and South Australia.

**Keywords:** biodiversity survey, Dasyuridae, marsupial, morphology, museum, phylogenetics, range extension, *Sminthopsis*.

## Introduction

Biodiversity surveys are essential to our understanding of species distributions, yet large areas of Australia remain under surveyed (How and Cowan 2006). In the past, government agencies significantly advanced biodiversity knowledge through surveys to remote areas, but they are increasingly being conducted by private companies as a requirement for development proposals. In Australia, surveys by environmental consultants have contributed greatly to our understanding of species distributions and have led to species discovery (Doughty *et al.* 2007, 2014; Ellis *et al.* 2015). A sound understanding of local fauna and their distributions is essential for field biologists to correctly identify unusual species or records.

In this paper, we report on a range extension and novel habitat for the stripe-faced dunnart (*Sminthopsis macroura*) resulting from an individual captured during a biodiversity survey. This widespread species occurs throughout the arid zone and northern savannahs of Australia (Dickman and Greenville 2023). It has been documented to prefer clay-loam soils in the Pilbara (Gibson and McKenzie 2009) and Sturt National Park, New South Wales, stony soils at Sandringham Station, Queensland (Morton *et al.* 1983), and a range of substrates in the Northern Territory (Cole and Gibson 1991). Molecular studies have revealed genetic structure between key areas of the distribution: animals in the Pilbara and mid-west regions in Western Australia are genetically distinct from those in South Australia and eastern Australia (Blackett *et al.* 2001; Umbrello *et al.* 2020). This genetic distinction also corresponds to an apparent gap of over 900 km in the distribution of *S. macroura*, from Yamarna Station in Western Australia to the Gawler Ranges in south-central South Australia (Owens and Graham 2009; Atlas of Living Australia 2024). This gap may represent a true break in the range, as fauna surveys in the Great Victoria Desert and Nullarbor regions that span this area have recorded other *Sminthopsis* species (Burbidge *et al.* 1976; McKenzie and Robinson 1987; How *et al.* 1988; Brennan *et al.* 2012), but not *S. macroura*. Our new record represents a significant southern extension of the known *S. macroura* distribution in Western Australia and highlights the importance of using genetic and morphological evidence to verify unusual species records.

## Materials and methods

### Field methods and site description

The specimen was captured on 7 April 2022, in a 20 L dry pitfall trap set on a coastal foredune 25 km south-west of Eucla, Western Australia (31.825°S, 128.679°E). The habitat at the site consisted of long unburnt, scattered tall shrubs (*Nitraria billardierei*, *Acacia* spp. and *Alyxia* spp.) over very open low shrubs (*Rhagodia*, *Tecticornia* and *Suaeda* spp.) and scattered herbs (including *Frankenia*, *Sonchus* and *Carpobrotus* spp.) on white sand.

### Molecular methods

The specimen was deposited at the Western Australian Museum for vouchering (registered as WAM M65257), and a liver sample was taken for genetic analysis. Total genomic DNA was extracted using a Qiagen DNeasy<sup>®</sup> tissue and blood kit according to manufacturer's instructions with an elution volume of 100 µL. We amplified the mitochondrial Control Region (CR) gene and 12S rRNA, as these loci are commonly used in barcoding studies to corroborate the identification of species, following the protocol described in Umbrello *et al.* (2017) (for further details, see Supplementary Information). DNA was Sanger sequenced at the Australian Genome Research Facility (Perth, Western Australia), and the resulting sequence reads were assembled and processed in Geneious Prime (Kearse *et al.* 2012), as shown in Umbrello *et al.* (2017).

To corroborate the identity of WAM M65257 a Maximum Likelihood phylogeny, partitioned by loci, using a GTR

nucleotide model and 1000 bootstrap replicates, was built in the RAxML (Stamatakis 2006) plug-in in Geneious with the new sequences aligned to exemplars from the published literature (Blacket *et al.* 1999; Blacket *et al.* 2001). To investigate the relationships between WAM M65257 and other *S. macroura* individuals, a Maximum Parsimony TCS haplotype network (Clement *et al.* 2000) was constructed for the CR sequence data including sequences from Umbrello *et al.* (2020) in the software program PopART (Leigh and Bryant 2015) with haplotypes grouped by Australian bioregion (Department of Climate Change, Energy, the Environment and Water 2020).

### Morphological methods

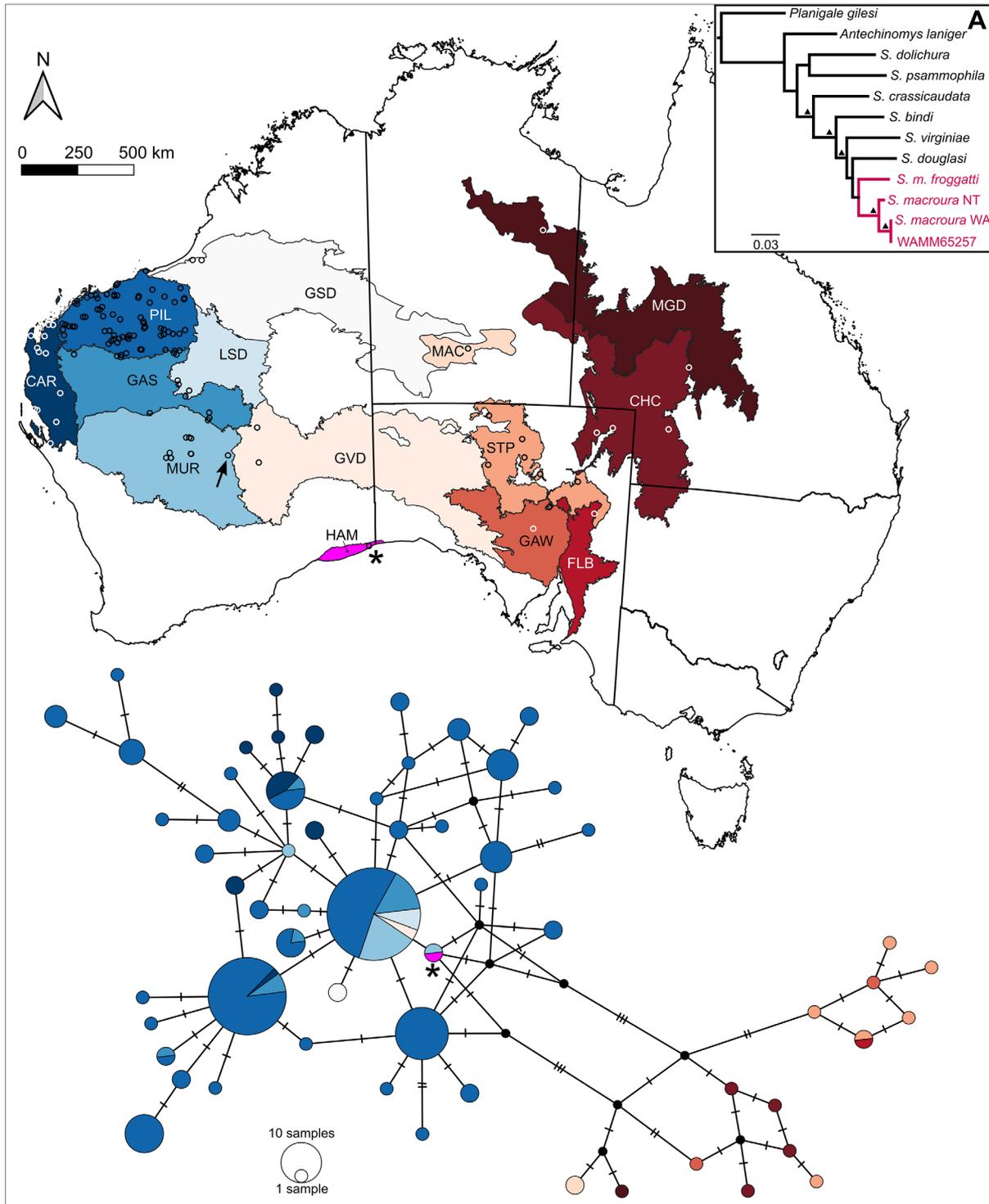
The skull and dentary of WAM M65257 was removed and cleaned with fine forceps. The skull was identified to species level by comparison with other *Sminthopsis* skull specimens held at the Western Australian Museum and by keying out craniodental features using the identification key outlined in Archer (1981).

## Results

The specimen was provisionally distinguished from other *Sminthopsis* occurring near the Eucla region (*S. crassicaudata*, *S. dolichura*, *S. fuliginosa* and *S. gilberti*) using external morphology, due to the combination of a prominent facial stripe, incrassated (fattened) tail and the enlarged, smooth granules on the interdigital pads on the underside of the foot (Fig. 1).



**Fig. 1.** (a) Photograph of WAM M65257 in life. Note the distinct facial stripe running from between the ears down to between the eyes and the incrassated (fattened) tail base. Photo copyright Joshua Keen/Biota. (b) Hind-foot morphology of M65257 showing the underside of the hindfoot with enlarged apical granules (see enlarged inset) on the interdigital footpads (Photo copyright Western Australian Museum).



**Fig. 2.** Mitochondrial haplotype network (Control Region) of *Sminthopsis macroura* samples coloured by bioregion (Department of Climate Change, Energy, the Environment and Water 2020) shown on a corresponding map of Australia. Circle size indicates the number of individuals sharing each unique haplotype, small black circles indicate unsampled nodes and hatch marks indicate number of nucleotide changes. Samples used in the haplotype network are shown as open circles on the map. The location of WAM M65257 is denoted by an asterisk on both the map and network, and WAM M50650 is indicated on the map by a black arrow. Inset (A) Maximum Likelihood phylogeny from combined mitochondrial loci (12S + CR) placing WAM M65257 with other *S. macroura* reference sequences from Blacket *et al.* (1999, 2001), black triangles indicate bootstrap support values greater than 70%.

The skull was identified as that of *S. macroura* following the key provided in Archer (1981) and differs from the aforementioned dunnart species by having large entoconids on M<sub>1-3</sub>, short premaxillary vacuities and the hypocristid separate from the entoconid on M<sub>3</sub>. Archer's (1981) revision precedes the splitting of *S. murina* into *S. dolichura*, *S. griseoverter* (note: now referred to as *S. fuliginosa*) and *S. gilberti* (Kitchener *et al.* 1984), but Kitchener *et al.* (1984) considered these three species to differ from all other *Sminthopsis* based on the same characters outlined in Archer (1981) for *S. murina*.

The CR genetic sequence was found to be identical to that of an individual (WAM M50650; Genbank Accession MT366297) captured at Duketon, Western Australia (27.79°S, 122.27°E), some 765 km north-west of our WAM M65257 *S. macroura* specimen (Fig. 2). The 12S sequence of our specimen was identical to published sequences AF339114 (Mardie Station, Pilbara) and AF339117 (Mileura, Murchison), which are over 1700 and 1200 km north-west of Eucla, respectively. Taken together, this places our WAM M65257 as part of the Western Australia genetic clade and not closely related to the *S. macroura* population in South Australia, the closest individuals of which are ~630 km east of Eucla. To our knowledge, there have previously been no records of *S. macroura* from the Hampton bioregion, where WAM M65257 was collected, or the adjacent bioregion (Nullarbor).

## Discussion

Based on total evidence (morphological features and mtDNA) we report a large range extension of the stripe-faced dunnart (*Sminthopsis macroura*) from coastal dune habitat near Eucla along the south-east coast of Western Australia. This location falls within the Roe Plains, a narrow coastal strip of sandy and clay soils bounded by the limestone escarpment of the Hampton range to the north (Greer *et al.* 1991). Prior to the surveys in which WAM M65257 was captured, there had been little systematic survey effort on the Roe Plains apart from targeted reptile surveys in which only two mammal species were captured: *Cercartetus concinnus* and *Mus musculus* (Porter 2019). WAM M65257 shares mitochondrial haplotypes with other specimens from Western Australia, rather than those in South Australia, which are found at similar latitudes (Fig. 2). There is a large gap in the records of *S. macroura* between mid-Western Australia and Eucla, mostly encompassing the Nullarbor region, and eastwards to the Gawler Ranges in South Australia (Atlas of Living Australia 2024). *Sminthopsis macroura* is also absent from subfossil material from Nullarbor caves, some 100–270 km west of Eucla (Lundelius 1983; Newman-Martin 2020), despite various other *Sminthopsis* species being found in these deposits, including *S. crassicaudata*, *S. fuliginosa* and *S. gilberti*, which suggests *S. macroura* is rare in the region. Further systematic survey work in the Eucla area and

adjacent Nullarbor may yield more records of *S. macroura*. This would help us to understand the habitat requirements of the species and better assess whether it is absent from the Nullarbor.

Mitochondrial haplotype sharing over vast distances is also present in the most commonly occurring haplotype in our dataset (shown as the largest circle in Fig. 2), which is shared by individuals from the south-eastern Pilbara to the central Goldfields region, a distance of over 837 km. Given the internal position of this widely shared ancestral haplotype in the network, it could be evidence for population expansion from historical refugia, with the Pilbara having been an important refugium for many taxa (Kingman 1982; Pepper *et al.* 2013; Umbrello *et al.* 2020). The apparent rarity of the CR haplotype that is shared between WAM M65257 and WAM M50650 (see black arrow and asterisk, Fig. 2) likely reflects the paucity of sampling in this area, and more genetic samples from this region may increase the frequency of this haplotype.

The new record reported here highlights the value of conducting biodiversity surveys in poorly studied regions and the substantial value of voucher specimens to verify identifications using a total evidence approach (Kemper *et al.* 2011). It also highlights the contribution that biologists working in the private sector make to our understanding of species distributions. Having a sound understanding of the local fauna is crucial for identifying when specimens warrant further investigation and can lead to improved knowledge of species distributions (Umbrello *et al.* 2022). New records such as that reported here provide valuable information that deepens our understanding of how small mammals are distributed across vast Australian landscapes. As mammal species continue to undergo population declines throughout Australia (Legge *et al.* 2023), building on and expanding existing knowledge assists with conservation assessments and management of poorly understood taxa and is a fundamental service provided by scientists working in museums, government and the private sector.

## Supplementary material

Supplementary material is available [online](#).

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**Data availability.** New sequence data generated in this study are available from the NCBI Genbank database with the accession numbers Control Region: OR778374 and 12S: OR789447.

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