Pleistocene climatic changes drive expansion and fragmentation in a widespread arid zone specialist, *Petrogale lateralis*

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Abstract

Organisms living in arid biomes are predicted to be at threat of extinction associated with ongoing climatic and anthropogenic change. Our understanding of species responses to Pleistocene climatic changes within these environments is still limited, particularly in Australia. Here we evaluate the demographic and evolutionary history of a widespread Australian marsupial, the black-footed rock-wallaby (*Petrogale lateralis*) whose contemporary distribution is highly fragmented across the arid biome and offshore islands. Combining genomic data from historical and modern samples we evaluate the divergence history of the five *P. lateralis* sub-species. The species has experienced a Pleistocene demographic expansion across the vast Australian arid biome, with subsequent fragmentation of populations and sub-species. Populations of the widespread sub-species *P. lateralis lateralis* are as divergent as sub-species within *P. lateralis* and there is negligible recent gene flow between most populations/sub-species. Individuals on islands have extremely low genetic diversity and high inbreeding coefficients, in contrast to the naturally fragmented mainland populations. Our results indicate historical connectivity of populations ~160-640 kya, and indications of bottlenecks for both island and some isolated mainland populations, providing important context for conservation management and potential genetic rescue. However, given the large ecological gradient and chromosomal variation within this widespread species, assessment of ecological differences will be important before decisions to mix across geographically distant populations and/or sub-species.

Keywords: phylogeography, *Petrogale lateralis*, arid biome, evolution, demographic history

Introduction

Arid biomes, including arid, hyper-arid and semi-arid regions (arid index <0.3; <100-300 mm annual precipitation), encompass ~30% of the global landmass and are under ongoing biodiversity loss and decline as a result of climate change and associated threats (Zhang et al., 2023). Unlike more mesic biomes (e.g., temperate and tropical regions) where we have a better understanding of organisms' responses to geologically recent climatic and environmental change, our understanding of arid adapted organisms is less well developed (Pepper & Keogh, 2020). Fossil and geological records in arid biomes are often limited and thus genetic information has been essential to understanding processes of speciation and diversification (e.g., Riddle & Hafner, 2006; Brito et al., 2014; Pepper & Keogh, 2020). Aridification began during the Miocene-Pliocene to form contemporary global arid biomes (Riddle & Hafner, 2006). Pleistocene climatic fluctuations caused range expansions from refugia in temperate areas of the Northern Hemisphere (Hewitt, 2000) yet led to localised persistence across multiple refugia during unfavourable times for low dispersal and/or habitat specialists, generating substantial phylogeographic structure in arid biomes (e.g., Brito et al., 2014; Burriel-Carranza et al., 2024*;* Riddle & Hafner, 2006). Genetic studies are now highlighting how these vast arid landscapes are associated with high levels of endemism and often "micro-hotspots" of biodiversity (Brito et al., 2014; Burriel-Carranza et al., 2024).

Today, many arid zone species are threatened due to the amplified impact of climate change along with ecological disturbance in desert habitats (Loarie et al., 2009). Understanding responses of species to recent climatic change is pertinent to understand how to manage species for conservation (Hewitt, 2004a, 2004b; Byrne et al., 2008). Australian deserts are a case in point. Encompassing ~70% of the continent, the arid biome represents one of the largest desert ecosystems in the world, dominated by stony and sandy desert systems that

formed during the late Pliocene and mid-Pleistocene (Fujioka et al., 2005, 2009; Byrne et al., 2008; Pepper & Keogh, 2020). The landscape is heterogeneous, with rocky outcrops and range systems forming habitat islands amidst the deserts (Pepper & Keogh, 2020). The unstable and variable climatic conditions began oscillating from the Pliocene and intensified into the Pleistocene (see Byrne et al., 2008), with fluctuating moisture and climates during the glacial interglacial cycles, although with varied evidence for whether the glacial periods were hyper-arid or moisture rich (see Weij et al., 2024). Either way, climatic changes and instability during the glacial interglacial periods had different responses amongst organisms in the arid regions. Some widespread species (ecological generalists) had little or no divergence among populations, compared to others that had substantial phylogeographic structure with scattered rocky ranges as likely refugia (reviewed in Byrne et al., 2008; Pepper & Keogh, 2021). This period of climatic change also resulted in some groups undergoing rapid speciation and divergence (e.g., *Pseudomys* – Smissen & Rowe, 2018; lizards - Tejero-Cicuéndez et al., 2022; *Heteronotia* geckos - Fujita et al., 2010). Compared to reptiles and birds, there have been rather few studies of widespread arid zone mammals. The studies to date reveal low genetic structure and signatures of widespread expansion (e.g., delicate mice in the genus *Pseudomys*, Roycroft et al., 2024; dasyurid marsupials, Umbrello et al., 2020, red kangaroo *Osphranter rufus*, Clegg et al., 1998).

Many Australian taxa are threatened or have already become extinct since European colonisation in 1788 (see Burbidge et al., 2009; Woinarski et al., 2019). Arid Australian mammals have been the focus of intensive conservation initiatives where species are released within feral predator-free fenced exclosures and islands to manage population numbers and reintroduce species from sites where they have gone locally extinct (Garnett et al., 2018). Arid regions have been subject to the greatest number of Australian mammal losses, both

local and global extinction, and this biome has been suggested to be at risk due to changed land use in some areas, introduced herbivores, impacts of altered fire regimes, and introduced predator access in open environments (McKenzie et al., 2007; Johnson & Isaac, 2009, Woinarski et al., 2019). Recent comparative analysis of extinct and threatened Australian rodents identified elevated extinction in the arid biome (Roycroft et al., 2021). Further research to understand diversification of extant Australian mammals across the arid region and the processes shaping their genetic diversity is important to ongoing conservation initiatives of Australia's unique mammal fauna. The ecologies of mammals in desert ecosystems have been shown to vary despite shared climatic and environmental conditions, with some species exhibiting fluctuating population dynamics (i.e., boom-bust) associated with the resource availability (see Greenville et al., 2016). This indicates diverse responses to past climatic changes across the arid zone. A recent long-term empirical study of small mammals in the Simpson desert found gene flow during periodic population booms was important in maintaining genetic diversity in a species with fluctuating population dynamics (e.g., many arid species) (Stringer et al., 2024). Yet we still lack a broad understanding of how diverse organisms maintain their genetic diversity and how their genetic variation is partitioned across the Australian arid biome. We have little knowledge of how species persist in ongoing refugia during climatic and resource fluctuations, whether multiple areas of refugia exist and persist over climatic cycles, whether refugial areas are common amongst diverse organisms, and how they differ between ecological generalists and habitat specialists. Understanding how populations and species persist across the heterogenous arid landscape of Australia will be important to identifying how we can best protect species moving forward and how mammals in desert ecosystems persist under such variable environmental conditions.

Rock-wallabies (genus *Petrogale*) are a good case study to understand diversification processes across the arid zone, as they are habitat specialists, restricted to rocky habitats which in the arid zone of Australia are separated by large expanses of low-relief sandy or stony deserts (reviewed in Pepper & Keogh, 2020). Of the 17 *Petrogale* species, four occur in the arid biome. Dispersal does occur in rock-wallabies, but it is generally localised and limited (e.g., Pope et al., 1996; Hazlitt et al., 2006; Piggott et al., 2006). *Petrogale lateralis*, the black-footed rock-wallaby, has a large (~2.65 million km^2) and naturally fragmented distribution across the central and western arid zone, within which five sub-species are recognised based on subtle differences in morphology and chromosome rearrangements (2n=20-22 karyotypes, including Robertsonian fusions and centric shifts; Briscoe et al., 1982; Sharman et al., 1990; Eldridge & Potter, 2020; Eldridge & Pearson, 2023; see Fig. 1). *Petrogale lateralis* offers a new biological perspective to explore how habitat specialists are genetically structured in the arid zone and their demographic response to past climatic changes. This will provide greater insight into where and how species have persisted across this heterogeneous landscape.

Petrogale lateralis has been the focus of numerous genetic studies that revealed low yet structured diversity among sub-species but with limited sampling across geographic isolates (Eldridge & Potter, 2020; Eldridge et al., 2021; Potter et al., 2012, 2017). Finer-scale genetic studies have been undertaken for *P. l. centralis* and *P. l. lateralis* and shown low diversity and limited contemporary gene flow between populations (Eldridge et al., 2004; Ruykys & Lancaster, 2015, West et al., 2019). A chromosomally heterogeneous population (2n=21-22) has been identified at Townsend Ridges in central eastern Western Australia (Eldridge & Pearson, 1997; Pearson, 2004), which mitochondrial data indicates is a hybrid population (Eldridge et al., 2021). Interestingly, experimental crosses between chromosomally divergent

P. l. centralis and *P. l. pearsoni* (fixed differences include a centric shift; see Fig. 1) produced fertile male and female hybrids and backcrosses (Close & Bell, 1997; R. L. Close, unpubl. data). However, these genetic studies have not yet had sufficiently comprehensive geographic and genomic coverage to fully understand the demographic history of the species and associated sub-species in response to past climatic changes.

Due to natural rocky habitat patchiness and widespread declines within the last 150 years the current distribution of *P. lateralis* is highly fragmented (Fig. 1). Two sub-species, *P. lateralis hacketti* and *P. l. pearsoni* are restricted to islands off the south coast of Australia.
Of the five sub-species, two are listed as Endangered (*P. l. lateralis* and *P. l. kimberleyensis*) and the other three are listed as Vulnerable under the Australian *Environment Protection and Biodiversity Conservation (EPBC) Act* 1999. *Petrogale l. centralis* and *P. l. lateralis* are actively managed for conservation with ongoing translocations, reintroductions, augmentations, and captive breeding used to bolster species numbers (e.g., Pearson et al., 2019; West et al., 2018; Nilsson et al., 2023). Some populations, particularly *P. l. lateralis* from Barrow Island and *P. l. pearsoni*, are highly inbred (Eldridge et al., 2001, 2004) and understanding the evolutionary history of *P. lateralis* across its' vast ecological and latitudinal gradient will assist in identifying future options for maximising genetic diversity through genetic rescue. In particular, how do island population dynamics compare to mainland populations, and do island populations need active management. In this study we incorporate both modern and historic museum samples to determine population structure and diversity across the range and evaluate their divergence history in response to past climatic changes. This study will not only shed light on how a widespread arid zone mammal has persisted and diversified across the Australian arid biome during the climatic changes of the

Pleistocene but also provide an important foundation for ongoing conservation management for the species.

Materials and Methods

Sampling and sequencing

Samples of *P. lateralis* were collected from the Australian Museum, Western Australian Department of Biodiversity, Conservation and Attractions, Western Australian Museum, and the Natural History Museum, London. In total, 97 samples were analysed from across the geographic range of *P. lateralis*, and included: *P. l. centralis* (n=10), *P. l. hacketti* (n=11), *P. l. kimberleyensis* (n=11), *P. l. lateralis* (n=41), and *P. l. pearsoni* (n=11), as well as six samples from Cotton Creek, Western Australia (karyotypes unknown) and seven samples from Townsend Ridges (putative hybrid population, Eldridge et al. 2020) (refer to Fig. 1 for distribution map of samples and Supp. Table 1 for sample information). Samples were collected from historical samples (1906-1959) and modern samples. The historical samples comprised biopsies from museum skins and some represented unique localities.

DNA was extracted from samples and sequenced as part of the Oz Mammal Genomics Framework initiative of BioPlatforms Australia. DNA from seven museum skin samples was extracted at the Australian National University's Ecogenomics and Bioinformatics Laboratory Trace DNA facility, using the DNeasy Blood and Tissue Kit (Qiagen) with modifications based on Joseph et al., (2016). Full details of this extraction method are available in Nistelberger et al., (2023). Extraction negative controls were included in each batch of extractions to monitor for contamination. DNA from two additional historical museum specimens (BMNH 1906.8.1.256 and BMNH 1939.2849) was extracted from approximately 10 mg of dried skin tissue, using the protocol described in Dabney et al., (2013) with

modifications as outlined in Brace et al., (2022). DNA extraction for these two samples was completed in the ancient DNA laboratory at the Natural History Museum, London. DNA from modern tissue samples was extracted either: 1) at the Australian Museum using a phenol chloroform method (Sambrook et al., 1989; 23 samples); 2) at the Australian Museum using a salting-out method (Sunnucks & Hales, 1996; 31 samples); or 3) by the Western Australian Department of Biodiversity, Conservation and Attractions using a salting-out method (34 samples). All DNA extracts were then prepared for a targeted exon capture approach where ~3000 exons were targeted for capture using a custom NimbleGen SeqCap EZ hybridisation kit (see Roycroft et al., 2022). Probes were designed from seven marsupial transcriptomes from across the order, as outlined in Bragg et al., (2016) and Duchene et al., (2018). Each sample was uniquely barcoded, and libraries prepared using the Meyer-Kircher library protocol (Meyer & Kircher, 2010), including some modifications from Bi et al., (2013). Samples were pooled in equimolar ratios (to a total of 1.2 ug) and hybridised with 5 ug of mouse cot-1 DNA following the manufacturers protocol for 72 hr. Hybridisation pools included libraries from 96 samples for DNA from modern specimens, and libraries from 64 samples for DNA from historical museum specimens (note that samples from other marsupial species were also included in each hybridisation pool to make up the total numbers). Post hybridisation, the sample was amplified in two separate enrichment PCRs (Phusion hot start kit, Thermo Scientific™; and IS5 and IS6 primers, Meyer and Kircher 2010) and cleaned up using the QIAquick PCR purification kit (QIAGEN). Quality control checks were made following the protocol of Potter et al. (2022). Samples were then sequenced across Illumina HiSeq 2500 and Illumina NovaSeq 6000 (100bp paired-end run) platforms at the ACRF Biomolecular Resource Facility at the Australian National University.

Bioinformatics and datasets

The raw sequencing data was processed, assembled and aligned using the Exon Capture Pipeline for Phylogenetics (ECPP, https://github.com/Victaphanta/ECPP) following the protocol of Roycroft et al., (2020) with some modifications. Briefly, we deduplicated raw paired reads using dedupe.sh (part of the BBTools package, Bushnell B. 2015, sourceforge.net/projects/bbmap) and quality trimmed using Trimmomatic (Bolger et al., 2014). We then *de novo* assembled the cleaned reads from each sample using Trinity v2.0.6 (Grabherr et al., 2011; Haas et al., 2014), and selected the highest-quality *de novo* assembly for each clade to be used as a reference for mapping. This approach has been shown to substantially improve in final data completeness and quality, especially from historical skins (Roycroft et al., 2022). We mapped the cleaned reads to the clade-specific reference using BBmap (version 35.82, Bushnell B. 2015, sourceforge.net/projects/bbmap) with a minimum depth of 10 to retain sites, and called variants using the mpileup2cns command in VarScan v2.3.7 (Koboldt et al., 2012). Resulting consensus sequences of all exons captured per sample were converted to fasta format and aligned using MAFFT (Katoh & Standley, 2013).

Loci with average per-locus heterozygosity >3% heterozygosity across samples (putative novel paralogs), and <90% sample completeness were removed from downstream analysis, leaving 1934 filtered exon alignments for final analysis. Final alignments were processed with BMGE (Criscuolo & Gribaldo, 2010) to remove poorly represented regions. From these final filtered alignments, single nucleotide polymorphism (SNP) datasets were extracted (not including the outgroups) using SNP-sites and scripts from https://github.com/tandermann/snp_extraction_from_alignments. Two SNP datasets were generated, one consisting of all the SNPs ('all SNP' dataset) and another consisting of a randomly selected SNP per exon ('single SNP' dataset).

Population structure and diversity

We estimated genetic clustering of individuals using the two SNP datasets. We used a hierarchical principal coordinate analysis (PCoA) using the package dartR (Gruber et al., 2018) in R (v. 3.6.3; R Core Team), where we sequentially removed the most divergent populations from the analysis and reanalysed the data to assess more fine-scale genetic clustering. This analysis was conducted on the 'all SNP' dataset. We also assessed population genetic structure using a spatial genetic clustering algorithm which estimates ancestry proportions from ancestral allele frequencies and geographic data in tess3r (Caye et al., 2018). We tested various numbers of *K* (number of genetic clusters) from 1-14 and used the cross-validation plot to assess the best value of *K.* As this approach can be arbitrary (François & Durand, 2010), we explored multiple values of *K* and also applied a hierarchical approach where divergent populations were removed to assess more fine-scale structure. This analysis was performed on both the 'all SNP' and 'single SNP' datasets.

We calculated average individual heterozygosity (Ho) of exon alignments for populations using AMAS (Borowiec, 2016), a tool for computing summary statistics. This summarises the data and enables estimation of heterozygous sites as a proportion of the entire dataset. We also calculated population inbreeding coefficients using dartR (Gruber et al., 2018) in R (v. 3.6.3; R Core Team) on the 'all SNP' dataset and the gl.report.heterozygosity function. We estimated effective inbreeding (equation (1-(Ho/uHe)), where uHe represents average uHe of mainland populations (Frankham, 1997). We calculated pairwise sequence divergence between populations (Dxy) from the exon alignments, as well as within population variation (theta) in PopGenome R package (Pfeifer et al., 2014) using all sites (i.e., including missing data).

We tested for isolation by distance between mainland populations and for *P. l. centralis* using a Mantel test in dartR (gl.ibd function; Gruber et al., 2018). We used the individual approach using a Euclidean distance matrix compared to genetic distance. Analyses were run with 999 permutations on the 'all SNP' dataset.

Divergence history

Phylogenetic analysis of the concatenated dataset for all individuals was estimated using IQTree2 (Minh et al., 2020). The analysis was run using the MFP criterion and 1000 bootstrap replicates. We also assessed relationships using a phylogenetic network approach in SplitsTree4 using the NeighborNet analysis (Bryant & Moulton, 2002; Huson & Bryant, 2006). This approach allows visualisation of reticulation in a network as it clusters individuals and uses a matrix of uncorrected P distances to link individuals.

We then estimated divergence time of populations using a single individual per population using the concatenated nuclear dataset. We estimated the divergence time using MCMCTree (Rannala & Yang, 2007). We used soft bound calibrations based on the upper and lower confidence limits from a fossil calibrated divergence tree for *Petrogale* from Potter et al., (2012). Three calibrations were used: 0.53-1.79 mya for the node connecting all *P. lateralis* individuals, 0.13-0.59 mya for the node connecting the two *P. xanthopus* sub-species and 3.18-8.62 mya for the node connecting *P. xanthopus* to *P. lateralis.* The HKY nucleotide substitution model was applied with four discrete gamma categories and 0.5 alpha for gamma rates at sites. The analysis was run using the approximate likelihood approach (dos Reis & Yang, 2011), independent rates model and including all missing sites. The analysis was run for 10 million generations sampling every 1000 generations (total 10,000 samples) after a burnin of 1 million generations.

Population demographic history

We tested for evidence of population expansion of the mainland populations of *P. lateralis* as a species as well as for individual populations using the concatenated exon alignment data. We assessed evidence of expansion by estimating *Tajima's D* (Tajima, 1989) in the PopGenome R package (Pfeifer et al., 2014) which assesses signals of non-neutral processes. We ran 1000 coalescent simulations for Tajima's *D* using Hudson's ms (Hudson, 2002) and significance was determined by comparing the observed Tajima's *D* to the top 0.05% of simulated data. We do not apply more elaborate tests for population demographic histories because of the low diversity overall, this would require full genome data.

As we were interested in exploring the degree of recent connectivity or isolation between currently fragmented mainland populations, we also estimated migration between populations and sub-species of *P. lateralis* using MIGRATE 4.0 (Beerli & Palczewski, 2010, Beerli et al., 2019). This Bayesian coalescent-based approach estimates mutation-scaled immigration rates (M) and population sizes (Θ). We evaluated all pairwise migration rates between modern samples of mainland populations of *P. lateralis* for independent datasets of 100 loci due to computational limitations to ensure convergence on the same results. The analysis was run using a random starting seed, random starting values from the prior, the Jukes-Cantor sequence model with base frequencies 0.25, varying mutation rate estimated from the data and a uniform prior distribution for Θ (0,0.01,0.001; minimum, maximum, Delta respectively) and M (0, 2000, 200). Two replicates were run for each analysis and included one long chain and four heated chains. A static heating scheme was used with temperatures set to 1, 1.5, 3 and 10^6 ordered from cold to hot, with sampling every 100 steps and run for 10 million steps after a burnin of one million. The mutation-scaled estimates were then

converted to real estimates from the following equations $\Theta i = xNe\mu$ and $M=m/\mu$, where μ is the mutation rate per generation and x is a multiplier that depends on the ploidy and inheritance of the data (x=4 for nuclear data). Here we used the mutation rate from Johnson et al., (2018). The product of $\Theta/4$ and M estimates the absolute rate of gene flow, here, the number of heterospecific genomes entering the population per generation.

Lastly, we evaluated the role of drift and migration in the evolutionary history of *P. lateralis*. We ran *TreeMix* (Pickrell & Pritchard, 2012) on the 'single SNP' dataset to estimate the population splitting history using allele frequency data. We used *P. l. centralis* as the outgroup based on the phylogenetic results above (IQTree2) and compared different admixture events (m=0-30). We ran the analysis with 1000 bootstraps, k=1 window size (since independent SNPs) with 10 replicates per iteration. We determined the best model of migration given the data using the package OptM in R (Fitak, 2021). OptM infers delta m based on the second-order rate of change in the log likelihood between different models. We ran the plotting funcs.R script associated with the *TreeMix* package in R and used the commands *plot_tree* and *plot_resid* to examine the *TreeMix* results and visualize the fit of the model to the data. The residual plots of covariance indicates populations that are not well-modelled, with positive residuals indicating underestimation of observed covariance between population pairs and negative values implying overestimation of the model. Good fit of the model to the data should be close to zero.

Results

Genomic datasets

We generated three different datasets to investigate the evolutionary and population history of *P. lateralis* using different approaches: (1) a diplotype sequence dataset of nuclear loci for 97

individuals (1,103,673 bp); (2) ‘all SNP’ dataset - a SNP dataset incorporating all SNPs across all exons (9168 SNPs); and (3) ‘single SNP’ dataset - a single SNP per exon dataset consisting of 1934 SNPs. Depending on the comparison for downstream analyses (pairwise analysis vs. all population), subsampled SNP datasets were generated from the full dataset to include only biallelic sites for that comparison. Most samples had low missing data (0.2-4%), including the skins (0.4-7%), with only one sample having more than 7% missing data (a modern *P. l. hacketti* sample with 27%) for the exon sequences (refer to Supp. Table 1 for missing data metrics).

Population structure and diversity

The hierarchical approach we applied identified multiple levels of population differentiation within *P. lateralis*. The island populations/sub-species were the most differentiated based on the PCoA analysis of ‘all SNPs’, with *P. l. pearsoni* diverging on PC1 (10.2%) and *P. l. hacketti* and *P. l. lateralis* from Salisbury Island and Barrow Island diverging on PC3 (6.6%). With individuals from islands removed, analysis of mainland individuals indicated differentiation of *P. l. centralis* (PC2 - 7.9%) and *P. l. kimberleyensis* individuals (PC3 – 5.5%), as well as individuals from the Kalbarri population of *P. l. lateralis* (PC3; Supp. Fig. 1). When mainland *P. l. lateralis* populations were analysed alone, individuals from Calvert Range separated on PC2 (10.4%), whilst individuals from Cape Range and Wheatbelt diverged on PC3 (8.5%; Supp. Fig. 1). The tess3r results, based on the ‘single SNP’ dataset, supported K=4 for all *P. lateralis* individuals. Genetic clustering resolved three island populations as discrete clusters, along with a cluster of mainland individuals, and some evidence of admixture (Supp. Fig. 2a). *Petrogale l. hacketti* and *P. l. lateralis* from Salisbury Island formed one genetic cluster, *P. l. lateralis* from Barrow Island a second, and *P. l. pearsoni* the third genetic cluster. Analysis of only the mainland populations and sub-species

indicated *K*=8 genetic clusters with some varied levels of admixture (Supp. Fig 2b). Most discrete geographic populations formed independent genetic clusters with small amounts of admixture; however, *P. l. kimberleyensis* split into two genetic clusters, as did *P. l. centralis*. Samples from Cotton Creek, Townsend Ridges and some of the *P. l. centralis* individuals were genetically admixed with ancestry from multiple mainland populations. When *P. l. kimberleyensis* and *P. l. centralis* were analysed separately, *P. l. kimberleyensis* supported two genetic clusters (Supp. Fig. 2c) whilst *P. l. centralis* did not show support for discrete genetic clustering but more a pattern of isolation-by-distance.

Genetic divergence between populations/sub-species (Dxy) revealed very low levels of divergence between populations of *P. l. lateralis*, populations of *P. l. kimberleyensis*, as well as between these populations and the other sub-species (0.0005-0.0007; Supp. Table 2). The highest divergence was between *P. l. centralis* and *P. l. pearsoni,* and between *P. l. centralis* and *P. l. lateralis* from Calvert Range (~0.0007). The lowest diversity was between *P. l. hacketti* and *P. l. lateralis* from Salisbury Island (0.0004). Despite low genetic divergence overall, significant isolation by distance was detected on the mainland and for *P. l. centralis* when analysed independently (Supp. Fig. 3).

Within each genetic cluster individual heterozygosity based on the diplotype sequence dataset was low, ~0.0002 for island populations and sub-species up to ~0.0007 for *P. l. centralis* (Fig. 3). Townsend Ridges had the second highest heterozygosity (~0.0005), midway between *P. l. centralis* and *P. l. kimberleyensis* populations. Mainland *P. l. lateralis* populations had similar heterozygosity levels (~0.0004) to other arid zone *Petrogale* taxa e.g., sub-species of *P. xanthopus*. Genetic diversity within these populations showed similar trends to heterozygosity, with the islands generally having almost an order of magnitude

lower theta values (~0.00003) compared to mainland populations (~0.0004), though *P. l. kimberleyensis* north also had lower theta values (0.0001) (Supp. Table 2). Again, *P. l. centralis* had the highest theta value (~0.0006), with as much diversity within this sub-species as comparisons between it and other populations/sub-species. The inbreeding coefficients showed similar trends to the heterozygosity results, with the islands and the mainland *P. l. kimberleyensis* north and *P. l. lateralis* Kalbarri populations having higher values (0.1-0.6) (Supp. Table 3). The remaining mainland populations/sub-species had lower inbreeding coefficients with *P. l. centralis* and Townsend Ridges having the lowest values.

Divergence history

Phylogenetic analysis of the nuclear exon sequence data supported monophyletic lineages for only two of the sub-species, *P. l. pearsoni* and *P. l. kimberleyensis* (Fig. 2). *P. l. centralis* formed a paraphyletic clade at the base of the phylogeny. *Petrogale l. hacketti* formed a lineage which included the proximate *P. l. lateralis* from Salisbury Island which have a different karyotype, as well as an individual from the now extinct Lucky Bay (ID: 364035) site on the adjacent mainland. *Petrogale l. lateralis* formed multiple well supported lineages (bootstrap support (bs) = 100) associated with identified genetic clusters (Supp. Figs. 1, 2). These lineages represented fragmented populations of *P. l. lateralis* clustered with *P. l. pearsoni* and *P. l. hacketti*, but with low support connecting these lineages (bs = 48-99). For *P. l. lateralis* there was strong support for Wheatbelt and Kalbarri populations to group together and weaker support for the placement of these populations with respect to populations at Barrow Island, Calvert Range and Cape Range. *P. l. kimberleyensis* supported two monophyletic populations (bs = 86). Individuals from Cotton Creek formed a monophyletic lineage (bs=100) separate from the other *P. l. lateralis* populations (bs=80).

The Townsend Ridges hybrid population formed a monophyletic lineage (bs=100) at the base of the tree, between *P. l. centralis* and individuals from Cotton Creek (bs=100).

The phylogenetic network largely clustered *P. lateralis* into sub-species, but again with the individual populations of *P. l. lateralis* showing distinct clustering (e.g., populations as divergent as sub-species; Fig. 2). There is evidence of reticulation amongst populations and sub-species, represented by webs towards the base of the network. *Petrogale l. kimberleyensis* forms two separate clusters in the network. *Petrogale l. lateralis* from Salisbury Island clustered at the base of *P. l. hacketti*. Townsend Ridges was placed between *P. l. centralis* and *P. l. kimberleyensis* in the network. Unlike the phylogenetic tree, Cotton Creek clustered amongst the *P. l. lateralis* populations. There were long branches leading to island populations for *P. l. pearsoni* and *P. l. lateralis* from Barrow Island.

The divergence of populations of *P. lateralis* were estimated during the Pleistocene ~640 kya continuing to ~160 kya (Supp. Fig. 4). *Petrogale l. centralis* was the earliest sub-species to diverge (640 kya), followed by potentially admixed populations from Townsend Ridges and Cotton Creek (350-410 kya). *P. l. kimberleyensis* diverged ~320 kya and *P. l. pearsoni* diverged ~250 kya from the remaining *P. lateralis*. The proximate *P. l. hacketti* and *P. l. lateralis* from Salisbury Island diverged ~160 kya and the remaining *P. l. lateralis* populations diverged 190-260 kya. The two populations of *P. l. kimberleyensis* diverged ~260 kya. We note here that these estimates should be taken with caution due to potential overestimation below the species level (see Ho et al., 2005).

Population demographic history

Given low genetic differentiation overall, some evidence of admixture between genetic clusters, isolation by distance and recent branching in the phylogenetic analysis, we tested for spatial expansion using modern samples for all populations/sub-species, as well as a second analysis only including populations present on the mainland. Estimates of Tajima's *D* supported a signal of population expansion with significant negative values for both analyses ($p < 0.05$) (Supp. Table 2). Evaluation of Tajima's *D* for individual populations did not indicate any significant values.

Estimates of migration between genetic clusters indicated low levels of gene flow between populations/sub-species (0.11-0.34 immigrants per generation). The two independent analyses of 100 loci produced comparable results, with similar theta estimates between populations and sub-species but slightly higher for *P. l. centralis*, and some *P. l. lateralis* populations (Wheatbelt and Cape Range; Supp. Table 4). The highest levels of gene flow came from *P. l. centralis* and *P. l. lateralis* from Cape Range and the lowest were for migration into the Kalbarri population.

When evaluating the role of drift and migration in the evolutionary history of *P. lateralis* we see that genetic drift plays a major role in population divergence, most prominent for island populations/sub-species and very small remnant mainland populations (Fig. 3). Our results from *TreeMix* indicate one migration event best fits the data (Supp. Fig. 5). The migration event varied between different replicates but was more generally between *P. l. centralis* and the ancestor of the two *P. l. kimberleyensis* populations, however the direction of this migration varied but was more often from *P. l. centralis* into *P. l. kimberleyensis*. We note the best model was based on the delta m rather than the 99.8% threshold outlined by Pickrell & Pritchard, (2010) and caution at inferring too much from the migration edges, but rather

focus on the drift in the populations. The residual plot of covariance indicated a good fit of the model to the data for most pairwise comparisons, however some were slightly more positive implying an underestimation of the model to the data (Supp. Fig. 5).

Discussion

Arid environments represent heterogeneous landscapes impacted by irregular and fluctuating environmental changes that impact population dynamics in space and time. The organisms inhabiting these arid habitats show diverse and unique adaptations to persist in these often-harsh environments, yet in Australia we still lack a good understanding of the dynamics influencing species persistence. Incorporation of historical specimens into widespread genomic and geographic sampling of *Petrogale lateralis* has increased understanding of the demographic history of the species across the vast Australian arid biome. Our study exposes a highly fragmented distribution, with exceptionally low diversity and divergence between populations/sub-species caused by two disparate evolutionary processes in close succession. We see evidence of a demographic expansion of *P. lateralis* widely across the vast Australian arid biome during the intense climatic fluctuations of the Pleistocene. This was followed by more recent fragmentation of populations and sub-species, leading to small, isolated populations that diverged ~160-640 kya. Effects of this fragmentation were seen in the significant isolation-by-distance detected between mainland populations, and negligible gene flow between the now geographically isolated regions on the mainland. The lack of recent gene flow for such a widespread species likely drives low genetic diversity within populations and drift driving population divergence (Fig. 3).

The restriction of rock-wallabies to topographically complex rocky outcrops, has likely driven the contemporary divergence pattern we find in *P. lateralis*. This fragmentation has

been further exacerbated by local extinction of populations due to more recent anthropogenic impacts, including introduced predators and herbivores, as well as altered fire regimes (Woinarski et al., 2019; Lavery et al., 2021). Although restriction to isolated rocky range systems is characteristic of this genus, the low heterozygosity estimated for *P. lateralis* is far lower than for other conspecifics with similar habitat requirements (Fig. 3). Interestingly, we see here that other arid zone *Petrogale* taxa (*P. xanthopus celeris* and *P. x. xanthopus*) also show lower levels of heterozygosity than their more mesic relatives. This could be due to more recent divergence and differing ancestral population sizes, or due to fluctuating population dynamics (e.g., recent expansions) compared to more stable populations in mesic relatives. More broadly, mammals in the arid region, have either gone extinct locally or globally (e.g., Moritz et al., 1997; Hogg et al., 2024; Eldridge et al., 2018; White et al., 2018; Nistelberger et al., 2023), or have persisted widely (e.g., Roycroft et al., 2024; Neaves et al., 2012; Clegg et al., 1998; McLean et al., 2018; Umbrello et al., 2020). Most of the major declines and extinctions have involved Critical Weight Range mammals (Woinarski et al., 2015), with arid mammals having the greatest losses (McKenzie et al., 2007). These have been linked to both environment (mean annual rainfall and environmental change) but also species' specific differences (e.g., body weight, phylogenetic similarity, habitat preference) (McKenzie et al., 2007). Differing ecologies and habitat preferences are likely key drivers in diverse mammal responses to climatic changes across the arid zone, together with susceptibility to introduced predators.

Prior understanding of *Petrogale lateralis* evolution has largely come from shallow sampling at a sub-species level (e.g., Loupis & Eldridge, 2001; Potter et al., 2012, 2017; Eldridge & Potter, 2020), or broader geographic sampling with reduced genomic data to understand fine-scale evolutionary processes within a sub-species (e.g., Eldridge et al., 2001; West et al.,

2018; Nilsson et al., 2023). Here, the inclusion of historical museum specimens to increase geographic sampling has enabled robust species-wide analysis of broad evolutionary processes shaping current patterns of diversity. Our results reveal that some populations of *P. l. lateralis* are as divergent from each other as other *P. lateralis* sub-species are from one another, although this divergence amongst lineages is exceptionally low (0.0004-0.0007), particularly for rock-wallabies. These sub-species are currently differentiated primarily by karyotype and morphology (Eldridge & Potter, 2020), although our more extensive geographic and genomic sampling, and overall low genetic differentiation raises questions about their status. Related species from the east coast, which diverged across a similar timescale (Potter et al., 2012, 2017), show higher levels of divergence ~0.0006-0.001 (Potter et al., 2022), whilst the monsoonal *brachyotis* group display higher divergence again (0.008-0.002; Potter et al., 2024). This low population differentiation likely represents more recent processes of demographic expansion during the Pleistocene, sometime before 640 kya when populations started to diverge and become isolated.

The response of Australian arid biota from Pleistocene climatic changes appears to follow one of two patterns, either deep geographic structure particularly for low vagility species (e.g. Chapple et al., 2004; reviewed in Pepper & Keogh, 2020) where species have persisted across multiple localised refugia, or low diversity and demographic expansion in highly vagile widespread species (e.g., Kuch et al., 2005, Kearns et al., 2014; Roycroft et al., 2024). Like a majority of highly vagile species in this arid landscape, *P. lateralis* shows evidence of Pleistocene expansion across the Australian arid biome. However, *P. lateralis* differs from other studies to date, in that the recent expansion detected for this species has been followed in quick succession by fragmentation and isolation of populations, as well as reorganisation and fixation of chromosome variation at scale.

Habitat fragmentation and lack of contemporary connectivity in *P. lateralis* has resulted in small population sizes, especially for island populations that exhibit exceptionally low heterozygosity and increased inbreeding coefficients. These offshore islands were connected via land bridges to the mainland up until 8-12 kya when sea levels rose (Lewis et al., 2013). It is unclear from our results whether all of the island populations were isolated well before the rise of sea levels or whether this caused their fragmentation. We do find evidence of one individual from Lucky Bay on the mainland being closely connected to *P. l. hacketti* individuals on islands (Fig. 2) indicating these islands have not been isolated for a long period of time. We see an order of magnitude lower genetic diversity for island populations compared to mainland populations, consistent with previous genetic diversity results based on neutral loci (Eldridge et al., 2001; Lennon et al., 2011). Under increased risk of genetic drift and inbreeding, previous studies have found associations of small effective population sizes with fitness (Eldridge et al., 2001; Frankham et al., 2010). Our results (inbreeding, heterozygosity) indicate these islands have much lower diversity than their mainland counterparts despite becoming isolated at a similar time scale. These island populations need careful conservation planning, including consideration of reduced fitness and evolvability, genetic load, and loss of unique diversity if genetic rescue is contemplated.

Small population sizes have been suggested to play a role in fixation of chromosomal rearrangements in *Petrogale* (Eldridge & Close, 1993). Chromosome rearrangements have been associated with adaptation and can be a driver of divergence and speciation (Rieseberg, 2001; Navarro & Barton, 2003; Kirkpatrick & Barton, 2006; Guerrero & Kirkpatrick, 2014), yet they have also shown little effect on fertility and polymorphisms can persist in populations or be fixed through genetic drift (Walsh, 1982; Lande, 1985). *Petrogale lateralis*

represents an interesting species to explore the evolution of chromosome rearrangements because multiple novel karyotypes have formed in recent history. The polymorphic and hybrid karyotypes at Townsend Ridges provide an opportunity to examine these processes in action. The association of the Townsend Ridges with *P. l. centralis* and *P. l. kimberleyensis* supports previous hypotheses that it is a hybrid population of these two sub-species (Eldridge et al., 2021) based on genetic diversity and chromosome diversity. The low genetic differentiation between chromosomally divergent *P. l. hacketti* (found on three inner Recherche Archipelago islands) and proximate *P. l. lateralis* from Salisbury Island (an outer island in the Recherche Archipelago) is another interesting result that provides information on population dynamics. The recent connectivity of these island populations is further emphasised by their close relationship with a mainland individual at Lucky Bay. Our divergence dating suggests the Salisbury Island population diverged ~100 kya from *P. l. hacketti.* Fixation of the 6-10 fusion on the three inner islands of *P. l. hacketti* indicate this chromosome rearrangement was established in the area before sea levels rose (<15 kya). Further research is required to establish if chromosome variation is associated with localised adaptations or driven by genetic drift, as this will have important consequences for considerations of mixing populations for potential genetic rescue.

Petrogale lateralis covers a huge latitudinal and ecological gradient. Aside from the population structure detected for *P. lateralis lateralis,* our results indicate additional genetic structuring within *P. l. kimberleyensis*. Our results indicate isolation-by-distance (Supp. Fig. 3), consistent with a lack of phylogeographic structure from mtDNA from across most sites and historical connectivity across the vast distribution of *P. l. centralis* (West et al., 2018). *Petrogale l. centralis* centres on the vast rocky region in the centre of Australia, including the MacDonnell Ranges. Previous genetic studies using microsatellites found limited

contemporary dispersal and connectivity between populations within *P. l. centralis* in the Anangu Pitjantjatjara Yankunytjatjara (APY) Lands (West et al., 2018). The MacDonnell Ranges is a large ancient interconnected (~650 km long) mountain range composed of a variety of rock types, and has been identified as an area of refugia for arid zone specialists (Byrne et al., 2008; Pepper & Keogh, 2020). *Petrogale l. centralis* is the most divergent lineage in *P. lateralis* and additional sampling might detect more fine-scale population structure. As this sub-species inhabits the most arid areas of Australia it is likely that populations of *P. l. centralis* were better connected during wetter climates potentially during glacial maxima (see Weij et al., 2024). In contrast, *P. l. kimberleyensis* inhabits sandstone formations within the Fitzroy Trough at the arid-monsoon interface (Eldridge & Pearson, 2023). Our results indicate two genetic populations exist within this sub-species located north and south of the Fitzroy River. Large rivers are known to be barriers to gene flow within this genus (Bee & Close, 1993) and our results indicate these populations diverged ~260 kya.

The exceptionally low genetic diversity and lack of contemporary gene flow between populations of *P. lateralis*, emphasize the need for immediate and ongoing conservation management for this species. The islands harbour exceptionally low genetic diversity, illustrating potential genetic threats for isolated mainland populations if gene flow is not re-established. Mixing *P. lateralis* individuals between populations may be required to maintain genetic diversity. Successful recent mixing of *P. l. lateralis* from Kalbarri, Cape Range and Wheatbelt populations demonstrate the benefits of establishing gene flow between populations (i.e., higher genetic diversity), and showcases the need to think broadly about mixing in *P. lateralis* (Nilsson et al., 2023). Theory suggests that chromosome rearrangements could be associated with local adaptation and result in outbreeding depression (see Frankham et al., 2011). The presence of polymorphic chromosomal populations (i.e.,

Townsend Ridges) implies that change in structural variation may be frequent in this species and perhaps not such a significant factor in consideration of mixing. In addition, we know from experimental crosses that viable and fertile offspring are produced from crossing *P. l. pearsoni* with *P. l. centralis* (Close & Bell, 1997). However, given the large ecological and latitudinal gradient *P. lateralis* inhabits, we need to identify if local adaptation is present between populations/sub-species and if it is linked to chromosomal rearrangements. Small, isolated and inbred populations should be considered candidates for genetic rescue (Frankham, 2015). Where concerns exist about potential outbreeding depression or genetic swamping, mixing could be done experimentally and monitored. Lastly, chromosome information should be obtained for new populations (e.g., Cotton Creek; and Little Sandy Desert, Turpin et al., 2018) to inform their management.

This study builds on recent research showcasing how museum skins can enhance our understanding of the processes shaping species diversification and persistence in environments where the climatic and evolutionary history of organisms is less clear (e.g., Card et al., 2021; Roycroft et al., 2022; Potter et al., 2024). The inclusion of skin samples here revealed unique insight into the recent island connectivity with the mainland for *P. l. hacketti*, as well as sampling that enabled identification of two divergent populations for *P. l. kimberleyensis*. *Petrogale* always been a fascinating genus in which to explore chromosomal variation and its links to diversification. However, our results indicate that the simple chromosomal rearrangements within *P. lateralis* appear unlikely to cause outbreeding depression in this species and maximising genetic diversity is the most important priority for island and small remnant mainland populations. Our study highlights the need to look at the evolutionary history of species at genomic scale to understand the drivers of contemporary patterns to best inform conservation management. Further research is required to understand

similarities or idiosyncrasies in response to past climatic changes across arid Australia and how best to manage species and regions within the arid biome for conservation.

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Conflict of interest

The authors declare no conflicts of interest.

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Figures

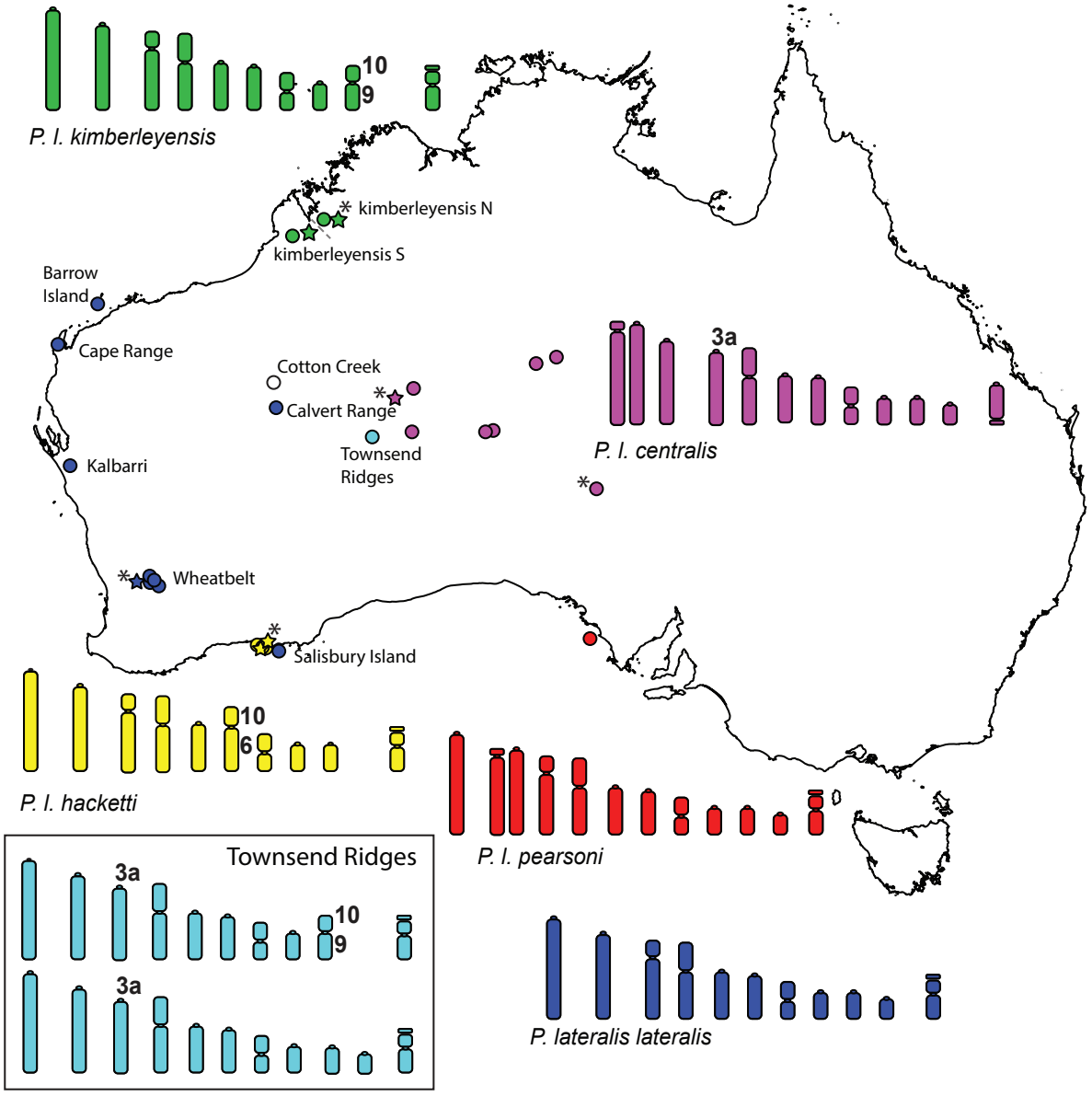


Figure 1 Sampling and karyotypes of *Petrogale lateralis* populations and sub-species across the arid biome of Australia and offshore islands. *Petrogale lateralis centralis* (purple), *P. l. hacketti* (yellow), *P. l. kimberleyensis* (green), *P. l. lateralis* (blue), and *P. l. pearsoni* (red). Sample locations are shown for modern (circle symbol), historical (star symbol), and extinct (asterisks) samples and coloured according to sub-species. Townsend Ridges are included in pale blue as this is a hybrid population of unknown sub-species and Cotton Creek is coloured

white also due to unknown sub-species allocation. There are various chromosomal rearrangements between sub-species. Here we highlight Robertsonian fusions by chromosome numbers in reference to the ancestral karyotype, (a) denotes acrocentric chromosome, and polymorphic karyotypes are shown for chromosome 1 for *P. l. centralis* and chromosome 2 for *P. l. pearsoni*. A single fusion is found in *P. l. kimberleyensis* and *P. l. hacketti*, a centric shift on chromosome 3 for *P. l. centralis* as well as a rearranged X chromosome, and Townsend Ridges has a polymorphic Robertsonian fusion and centric shift on chromosome 3.

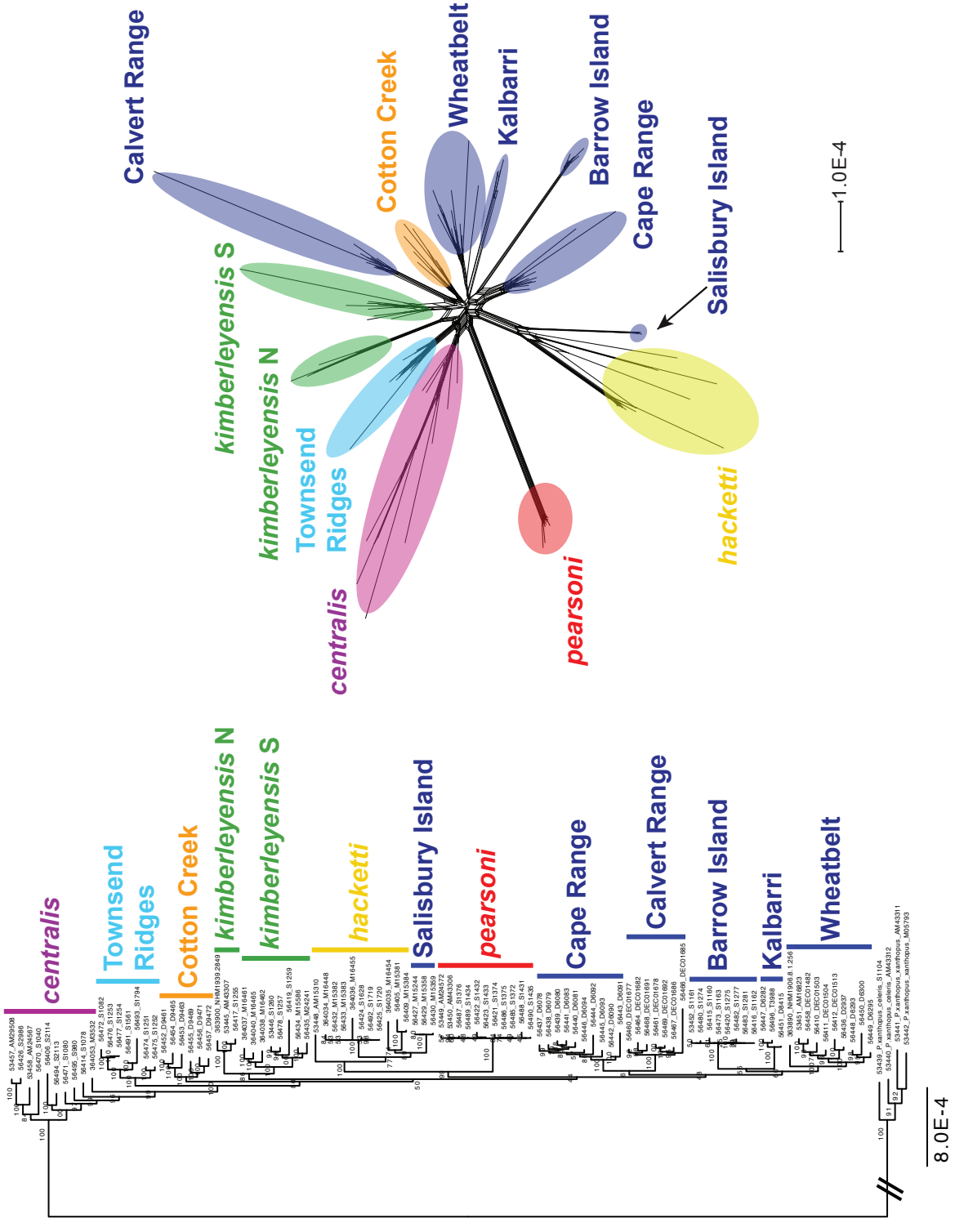
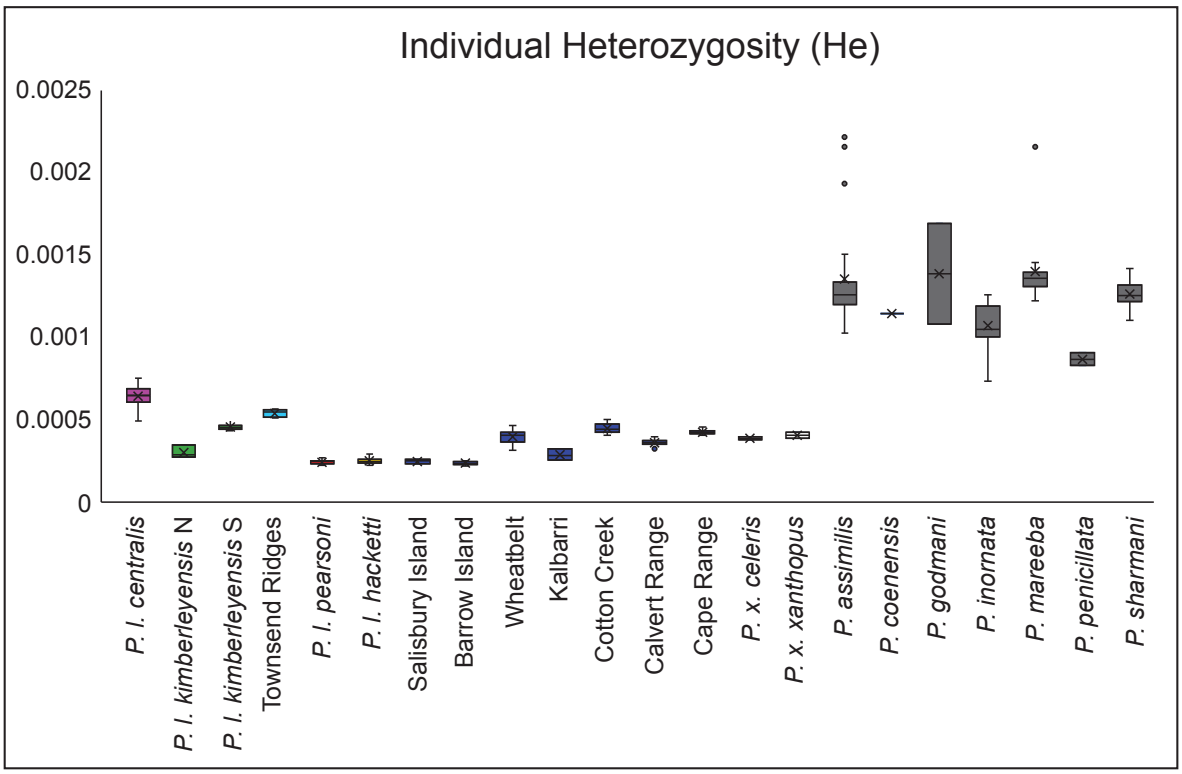


Figure 2 On left, a phylogeny of *Petrogale lateralis* populations and sub-species based on the concatenated nuclear alignment with bootstrap support values on nodes. *Petrogale xanthopus* sub-species are used to root the tree. On right, a phylogenetic network of the same dataset showing the star like shape of the populations/sub-species.

a)


Individual Heterozygosity (He)
0.0025
0.002
0.0015
0.001
0.0005
0
P. l. centralis
P. l. kimberleyensis N
P. l. kimberleyensis S
Townsend Ridges
P. l. pearsoni
P. l. hacketti
Salisbury Island
Barrow Island
Wheatbelt
Kalbarri
Cotton Creek
Calvert Range
Cape Range
P. x. celeris
P. x. xanthopus
P. assimilis
P. coenensis
P. godmani
P. inornata
P. mareeba
P. penicillata
P. sharmani

b)

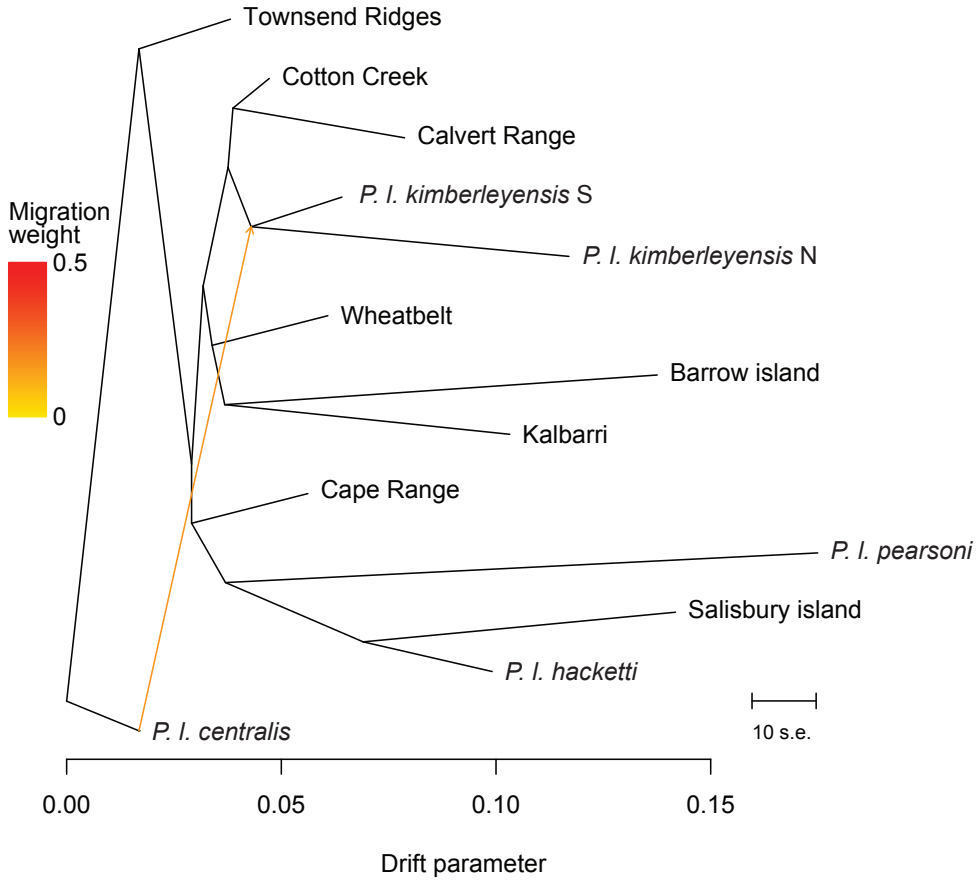

Townsend Ridges
Cotton Creek
Calvert Range
P. l. kimberleyensis S
P. l. kimberleyensis N
Wheatbelt
Barrow island
Kalbarri
Cape Range
P. l. pearsoni
Salisbury island
P. l. hacketti
P. l. centralis
Migration weight
0.5
0
10 s.e.
0.00
0.05
0.10
0.15
Drift parameter

Figure 3 a) Graph of range and average individual heterozygosity values for populations/sub-species of *Petrogale lateralis* based on nuclear exon dataset, as well as estimates from *Petrogale xanthopus* (arid species), and mesic *Petrogale assimilis*, *P. coenensis*, *P. godmani*, *P. inornata*, P. *mareeba*, *P. penicillata* and P. *sharmani*. b) Population splitting results from *TreeMix* highlighting the role of drift in divergence, as well as potential migration between *P. l. centralis* and *P. l. kimberleyensis*.

Supplementary Information

Table S1 Sample information

sequence ID	facility_sample_id	tissue_number	voucher_number	species	pop	longitude	latitude	state_or_region	subspecies	location_text	Sample type	% Missing	SRA number	Sample age	DNA_extraction_method	DNA_extraction_location	experimental_design	hyb_pool_size	sequencing_details	seq_pool_size	Individual He
363890_Pll_NHM1906_StockPool_WA_1906	363890_BHV5KMDRXX_CTATGGC	BMNH 1906.8.1.256	BMNH 1906.8.1.256	lateralis	wheatbelt	117.036726	-31.929225	Western Australia	lateralis	East Beverley	Historical skin	1.329	TBA	1906	Dabney modified	NHM, London aDNA lab	Nimblegen Exon Capture - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	192	0.000466265
363900_Plk_NHM1939_MtWynne_WA_1901	363900_BHV5KMDRXX_AAGCTAA	BMNH 1939.2849	BMNH 1939.2849	lateralis	kimberleyensis_north	124.509951	-17.848084	Western Australia	kimberleyensis	Mt Wynne	Historical skin	0.369	TBA	1939	Dabney modified	NHM, London aDNA lab	Nimblegen Exon Capture - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	192	0.000342713
364034_Plh_M16448_MondrainIs	364034_AHY7JTDRXX_GCCTACG	WAM M16448	WAM M16448	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Is	Historical skin	7.071	TBA	1906	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000257425
364035_Plh_M16454_MondrainIs	364035_AHY7JTDRXX_TAATCAT	WAM M16454	WAM M16454	lateralis	hacketti	122.235689	-33.991632	Western Australia	unknown	Lucky Bay	Historical skin	1.686	TBA	1906	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000287068
364036_Plh_M16455_MondrainIs	364036_AHY7JTDRXX_AACCTGC	WAM M16455	WAM M16455	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Is	Historical skin	0.355	TBA	1906	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000289468
364037_Plk_M16461_MtAlexander_WA	364037_AHY7JTDRXX_GACGATT	WAM M16461	WAM M16461	lateralis	kimberleyensis_south	123.690948	-18.304988	Western Australia	kimberleyensis	Mt Alexander	Historical skin	1.426	TBA	1911	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000453517
364038_Plk_M16462_MtAlexander_WA	364038_AHY7JTDRXX_TAGGCCG	WAM M16462	WAM M16462	lateralis	kimberleyensis_south	123.690948	-18.304988	Western Australia	kimberleyensis	Mt Alexander	Historical skin	1.511	TBA	1911	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000450297
364040_Plk_M16465_MtAlexander_WA	364040_AHY7JTDRXX_TTCAACC	WAM M16465	WAM M16465	lateralis	kimberleyensis_south	123.690948	-18.304988	Western Australia	kimberleyensis	Mt Alexander	Historical skin	1.57	TBA	1911	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.000492578
364053_Plc_M3532_LightningRocks_WA	364053_AHY7JTDRXX_GCCGCCT	WAM M3532	WAM M3532	lateralis	centralis	127.878653	-25.108817	Western Australia	centralis	Lightning Rocks	Historical skin	1.538	TBA	1959	Qiagen DNeasy modified	ANU Trace lab	Nimblegen Exon Capture, methods for trace samples - dual index - marsupial V2	64	Illumina NovaSeq SP 200 cycle - 100 bp	224	0.00061971
53445_Plk_AM43307_Erskine_WA_1995	53445_AHGVYVBCX2_AACTCCG	EBU47376	no voucher	lateralis	kimberleyensis_north	124.33	-17.81	Western Australia	kimberleyensis	Erskine Range, West Kimberley	Modern tissue	1.346	TBA	1995	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000281495
53446_Plk_S1260_Logues_WA_1995	53446_AHGVYVBCX2_TTGAAGT	S1260	no voucher	lateralis	kimberleyensis_south	123.08	-18.42	Western Australia	kimberleyensis	Logues Springs, West Kimberley	Modern tissue	0.802	TBA	1995	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.00045103
53448_Plh_AM15310_WestallIs_Recherche_1977	53448_AHGVYVBCX2_TTGGATC	S217	AM M.15310	lateralis	hacketti	122.97	-34.08	South Australia	hacketti	Westall Island, Recherche Archipelago	Modern tissue	2.343	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000223599
53449_Plp_AM24572_SPearsonIs_1991	53449_AHGVYVBCX2_CGACCTG	S997	AM M.24572	lateralis	pearsoni	134.27	-33.95	South Australia	pearsoni	South Pearson Island	Modern tissue	1.343	TBA	1991	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000222048
53450_Plp_AM43306_SPearsonIs_1997	53450_AHGVYVBCX2_TAATGCG	EBU47375	AM M.43306.001	lateralis	pearsoni	134.27	-33.95	South Australia	pearsoni	South Pearson Island	Modern tissue	1.165	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000244568
53451_Pll_AM16823_Nangeen_WA_1989	53451_AHGVYVBCX2_AGGTACC	S970	AM M.16823	lateralis	wheatbelt	117.68	-31.83	Western Australia	lateralis	Nangeen Hill	Modern tissue	0.847	TBA	1989	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000356188
53452_Pll_S1161_BarrowIs_1993	53452_AHGVYVBCX2_TGCGTCC	S1161	no voucher	lateralis	barrow_island	115.33	-20.77	Western Australia	lateralis	Barrow Island	Modern tissue	1.222	TBA	1993	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000218982
53457_Plc_AM29508_Alice_NT_1989	53457_AHGVYVBCX2_GATCTCG	EBU47377	AM M.29508	lateralis	centralis	133.87	-23.74	Northern Territory	centralis	Heavitree Gap, Alice Springs	Modern tissue	1.295	TBA	1989	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000608537
53458_Plc_AM24567_Alice_NT_1987	53458_AHGVYVBCX2_CAATATG	S955	AM M.24567	lateralis	centralis	133.88	-23.67	Northern Territory	centralis	Telegraph Station, Alice Springs	Modern tissue	0.549	TBA	1987	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - single index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000699883
56405_Plh_M15381_WilsonIs_Recherche_1977	56405_AHV5LWDRXX_TGCATGA	S233	ANWC M15381	lateralis	hacketti	121.9962	-34.1152	South Australia	hacketti	Wilson Island, Recherche Archipelago	Modern tissue	27.639	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000237318
56406_Plc_S2114_APY_SA_2005	56406_AHV5LWDRXX_TACTTAG	S2114	no voucher	lateralis	centralis	132.21031	-26.08349	South Australia	centralis	New Well, APY Lands	Modern tissue	2.848	TBA	2005	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000681891
56409_Plh_M15384_WilsonIs_Recherche_1977	56409_AHV5LWDRXX_TAGTCTA	S234	ANWC M15384	lateralis	hacketti	121.9962	-34.1152	Western Australia	hacketti	Wilson Island	Modern tissue	0.612	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000229838
56410_Pll_DEC01503_Wheatbelt_WA_2012	56410_AHV5LWDRXX_TAATGCG	DEC01503	no voucher	lateralis	wheatbelt	117.686603	-31.835969	Western Australia	lateralis	Wheatbelt, Nangeen Hill	Modern tissue	1.215	TBA	2012	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000416223
56411_Pll_DEC01504_Wheatbelt_WA_2012	56411_AHV5LWDRXX_CGACCTG	DEC01504	no voucher	lateralis	wheatbelt	117.686603	-31.835969	Western Australia	lateralis	Wheatbelt, Nangeen Hill	Modern tissue	0.284	TBA	2012	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000426615
56412_Pll_DEC01513_Wheatbelt_WA_2012	56412_AHV5LWDRXX_GAATCTC	DEC01513	no voucher	lateralis	wheatbelt	117.634683	-31.789175	Western Australia	lateralis	Wheatbelt, Mt Caroline	Modern tissue	1.69	TBA	2012	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000399468
56414_Plc_S1078_WalterJamesRange_WA_1993	56414_AHV5LWDRXX_GTCCGGC	S1078	no voucher	lateralis	centralis	128.72286	-24.62795	Western Australia	centralis	Walter James Range	Modern tissue	1.171	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000660786
56415_Pll_S1160_BarrowIs_1993	56415_AHV5LWDRXX_CGCAGCC	S1160	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island	Modern tissue	0.713	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000246586
56416_Pll_S1162_BarrowIs_1993	56416_AHV5LWDRXX_CGAGATC	S1162	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island	Modern tissue	0.359	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000238384
56417_Plk_S1255_Erskine_WA_1995	56417_AHV5LWDRXX_AACTAGA	S1255	no voucher	lateralis	kimberleyensis_north	124.3272	-17.8053	Western Australia	kimberleyensis	Erskine Range	Modern tissue	0.926	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000269039
56419_Plk_S1259_Logues_WA_1995	56419_AHV5LWDRXX_CTATGGC	S1259	no voucher	lateralis	kimberleyensis_south	123.0917	-18.4194	Western Australia	kimberleyensis	Logues Spring	Modern tissue	5.664	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000430646
56420_Pll_S1275_BarrowIs_1995	56420_AHV5LWDRXX_CGTATAT	S1275	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island (site Y23)	Modern tissue	0.5	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000248209
56421_Plp_S1374_SPearsonIs_1997	56421_AHV5LWDRXX_TAATCAT	S1374	no voucher	lateralis	pearsoni	134.2699	-33.9635	South Australia	pearsoni	South Pearson Island	Modern tissue	1.987	TBA	1997	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00025385
56422_Plp_S1432_NPearsonIs_1997	56422_AHV5LWDRXX_TTCAACC	S1432	no voucher	lateralis	pearsoni	134.2681	-33.9468	South Australia	pearsoni	North Pearson Island	Modern tissue	1.598	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000229884
56423_Plp_S1433_NPearsonIs_1997	56423_AHV5LWDRXX_GGCATAG	S1433	no voucher	lateralis	pearsoni	134.2681	-33.9468	South Australia	pearsoni	North Pearson Island	Modern tissue	0.425	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000248646
56424_Plh_S1628_MondrainIs_1998	56424_AHV5LWDRXX_AATAAGC	S1628	no voucher	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Island (nw corner)	Modern tissue	0.544	TBA	1998	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000252427
56425_Plh_S1720_MondrainIs_1999	56425_AHV5LWDRXX_AGCCTTG	S1720	no voucher	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Island	Modern tissue	0.739	TBA	1999	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000243802
56426_Plc_S2986_MelbZoo_source_ArltungaNT_1998	56426_AHV5LWDRXX_TCAGCTT	S2986	no voucher	lateralis	centralis	134.7197	-23.4495	Northern Territory	centralis	Arltunga	Modern tissue	1.418	TBA	1998	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000752976
56427_Pll_M15244_SalisburyIs_1977	56427_AHV5LWDRXX_AACGACC	S216	ANWC M15244	lateralis	salisbury	123.551	-34.3604	Western Australia	lateralis	Salisbury Island	Modern tissue	0.261	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000229287
56429_Pll_M15358_SalisburyIs_1977	56429_AHV5LWDRXX_GCCGCCT	S237	ANWC M15358	lateralis	salisbury	123.551	-34.3604	Western Australia	lateralis	Salisbury Island	Modern tissue	0.464	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000248088
56430_Pll_M15359_SalisburyIs_1977	56430_AHV5LWDRXX_CCGGATA	S238	ANWC M15359	lateralis	salisbury	123.551	-34.3604	Western Australia	lateralis	Salisbury Island	Modern tissue	0.619	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000259493
56432_Plh_M15382_MondrainIs_1977	56432_AHV5LWDRXX_AGAATTA	S235	ANWC M15382	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Island	Modern tissue	0.563	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000245164
56433_Plh_M15383_MondrainIs_1977	56433_AHV5LWDRXX_GCAGAAG	S236	ANWC M15383	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Island	Modern tissue	1.112	TBA	1977	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000241093
56434_Plk_M15586_Logues_WA_1977	56434_AHV5LWDRXX_GCAGTCC	S302	ANWC M15586	lateralis	kimberleyensis_south	123.0917	-18.4194	Western Australia	kimberelyensis	Logues Spring	Modern tissue	0.548	TBA	1977	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000465194
56435_Plk_M24241_Logues_WA_1977	56435_AHV5LWDRXX_CGGCGTA	S303	ANWC M24241	lateralis	kimberleyensis_south	123.0917	-18.4194	Western Australia	kimberelyensis	Logues Spring	Modern tissue	2.572	TBA	1977	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000442762
56436_Pll_D2937_Wheatbelt_WA_2016	56436_AHV5LWDRXX_ACGCAAC	D2937	no voucher	lateralis	wheatbelt	117.609285	-31.788315	Western Australia	lateralis	Wheatbelt, Dicksons Rock	Modern tissue	0.302	TBA	2016	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000369429
56437_Pll_D6078_CapeRange_WA_2018	56437_AHV5LWDRXX_AATTCAA	D6078	no voucher	lateralis	cape_range	113.88211	-22.150169	Western Australia	lateralis	Cape Range National Park, Mandu Mandu Gorge	Modern tissue	0.965	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000427257
56438_Pll_D6079_CapeRange_WA_2018	56438_AHV5LWDRXX_TTCGCAA	D6079	no voucher	lateralis	cape_range	113.88211	-22.150169	Western Australia	lateralis	Cape Range National Park, Mandu Mandu Gorge	Modern tissue	0.736	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000453646
56439_Pll_D6080_CapeRange_WA_2018	56439_AHV5LWDRXX_CGAATGC	D6080	no voucher	lateralis	cape_range	113.88211	-22.150169	Western Australia	lateralis	Cape Range National Park, Mandu Mandu Gorge	Modern tissue	0.361	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000450021
56440_Pll_D6081_CapeRange_WA_2018	56440_AHV5LWDRXX_AATACCT	D6081	no voucher	lateralis	cape_range	113.88211	-22.150169	Western Australia	lateralis	Cape Range National Park, Mandu Mandu Gorge	Modern tissue	0.307	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000428673
56441_Pll_D6083_CapeRange_WA_2018	56441_AHV5LWDRXX_CAGGAGG	D6083	no voucher	lateralis	cape_range	113.88211	-22.150169	Western Australia	lateralis	Cape Range National Park, Mandu Mandu Gorge	Modern tissue	0.513	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000409495
56442_Pll_D6090_CapeRange_WA_2018	56442_AHV5LWDRXX_TGGAATA	D6090	no voucher	lateralis	cape_range	113.87171	-22.19518	Western Australia	lateralis	Cape Range National Park, Pilgonoman Gorge	Modern tissue	0.507	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000414421
56443_Pll_D6091_CapeRange_WA_2018	56443_AHV5LWDRXX_AGAACCG	D6091	no voucher	lateralis	cape_range	113.87171	-22.19518	Western Australia	lateralis	Cape Range National Park, Pilgonoman Gorge	Modern tissue	3.577	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000403844
56444_Pll_D6092_CapeRange_WA_2018	56444_AHV5LWDRXX_TCATGGT	D6092	no voucher	lateralis	cape_range	113.87171	-22.19518	Western Australia	lateralis	Cape Range National Park, Pilgonoman Gorge	Modern tissue	3.956	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00041371
56445_Pll_D6093_CapeRange_WA_2018	56445_AHV5LWDRXX_CATCCGG	D6093	no voucher	lateralis	cape_range	113.87171	-22.19518	Western Australia	lateralis	Cape Range National Park, Pilgonoman Gorge	Modern tissue	0.548	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000428382
56446_Pll_D6094_CapeRange_WA_2018	56446_AHV5LWDRXX_AATAGTA	D6094	no voucher	lateralis	cape_range	113.87171	-22.19518	Western Australia	lateralis	Cape Range National Park, Pilgonoman Gorge	Modern tissue	0.402	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000421694
56447_Pll_D6282_Kalbarri_WA_2018	56447_AHV5LWDRXX_CCGGTAC	D6282	no voucher	lateralis	kalbarri	114.456793	-27.653573	Western Australia	lateralis	Kalbarri National Park, Z Bend	Modern tissue	1.08	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000255464
56448_Pll_D6293_Wheatbelt_WA_2018	56448_AHV5LWDRXX_ACTATCA	D6293	no voucher	lateralis	wheatbelt	117.605794	-31.853926	Western Australia	lateralis	Wheatbelt, Sales Rock	Modern tissue	0.379	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000408513
56449_Pll_D6295_Wheatbelt_WA_2018	56449_AHV5LWDRXX_TTGAAGT	D6295	no voucher	lateralis	wheatbelt	117.605794	-31.853926	Western Australia	lateralis	Wheatbelt, Sales Rock	Modern tissue	0.655	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000421144
56450_Pll_D6300_Wheatbelt_WA_2018	56450_AHV5LWDRXX_AGGTACC	D6300	no voucher	lateralis	wheatbelt	117.601592	-31.83235	Western Australia	lateralis	Wheatbelt, Mt Stirling	Modern tissue	5.73	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000384679
56451_Pll_D8415_Kalbarri_WA_2018	56451_AHV5LWDRXX_AACTCCG	D8415	no voucher	lateralis	kalbarri	114.473056	-27.635	Western Australia	lateralis	Kalbarri National Park	Modern tissue	0.428	TBA	2019	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000323704
56452_Pll_D9461_GeorgiaBore_WA_2018	56452_AHV5LWDRXX_ATGGAGA	D9461	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 1	Modern tissue	0.822	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00046204
56453_Pll_D9463_GeorgiaBore_WA_2018	56453_AHV5LWDRXX_GCAAGAT	D9463	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 1	Modern tissue	0.576	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000426153
56454_Pll_D9465_GeorgiaBore_WA_2018	56454_AHV5LWDRXX_GGATCAA	D9465	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 1	Modern tissue	2.408	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000440791
56455_Pll_D9469_Kumpupintil_WA_2018	56455_AHV5LWDRXX_CCTAGGT	D9469	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 2	Modern tissue	0.473	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000500478
56456_Pll_D9471_Kumpupintil_WA_2018	56456_AHV5LWDRXX_CTCTGCA	D9471	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 2	Modern tissue	0.251	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000405608
56457_Pll_D9472_Kumpupintil_WA_2018	56457_AHV5LWDRXX_TCGCAGG	D9472	no voucher	lateralis	cotton_creek	123.18601	-22.54324	Western Australia	unknown	Cotton Creek 2	Modern tissue	0.706	TBA	2018	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000443524
56458_Pll_DEC01482_Wheatbelt_2013	56458_AHV5LWDRXX_TTGGATC	DEC01482	no voucher	lateralis	wheatbelt	117.93132	-31.99416	Western Australia	lateralis	Wheatbelt, Querekin	Modern tissue	0.482	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000311825
56460_Pll_DEC01677_CalvertRange_WA_2013	56460_AHV5LWDRXX_CAGTACT	DEC01677	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	0.452	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000352047
56461_Pll_DEC01678_CalvertRange_WA_2013	56461_AHV5LWDRXX_ATGCCGC	DEC01678	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	0.962	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000353774
56464_Pll_DEC01682_CalvertRange_WA_2013	56464_AHV5LWDRXX_CAATTAC	DEC01682	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	1.151	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000360769
56466_Pll_DEC01685_CalvertRange_WA_2013	56466_AHV5LWDRXX_TGACGTC	DEC01685	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	6.176	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000320993
56467_Pll_DEC01686_CalvertRange_WA_2013	56467_AHV5LWDRXX_CAATATG	DEC01686	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	0.329	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000372727
56468_Pll_DEC01691_CalvertRange_WA_2013	56468_AHV5LWDRXX_GATCTCG	DEC01691	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	1.552	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000359852
56469_Pll_DEC01692_CalvertRange_WA_2013	56469_AHV5LWDRXX_GCATTGG	DEC01692	no voucher	lateralis	calvert_range	122.96926	-23.9667	Western Australia	lateralis	Calvert Ranges	Modern tissue	0.695	TBA	2013	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000394144
56470_Plc_S1040_DavenportRange_SA_1992	56470_AHV5LWDRXX_ACGTATG	S1040	no voucher	lateralis	centralis	136.01577	-28.40204	South Australia	centralis	Davenport Range	Modern tissue	1.816	TBA	1992	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000493664
56471_Plc_S1080_WalterJamesRange_WA_1993	56471_AHV5LWDRXX_AGAAGAC	S1080	no voucher	lateralis	centralis	128.72286	-24.62795	Western Australia	centralis	Walter James Range	Modern tissue	0.435	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000677984
56472_Pl_S1082_Townsend_WA_1993	56472_AHV5LWDRXX_AGTCAGA	S1082	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	1.719	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000560213
56473_Pll_S1163_BarrowIs_1993	56473_AHV5LWDRXX_GTACTAT	S1163	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island	Modern tissue	0.176	TBA	1993	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000235289
56474_Pl_S1251_Townsend_WA_1995	56474_AHV5LWDRXX_AATGATG	S1251	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	0.59	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000527161
56475_Pl_S1252_Townsend_WA_1995	56475_AHV5LWDRXX_GGTCAAG	S1252	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	0.166	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00056306
56476_Pl_S1253_Townsend_WA_1995	56476_AHV5LWDRXX_GTACCGG	S1253	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	0.299	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000545694
56477_Pl_S1254_Townsend_WA_1995	56477_AHV5LWDRXX_AGCAGGT	S1254	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	0.882	TBA	1995	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000509879
56478_Plk_S1257_Logues_WA_1995	56478_AHV5LWDRXX_AACCAAG	S1257	no voucher	lateralis	kimberleyensis	123.0917	-18.4194	Western Australia	kimberelyensis	Logues Spring	Modern tissue	1.297	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000438959
56480_Pll_S1274_BarrowIs_1995	56480_AHV5LWDRXX_GCTAATC	S1274	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island (site Y23)	Modern tissue	0.97	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000231159
56482_Pll_S1277_BarrowIs_1995	56482_AHV5LWDRXX_TAGTTCC	S1277	no voucher	lateralis	barrow_island	115.3954	-20.718	Western Australia	lateralis	Barrow Island (site Y23)	Modern tissue	0.885	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00022737
56483_Pll_S1281_BarrowIs_1995	56483_AHV5LWDRXX_CCAGCGG	S1281	no voucher	lateralis	barrow_island	115.3682	-20.7525	Western Australia	lateralis	Barrow Island (site JWC)	Modern tissue	0.446	TBA	1995	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000228331
56485_Plp_S1372_SPearsonIs_1997	56485_AHV5LWDRXX_AACCTGC	S1372	no voucher	lateralis	pearsoni	134.2699	-33.9635	South Australia	pearsoni	South Pearson Island	Modern tissue	0.354	TBA	1997	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000251033
56486_Plp_S1375_SPearsonIs_1997	56486_AHV5LWDRXX_GCCTACG	S1375	no voucher	lateralis	pearsoni	134.2699	-33.9635	South Australia	pearsoni	South Pearson Island	Modern tissue	0.583	TBA	1997	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00026649
56487_Plp_S1376_SPearsonIs_1997	56487_AHV5LWDRXX_AGAGCGC	S1376	no voucher	lateralis	pearsoni	134.2699	-33.9635	South Australia	pearsoni	South Pearson Island	Modern tissue	0.465	TBA	1997	Phenol chloroform (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000229288
56488_Plp_S1431_NPearsonIs_1997	56488_AHV5LWDRXX_TTAACTC	S1431	no voucher	lateralis	pearsoni	134.2681	-33.9468	South Australia	pearsoni	North Pearson Island	Modern tissue	2.587	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00022307
56489_Plp_S1434_NPearsonIs_1997	56489_AHV5LWDRXX_TAGGCCG	S1434	no voucher	lateralis	pearsoni	134.2681	-33.9468	South Australia	pearsoni	North Pearson Island	Modern tissue	0.412	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000251295
56490_Plp_S1435_NPearsonIs_1997	56490_AHV5LWDRXX_GACGATT	S1435	no voucher	lateralis	pearsoni	134.2681	-33.9468	South Australia	pearsoni	North Pearson Island	Modern tissue	0.401	TBA	1997	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000235946
56491_Pl_S1561_Townsend_WA_1998	56491_AHV5LWDRXX_AAGGTCT	S1561	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	0.428	TBA	1998	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000545704
56492_Plh_S1719_MondrainIs_1999	56492_AHV5LWDRXX_CCAACCT	S1719	no voucher	lateralis	hacketti	122.25	-34.1333	Western Australia	hacketti	Mondrain Island	Modern tissue	0.554	TBA	1999	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.00023431
56493_Pl_S1794_Townsend_WA_2000	56493_AHV5LWDRXX_CGCGCAG	S1794	no voucher	lateralis	townsend_ridges	126.9389	-26.3417	Western Australia		Townsend Ridges	Modern tissue	5.011	TBA	2000	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000516032
56494_Plc_S2113_Alalka_SA_2005	56494_AHV5LWDRXX_ATACTGA	S2113	no voucher	lateralis	centralis	132.11517	-26.1402	South Australia	centralis	Alalka	Modern tissue	0.889	TBA	2005	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000632725
56495_Plc_S980_BellRock_WA_1990	56495_AHV5LWDRXX_GACGGCG	S980	no voucher	lateralis	centralis	128.71689	-26.20593	Western Australia	centralis	Bell Rock Range	Modern tissue	0.509	TBA	1990	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000602878
56496_Pll_T3988_Kalbarri_WA_2009	56496_AHV5LWDRXX_ACCAACT	T3988	no voucher	lateralis	kalbarri	114.456793	-27.653573	Western Australia	lateralis	Kalbarri National Park, Z Bend	Modern tissue	1.276	TBA	2009	High salt (DBCA)	DBCA	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina NovaSeq SP 200 cycle - 100 bp	288	0.000279516
53439_Petrogale_xanthopus_celeris_S1104	53439_AHGVYVBCX2_GCAAGAT	S1104	no voucher	xanthopus		145.16	-25	Queensland	celeris	Captive, Queensland Parks and Wildlife Services, C	Modern tissue			1993	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000394484
53440_Petrogale_xanthopus_celeris_AM43312	53440_AHGVYVBCX2_ATGGAGA	EBU47383	no voucher	xanthopus		145.16	-25	Queensland	celeris	Captive, Queensland Parks and Wildlife, Charlevill	Modern tissue			1993	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000378468
53441_Petrogale_xanthopus_xanthopus_AM43311	53441_AHGVYVBCX2_CTCGATG	EBU47382	no voucher	xanthopus		138.04	-32.17	South Australia	xanthopus	Middle Gorge, Quorn	Modern tissue			1980	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000424064
53442_Petrogale_xanthopus_xanthopus_M05793	53442_AHGVYVBCX2_GCTCGAA	S384	ANWC M05793	xanthopus		142.08	-31.05	New South Wales	xanthopus	Cootawundi Station	Modern tissue			1981	High salt (AustMus)	Australian Museum	Nimblegen Exon Capture - dual index - marsupial V2	96	Illumina HiSeq 2500 RAPID - 100bp PE	96	0.000387799

Table S2 Estimates of theta and Tajima's D for populations/sub-species of *Petrogale lateralis* from PopGenome, and Dxy estimates between populations/sub-species.

Population	Wattersons theta (sites)	Theta	Segregating sites	Tajima D	Tajima D significance
kimberleyensis_north	159.6667	0.000145	210	N/A	
kimberleyensis_south	397.3381	0.000360	957	0.4106	not significant
pearsoni	74.53357	0.000068	194	-1.1838	not significant
centralis	709.0259	0.000642	1747	0.6849	not significant
Townsend	366.664	0.000332	671	1.2914	not significant
hacketti	444.4275	0.000403	1242	-0.8423	not significant
Salisbury	13.33333	0.000012	16	N/A	
CapeRange	319.5914	0.000290	755	-0.0549	not significant
Kalbarri	75.33333	0.000068	88	N/A	
Wheatbelt	367.3995	0.000333	831	0.4173	not significant
Cotton Creek	375.2319	0.000340	681	1.2556	not significant
CalvertRange	341.8787	0.000310	682	0.4028	not significant
Barrow	52.94532	0.000048	123	-0.8226	not significant
all modern samples				-1.824427	significant
all modern mainland samples				-1.909045	significant
*islands lowest diversity, centralis highest					

Dxy	kimberleyensis_north	kimberleyensis_north	pearsoni	centralis	Townsend	hacketti	Salisbury	CapeRange	Kalbarri	Wheatbelt	Cotton Creek	CalvertRange
kimberleyensis_south	0.000540859											
pearsoni	0.000656027	0.000640861										
centralis	0.00066783	0.000688387	0.000723508									
Townsend	0.000565015	0.000572726	0.000620671	0.00062034								
hacketti	0.00062129	0.000608321	0.000637416	0.00073543	0.000608175							
Salisbury	0.000545961	0.00055348	0.000595339	0.0006632	0.000552401	0.00040848						
CapeRange	0.000529665	0.000512077	0.000599242	0.00064705	0.000513757	0.000559948	0.00049029					
Kalbarri	0.000544451	0.000541006	0.000593729	0.00067565	0.00051165	0.000559958	0.000505939	0.00045754				
Wheatbelt	0.000541862	0.000525154	0.000594908	0.0006605	0.000538608	0.000572771	0.000507632	0.00045518	0.00045579			
Cotton Creek	0.000530843	0.000509888	0.000564161	0.00063271	0.000499973	0.000560988	0.000509065	0.00046699	0.00046258	0.00046666		
CalvertRange	0.000585068	0.000556101	0.000641185	0.00071706	0.000583121	0.000618444	0.000558768	0.00050852	0.000514	0.00053694	0.000493415	
Barrow	0.000571143	0.000553811	0.000614425	0.00068289	0.000567124	0.000592177	0.000520489	0.00046579	0.00049393	0.00048709	0.000475619	0.000559832

1103559 valid sites in analysis

Table S3 Estimates of inbreeding coefficients where observed heterozygosity (Ho) was divided by average mainland unbiased expected heterozygosity (uHe) for all populations/sub-species of *Petrogale lateralis*.

Population/Sub-species	Ho	He	uHe	inbreeding coefficient
barrow_island	0.06494642	0.04863	0.051871	0.4874
calvert_range	0.13083003	0.111424	0.119995	-0.032596922
cape_range	0.12696261	0.109544	0.11531	-0.002072691
centralis	0.15604636	0.155634	0.163825	-0.231620837
cotton_creek	0.12854435	0.108663	0.118542	-0.014556827
hacketti	0.11063952	0.11448	0.119932	0.126759905
kalbarri	0.11181573	0.074641	0.089569	0.11747648
kimberleyensis_north	0.09978861	0.080946	0.097135	0.212402447
kimberleyensis_south	0.14230265	0.126384	0.134809	-0.123146409
pearsoni	0.07931932	0.060683	0.063573	0.37395959
salisbury_island	0.05251841	0.033488	0.040185	0.585490055
townsend_ridges	0.14366936	0.119845	0.129064	-0.133933386
wheatbelt	0.1428056	0.128249	0.134999	-0.127116022

average mainland uHe
0.126709875

Table S4 Estimates of theta and migration rates for 100 nuclear loci for populations/sub-species of mainland *P. lateralis*.

Population number	Population ID
1	kimberleyensis
2	centralis
3	wheatbelt
4	cape range
5	kalbarri
6	cotton creek
7	calvert range
8	townsend ridges

* samples combined for kimberleyensis as not enough individuals to split to two populations

dataset 100b	Population	Theta	dataset 100	Population	Theta
1	kimberleyensis	*0.00116*	1	kimberleyensis	*0.0016*
2	centralis	*0.00147*	2	centralis	*0.00175*
3	wheatbelt	*0.00142*	3	wheatbelt	*0.00177*
4	cape range	*0.00127*	4	cape range	*0.00223*
5	kalbarri	*0.00077*	5	kalbarri	*0.00103*
6	cotton creek	*0.00105*	6	cotton creek	*0.0015*
7	calvert range	*0.00105*	7	calvert range	*0.0015*
8	townsend ridges	*0.00118*	8	townsend ridges	*0.0016*

Migration	dataset100b	m*theta	/4 (4Ne)	Migration	dataset 100	m*theta	/4 (4Ne)
M2->1	*576.994*	0.66931304	0.16732826	*M2->1*	*588.292*	0.9412672	0.2353168
M3->1	*553.214*	0.64172824	0.16043206	*M3->1*	*590.574*	0.9449184	0.2362296
M4->1	*589.097*	0.68335252	0.17083813	*M4->1*	*570.884*	0.9134144	0.2283536
M5->1	*608.066*	0.70535656	0.17633914	*M5->1*	*601.04*	0.961664	0.240416
M6->1	*565.888*	0.65643008	0.16410752	*M6->1*	*582.036*	0.9312576	0.2328144
M7->1	*558.897*	0.64832052	0.16208013	*M7->1*	*608.737*	0.9739792	0.2434948
M8->1	*570.586*	0.66187976	0.16546994	*M8->1*	*578.164*	0.9250624	0.2312656
M1->2	*564.659*	0.83004873	0.207512183	*M1->2*	*547.998*	0.9589965	0.23974913
M3->2	*546.458*	0.80329326	0.200823315	*M3->2*	*552.547*	0.96695725	0.24173931
M4->2	*581.935*	0.85544445	0.213861113	*M4->2*	*531.069*	0.92937075	0.23234269
M5->2	*602.605*	0.88582935	0.221457338	*M5->2*	*582.448*	1.019284	0.254821
M6->2	*550.447*	0.80915709	0.202289273	*M6->2*	*564.12*	0.98721	0.2468025
M7->2	*564.589*	0.82994583	0.207486458	*M7->2*	*563.804*	0.986657	0.24666425
M8->2	*578.333*	0.85014951	0.212537378	*M8->2*	*559.139*	0.97849325	0.24462331
M1->3	*575.26*	0.8168692	0.2042173	*M1->3*	*551.269*	0.97574613	0.24393653
M2->3	*564.08*	0.8009936	0.2002484	*M2->3*	*554.717*	0.98184909	0.24546227
M4->3	*588.259*	0.83532778	0.208831945	*M4->3*	*557.872*	0.98743344	0.24685836
M5->3	*593.675*	0.8430185	0.210754625	*M5->3*	*568.229*	1.00576533	0.25144133
M6->3	*578.075*	0.8208665	0.205216625	*M6->3*	*552.131*	0.97727187	0.24431797
M7->3	*596.723*	0.84734666	0.211836665	*M7->3*	*580.375*	1.02726375	0.25681594
M8->3	*563.361*	0.79997262	0.199993155	*M8->3*	*563.576*	0.99752952	0.24938238
M1->4	*510.66*	0.6485382	0.16213455	*M1->4*	*608.246*	1.35638858	0.33909715
M2->4	*501.687*	0.63714249	0.159285623	*M2->4*	*575.904*	1.28426592	0.32106648
M3->4	*493.611*	0.62688597	0.156721493	*M3->4*	*600.497*	1.33910831	0.33477708
M5->4	*553.323*	0.70272021	0.175680053	*M5->4*	*598.58*	1.3348334	0.33370835
M6->4	*518.529*	0.65853183	0.164632958	*M6->4*	*585.213*	1.30502499	0.32625625
M7->4	*525.757*	0.66771139	0.166927848	*M7->4*	*598.804*	1.33533292	0.33383323
M8->4	*511.059*	0.64904493	0.162261233	*M8->4*	*586.496*	1.30788608	0.32697152
M1->5	*580.378*	0.44689106	0.111722765	*M1->5*	*596.306*	0.61419518	0.1535488
M2->5	*535.099*	0.41202623	0.103006558	*M2->5*	*606.623*	0.62482169	0.15620542
M3->5	*565.41*	0.4353657	0.108841425	*M3->5*	*599.195*	0.61717085	0.15429271
M4->5	*572.692*	0.44097284	0.11024321	*M4->5*	*590.14*	0.6078442	0.15196105
M6->5	*571.461*	0.44002497	0.110006243	*M6->5*	*612.336*	0.63070608	0.15767652
M7->5	*593.176*	0.45674552	0.11418638	*M7->5*	*615.159*	0.63361377	0.15840344
M8->5	*561.304*	0.43220408	0.10805102	*M8->5*	*601.965*	0.62002395	0.15500599
M1->6	*586.334*	0.6156507	0.153912675	*M1->6*	*589*	0.8835	0.220875
M2->6	*552.614*	0.5802447	0.145061175	*M2->6*	*574.226*	0.861339	0.21533475
M3->6	*573.488*	0.6021624	0.1505406	*M3->6*	*603.445*	0.9051675	0.22629188
M4->6	*604.15*	0.6343575	0.158589375	*M4->6*	*606.587*	0.9098805	0.22747013
M5->6	*605.807*	0.63609735	0.159024338	*M5->6*	*629.522*	0.944283	0.23607075
M7->6	*592.149*	0.62175645	0.155439113	*M7->6*	*617.516*	0.926274	0.2315685
M8->6	*565.607*	0.59388735	0.148471838	*M8->6*	*588.657*	0.8829855	0.22074638
M1->7	*547.731*	0.57511755	0.143779388	*M1->7*	*568.864*	0.853296	0.213324
M2->7	*519.444*	0.5454162	0.13635405	*M2->7*	*569.622*	0.854433	0.21360825
M3->7	*537.675*	0.56455875	0.141139688	*M3->7*	*567.189*	0.8507835	0.21269588
M4->7	*538.774*	0.5657127	0.141428175	*M4->7*	*550.701*	0.8260515	0.20651288
M5->7	*572.152*	0.6007596	0.1501899	*M5->7*	*581.196*	0.871794	0.2179485
M6->7	*544.101*	0.57130605	0.142826513	*M6->7*	*553.281*	0.8299215	0.20748038
M8->7	*542.192*	0.5693016	0.1423254	*M8->7*	*551.644*	0.827466	0.2068665
M1->8	*570.914*	0.67367852	0.16841963	*M1->8*	*611.209*	0.9779344	0.2444836
M2->8	*561.443*	0.66250274	0.165625685	*M2->8*	*583.183*	0.9330928	0.2332732
M3->8	*547.728*	0.64631904	0.16157976	*M3->8*	*591.693*	0.9467088	0.2366772
M4->8	*569.279*	0.67174922	0.167937305	*M4->8*	*560.975*	0.89756	0.22439
M5->8	*577.207*	0.68110426	0.170276065	*M5->8*	*595.166*	0.9522656	0.2380664
M6->8	*568.825*	0.6712135	0.167803375	*M6->8*	*590.685*	0.945096	0.236274
M7->8	*585.958*	0.69143044	0.17285761	*M7->8*	*597.431*	0.9558896	0.2389724

Figure S1 PCoA results from hierarchical analysis of individuals of *Petrogale lateralis* based on 'all SNP' dataset, where divergent populations/sub-species were removed to find additional sub-structure.

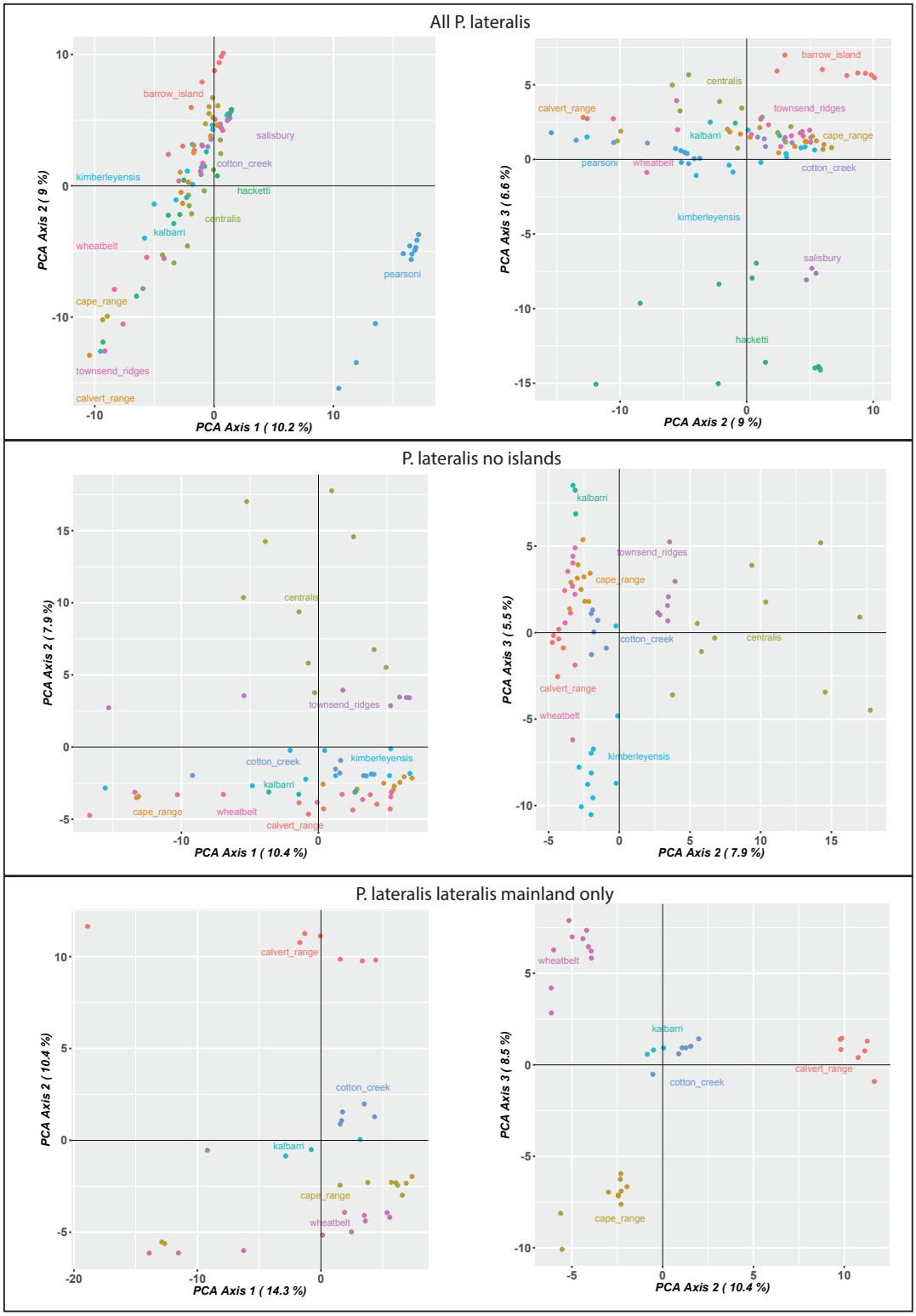
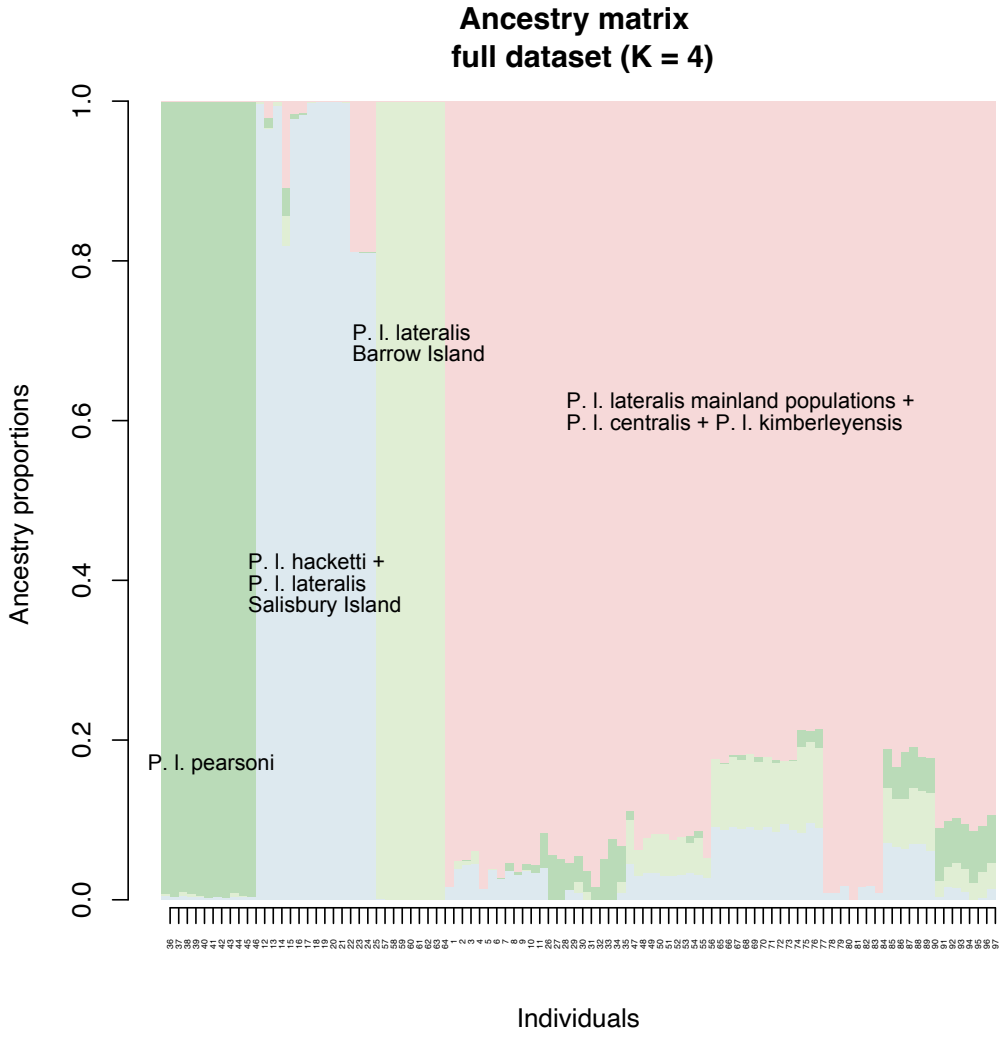
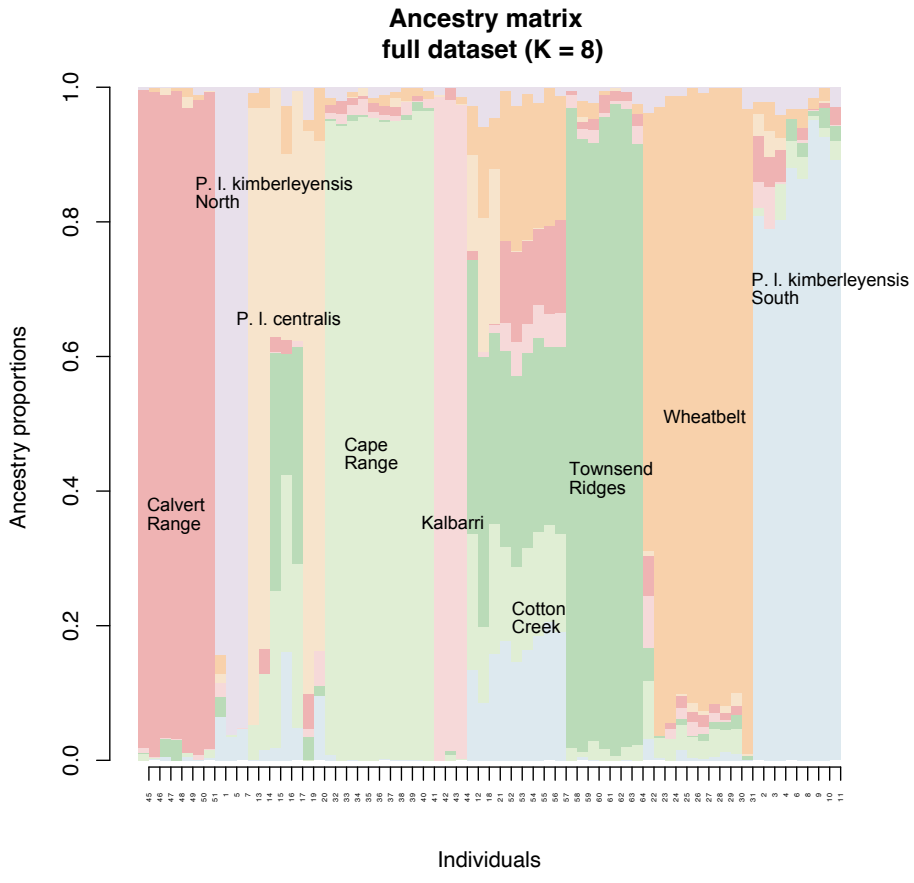


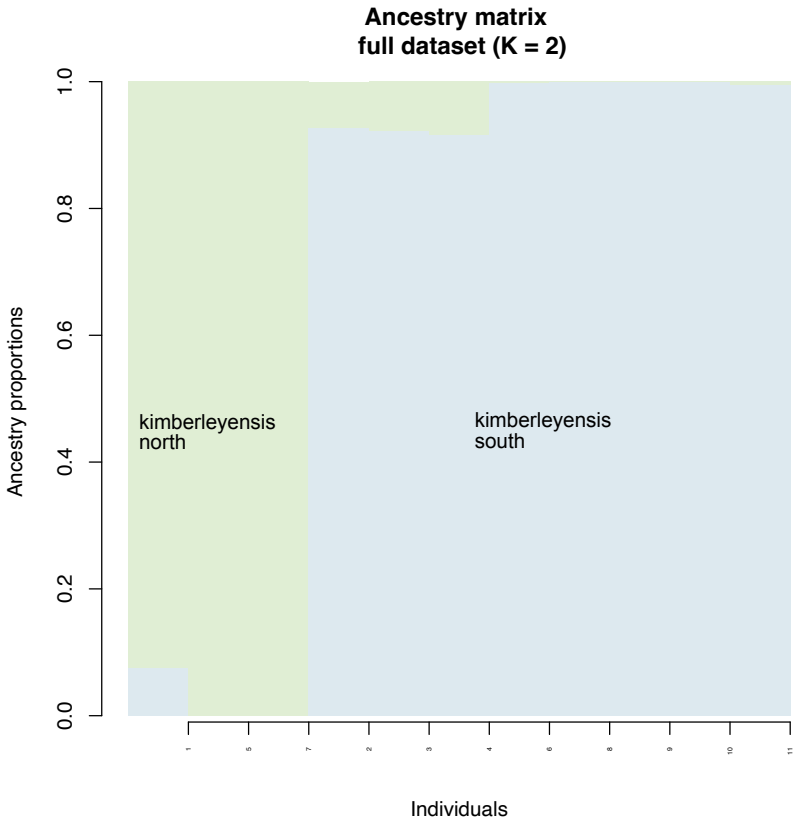
Figure S2 Tess3r results revealing genetic clustering of a) islands separate from mainland *Petrogale lateralis*, b) genetic clustering of mainland populations/sub-species, and c) genetic clustering of *P. l. kimberleyensis*.



a)


Ancestry matrix
full dataset (K = 8)
Ancestry proportions
0.0
0.2
0.4
0.6
0.8
1.0
P. l. kimberleyensis
North
P. l. centralis
Cape
Range
Calvert
Range
Kalbarri
Cotton
Creek
Townsend
Ridges
Wheatbelt
P. l. kimberleyensis
South
Individuals

b)


Ancestry matrix
full dataset (K = 2)
Ancestry proportions
0.0
0.2
0.4
0.6
0.8
1.0
kimberleyensis
north
kimberleyensis
south
Individuals

c)

Figure S3 Isolation-by-distance of (a) all modern mainland individuals, and (b) modern *P. l. centralis* individuals. Both plots indicate significant isolation-by-distance ($p < 0.05$) based on 999 permutations.

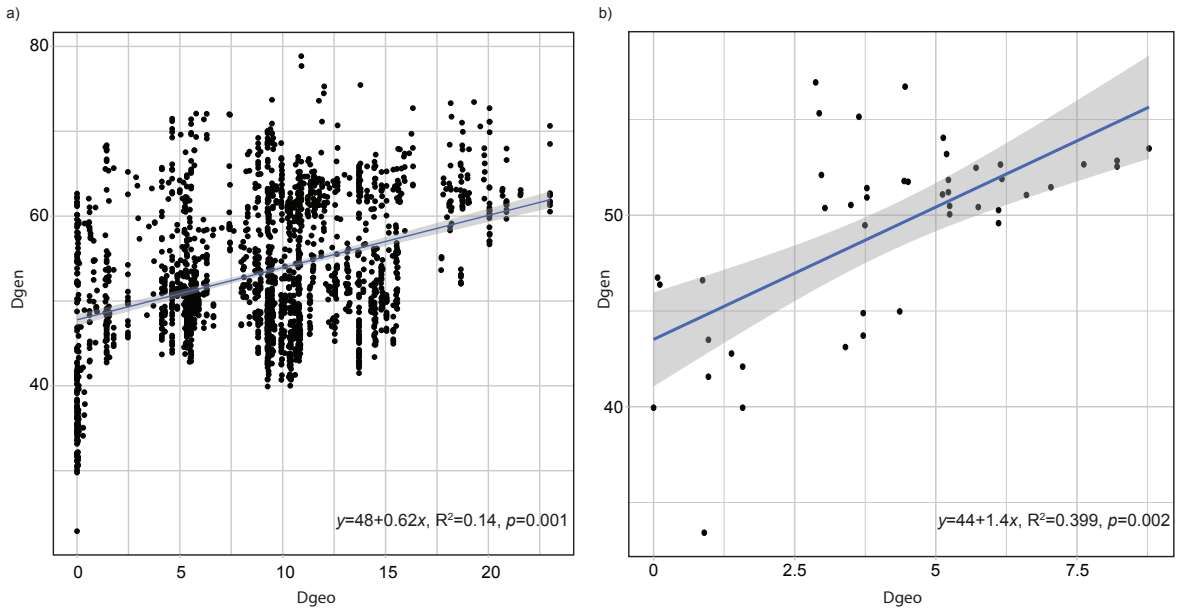


Figure S4 Phylogeny showing the divergence estimates based on MCMCTree analysis. The divergence times are highlighted at each node as well as the scale bar. The blue bars at each node represent the 95% HPD around the divergence estimates.

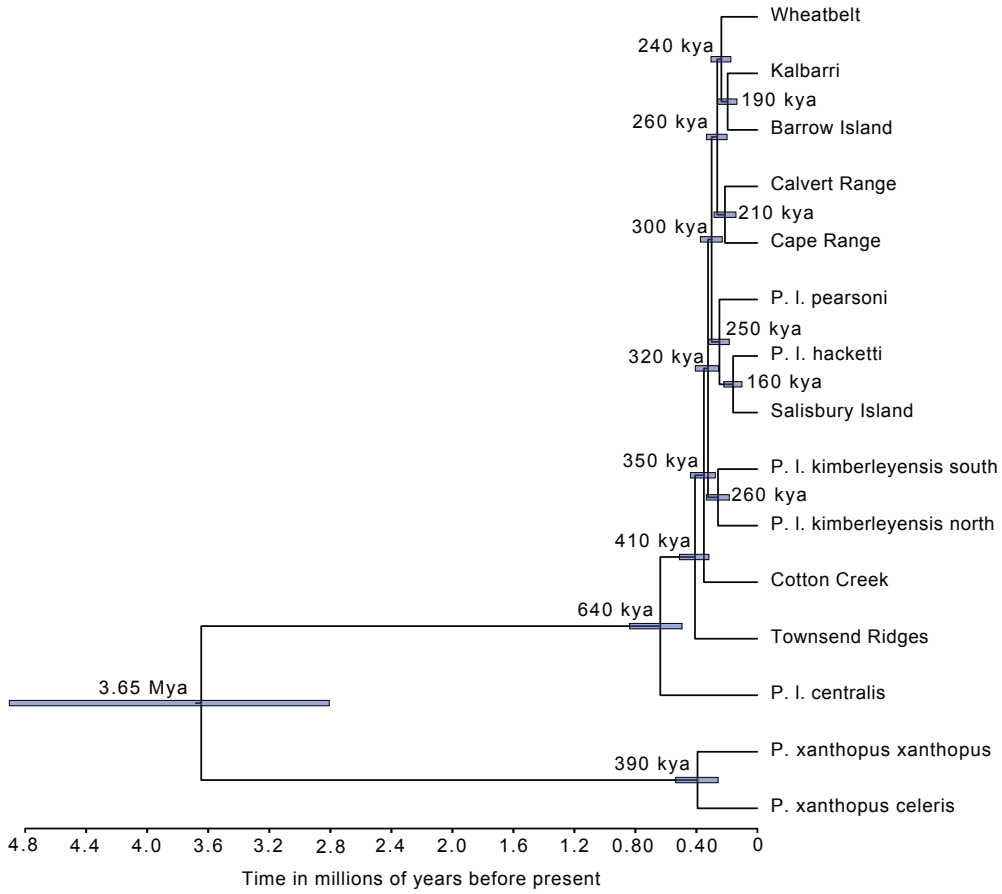


Figure S5 The OptM results showing (a) the mean log likelihood values of the varied migration edge estimates in *TreeMix* from the 10 replicate runs, (b) the delta m estimates highlighting m=1 as the best model fit for the data, and (c) the residual plot of covariance for one replicate of m=1, indicating some populations/sub-species are not well-modelled, with underestimation of observed covariance but in general most are good (close to zero).