

Supplementary Material

Persistence of social structuring in an arid zone mammal following reintroduction

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Supplementary Information

Table S1: Details of microsatellite primers and PCR multiplexes used to assess relatedness within *Bettongia lesueur*. Each PCR multiplex is amplified and electrophoresed separately during fragment analysis due to the overlap in product sizes, with the exception of 3a and 3b that are co-loaded during fragment analysis.

Multiplex	Ta (°C)	Primer	Label	Size Range (bp)	Primer source
1	57	P13	Fam	134 – 168	Luikart et al. 1997
		Bt76	Ned	200 – 240	Pope et al. 2000
		Bt64	Pet	180 - 220	Pope et al. 2000
2	54	Bt80	Fam	140 – 210	Pope et al. 2000
		T31-1	Vic	220 – 240	Zenger & Cooper 2001
3a	57	Pa593	Pet	105 – 133	Spencer et al. 1995
		T17-2	Fam	95 – 115	Zenger & Cooper 2001
3b	62	Y170	Ned	130 - 160	Pope et al. 1996
		Y105	Vic	228 – 245	Pope et al. 1996
4	54	P122	Fam	124 - 145	Luikart et al. 1997
		P126	Pet	161 - 167	Luikart et al. 1997
5	57	Pa385	Fam	140 - 150	Spencer et al. 1995
		Y112	Vic	179 - 215	Pope et al. 1996
		Y175	Ned	266 - 290	Pope et al. 1996

References

- Luikart G, Painter J, Crozier R, Westerman M, Sherwin W. 1997. Characterization of microsatellite loci in the endangered long-footed potoroo *Potorous longipes*. . *Molecular Ecology* **6**:497 - 498.
- Pope L, Estoup A, Moritz C. 2000. Phylogeography and population structure of an ecotonal marsupial, *Bettongia tropica*, determined using mtDNA and microsatellites. . *Molecular Ecology* **9**:2041–2053.
- Pope L, Sharp A, Mortiz C. 1996. Population structure of the yellow-footed rock-wallaby *Petrogale xanthopus* (Gray, 1854) inferred from mtDNA sequences and microsatellite loci. *Molecular Ecology* **5**:629–640.
- Spencer PB, Odorico DM, Jones SJ, Marsh HD, Miller DJ. 1995. Highly variable microsatellites in isolated colonies of the rock-wallaby (*Petrogale assimilis*). *Molecular Ecology* **4**:523–525.
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Table S2: Genetic differentiation detected between boodie warren using pairwise F_{ST} (below diagonal) and D_{EST} values (above diagonal). Significant difference after Bonferroni correction: ** $P < 0.0001$. D_{EST} was not calculated for warren BW503 due to low sample size ($n = 5$).

Warren	BW001	BW003	BW004	BW007	BW239	BW503	BW511
BW001	-	0.050	0.053	0.059	0.038	-	0.061
BW003	0.018	-	0.069	0.050	0.029	-	0.097
BW004	0.012	0.041**	-	0.081	0.021	-	0.006
BW007	0.020	0.020	0.024	-	0.038	-	0.089
BW239	0.016	0.025	0.013	0.005	-	-	0.016
BW503	0.051	0.113**	0.089	0.092**	0.084	-	-
BW511	0.023	0.056**	0.007	0.036	0.010	0.103	-

Table S3: AMOVA on microsatellite and mitochondrial haplotype data apportioning genetic variation within and among boodie warrens.

Source of variation	Microsatellite				mtDNA			
	d.f.	Sum of squares	Variance components	% variation	d.f.	Sum of squares	Variance components	% variation
Among	6	35.7	0.091	3.1	6	4.0	0.025	8.7
Within	233	668.3	2.868	96.9	107	28.5	0.266	91.3
Total	239	704.0	2.959		113	32.5	0.292	

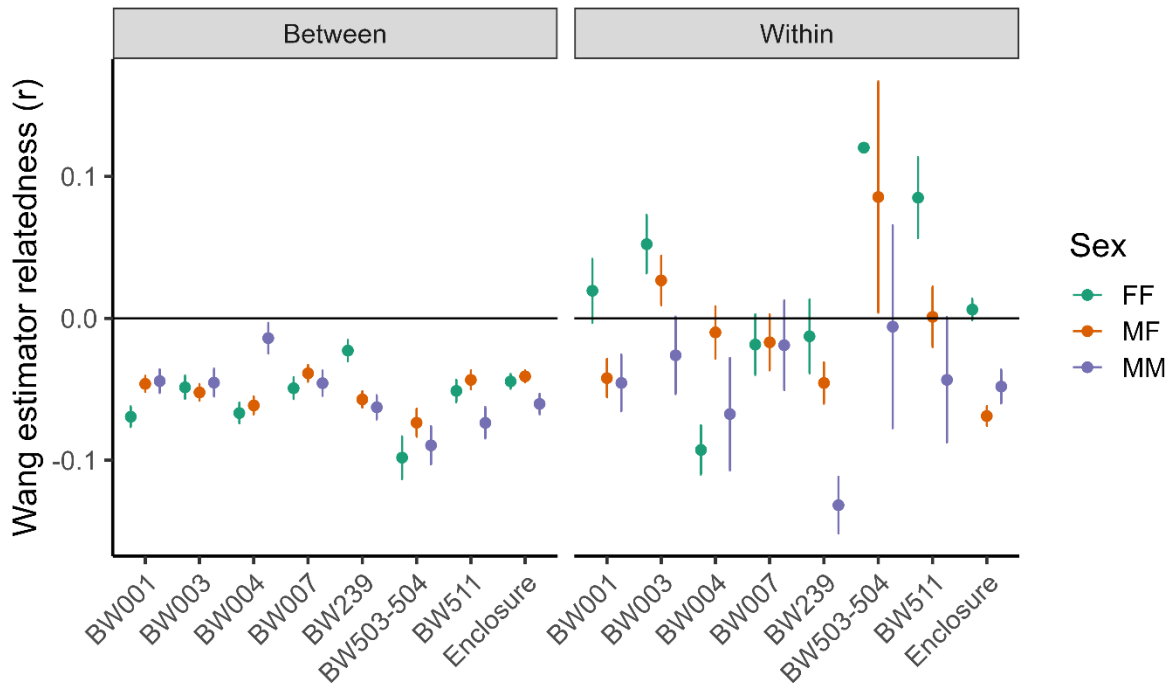
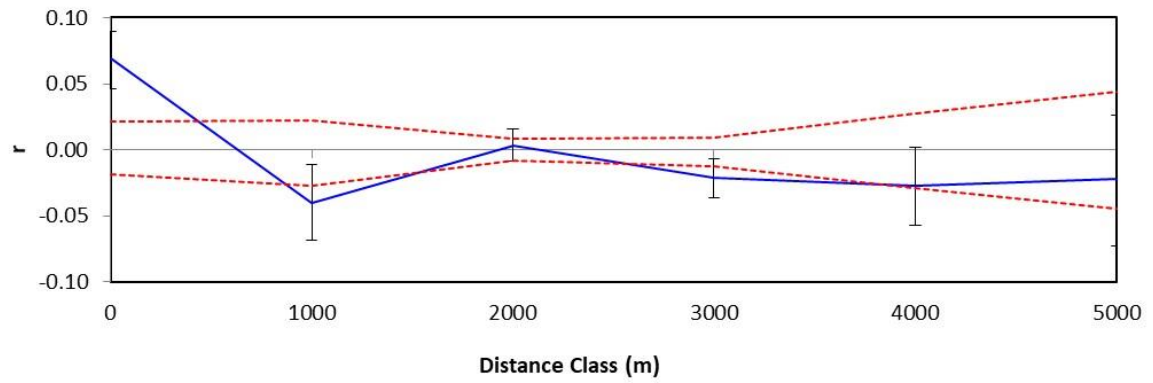


Figure S1: Wang (2002) relatedness values (mean and standard error) for pairs of boodies sampled within the same and between different warrens. Pairs of boodies may be female-female (FF), male-female (MF), or male-male (MM).

Females



Males

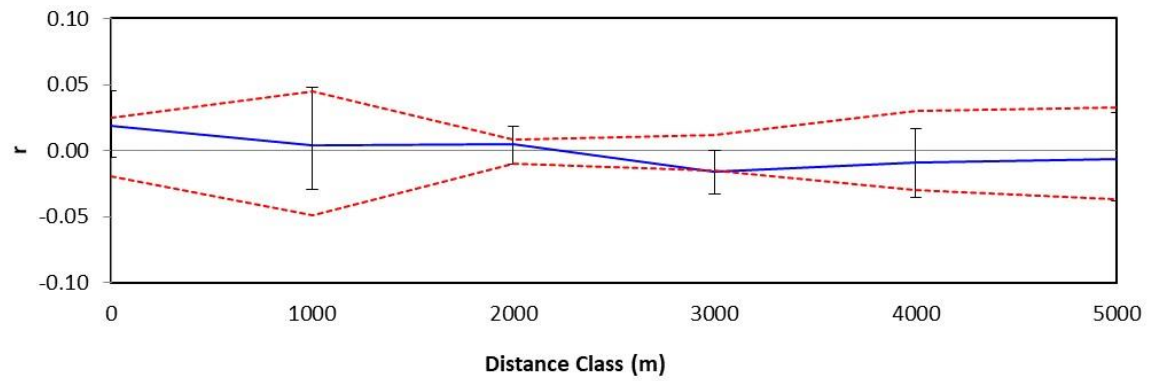


Figure S2. Spatial autocorrelation plots of boodies sampled within warrens at Matuwa. The dashed red lines are the upper and lower 95% confidence intervals about the null hypothesis of no genetic structure. Error bars are the 95% confidence intervals determined by bootstrapping.