

Supplementary Material

Small marsupial, big dispersal? Broad and fine-scale genetic structure of an endangered marsupial from the Australian arid zone

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Supp Table S1

Genotypes of 107 *S. psammophila* individuals captured from Middleback Ranges and genotyped at 16 microsatellite loci.

Sample	Site	Sp1	Sp6	Sp7	Sp8	Sp9	Sp10	Sp11	Sp12	Sp13	Sp14	Sp15	Sp16	Sp17	Sp18	Sd4	Sd25																
M06	8	114	122	115	139	130	138	128	148	139	142	155	159	124	140	183	187	164	168	160	184	189	189	195	195	200	200	214	246	198	204	104	120
M22	8	114	126	135	139	140	140	120	148	139	151	155	159	152	152	199	203	164	164	160	160	189	193	195	195	200	200	214	218	206	206	120	138
F27	8	114	128	115	115	140	140	140	140	148	151	159	159	152	152	199	247	164	176	172	184	187	197	195	199	198	208	214	220	198	206	112	112
F42	8	114	126	139	139	130	136	120	152	139	154	159	159	124	152	203	203	164	166	160	172	189	195	195	211	200	200	246	248	202	208	104	104
F01	3	114	114	115	143	116	138	128	140	151	157	155	163	124	124	167	187	168	176	160	184	189	189	195	207	200	200	248	248	206	206	120	130
F08	3	112	126	115	139	130	138	128	152	148	157	157	159	132	164	199	247	164	168	160	184	185	193	199	211	198	208	246	246	206	208	130	130
F0851	3	114	114	115	135	130	140	152	152	139	157	159	159	140	152	171	183	164	168	160	184	183	189	195	195	198	200	214	248	192	204	120	120
M05	3	112	128	115	115	128	140	144	144	151	154	159	159	124	124	171	199	164	168	184	184	189	189	211	211	200	200	214	248	190	198	112	130
M5074	3	114	126	131	139	140	140	144	152	151	157	159	159	164	164	187	203	164	164	160	160	189	189	195	215	200	200	218	246	204	206	0	0
M7DDA	3	114	126	115	115	130	140	148	152	151	154	0	0	124	152	171	247	164	166	160	160	183	185	195	203	198	200	214	246	198	208	104	112
F20	3	114	114	131	135	140	140	120	148	151	154	155	159	124	124	183	199	168	176	172	172	183	189	211	211	198	200	246	246	198	206	112	112
F53BE	3	112	112	135	143	138	140	140	140	148	151	159	167	152	164	183	187	176	180	172	184	189	193	207	207	200	208	246	246	204	206	112	112
M8445	3	114	126	115	139	128	140	140	152	142	151	163	163	152	152	247	263	164	172	160	184	193	197	211	211	200	200	214	246	206	206	104	120
F6ED8	3	114	114	115	139	138	138	144	148	142	157	159	159	124	152	183	183	164	164	160	184	183	189	207	211	198	200	246	248	198	208	104	104
F6374	3	112	114	115	139	140	144	144	152	151	151	155	167	124	140	171	187	164	176	160	164	189	189	195	203	198	198	246	246	198	208	112	112
M7159	3	114	114	139	139	128	130	144	144	154	157	155	159	124	124	167	199	164	164	160	176	183	187	207	211	198	200	246	246	198	204	112	112
M74	3	112	112	135	139	130	140	140	144	151	154	163	163	152	152	183	187	164	172	160	184	183	195	195	195	200	200	248	248	198	206	120	120
Fnn	3	114	114	115	139	130	140	128	152	148	154	157	159	152	164	183	247	164	164	160	160	183	195	195	195	198	198	214	246	204	206	104	112
FE4CE	3	114	114	139	139	130	140	148	152	151	151	155	159	152	152	167	247	164	168	176	184	187	189	195	195	194	198	214	246	204	204	104	104
F0309	5	112	114	115	139	116	118	120	152	139	151	159	159	124	124	187	247	164	168	176	184	189	197	195	199	200	200	228	228	198	204	112	112
M04	5	122	122	131	139	128	140	148	144	139	157	155	159	0	0	199	247	164	164	160	176	183	189	195	207	194	200	214	248	204	206	112	130
M14	5	114	114	115	139	130	138	120	148	151	154	155	159	140	152	167	171	164	164	172	176	189	189	195	207	200	200	214	246	198	204	104	112

F24	5	114	128	115	115	128	138	116	144	142	151	159	159	124	152	171	247	164	164	160	184	183	189	195	195	200	200	214	246	206	208	130	130
F40	5	114	128	115	115	128	138	116	144	142	151	159	159	124	152	171	247	164	164	160	184	183	189	195	195	200	200	214	246	204	208	130	130
M50	5	112	114	115	143	140	140	144	152	151	154	155	163	0	0	171	187	164	166	160	172	187	189	195	199	208	208	246	246	204	204	104	112
M5893	5	114	114	135	139	130	140	144	152	142	151	155	159	124	140	199	247	164	180	172	172	187	189	195	195	200	200	246	246	206	208	112	112
F8557	5	112	114	131	139	128	130	152	152	154	154	157	159	124	152	187	247	168	176	184	184	187	195	195	195	200	200	214	214	198	198	104	104
FE6E6	5	112	114	115	139	116	140	116	128	139	154	159	159	124	124	171	247	168	176	160	176	183	189	195	203	200	202	246	246	198	206	120	120
M9233	5	114	128	115	139	116	136	152	152	151	154	155	159	124	124	187	203	164	168	160	172	189	195	195	195	200	200	214	214	206	206	104	104
F37C3	9	114	128	139	139	130	140	128	152	142	148	155	159	124	152	187	247	164	172	160	184	187	189	195	199	200	200	214	214	204	206	104	130
F09	9	126	126	135	139	130	140	144	152	154	154	159	159	152	152	247	247	164	172	160	172	189	197	195	211	198	198	214	218	198	206	112	120
F10	9	112	114	135	139	130	130	144	144	148	154	159	159	152	152	183	187	164	164	160	172	189	189	195	195	198	200	214	246	206	206	0	0
M09	9	112	114	135	135	130	138	140	152	151	151	155	159	152	152	171	247	164	176	160	160	187	189	195	203	198	198	246	246	204	204	120	120
M11	9	112	114	139	139	130	140	128	148	142	148	159	159	152	164	167	247	164	164	160	184	189	189	207	211	198	200	214	246	204	204	112	120
F1287	9	128	128	139	139	140	140	152	152	148	151	159	159	124	124	171	183	164	164	184	184	183	189	195	195	200	200	246	246	204	204	104	122
F17	9	122	126	115	139	130	140	116	144	139	154	155	159	124	164	171	263	164	168	172	184	189	193	203	211	200	200	214	246	202	206	130	130
F21	9	114	128	135	135	130	130	144	152	151	154	155	159	124	164	187	247	168	168	172	176	187	189	195	199	198	200	214	246	206	206	104	120
F4EDD	9	114	126	115	115	140	140	140	144	151	154	159	167	124	124	171	187	164	180	172	184	189	197	195	195	200	200	246	246	202	206	104	120
F8903	9	114	128	139	139	140	140	144	152	151	151	159	163	124	152	183	247	164	168	172	184	189	195	195	195	200	200	246	246	198	206	104	104
M02	9	112	114	139	139	140	140	152	152	151	154	159	159	152	152	247	247	164	170	160	172	189	189	211	211	200	200	246	248	198	204	120	120
M6464	9	112	126	139	139	130	140	140	144	139	154	155	157	124	124	167	263	164	172	160	160	185	193	195	211	200	200	214	246	204	204	104	120
M27	9	114	114	131	139	130	140	148	152	151	157	159	159	140	140	183	263	164	180	160	184	189	193	211	211	198	208	246	246	198	204	112	112
M41	9	114	128	115	135	116	130	128	140	139	151	159	167	124	124	183	187	168	168	176	184	183	189	195	199	200	200	228	228	204	208	104	112
M6CD9	9	112	114	115	131	130	130	116	144	142	154	159	163	124	124	247	163	164	164	160	184	183	195	211	211	200	200	218	246	198	202	104	104
MCD57	9	124	128	115	139	140	140	144	152	154	157	155	159	124	132	171	183	164	168	160	176	189	189	195	203	200	200	246	246	190	208	112	112
M60	9	114	114	115	143	128	140	120	140	154	157	157	159	124	152	171	187	164	164	160	160	189	195	203	203	200	200	246	246	204	206	104	104
M6666	9	114	128	115	135	130	140	128	148	151	157	157	159	128	128	171	187	168	172	172	184	185	189	195	195	198	200	214	246	202	204	104	104
M77	9	114	126	139	143	130	140	144	152	154	154	155	155	140	152	167	263	176	176	172	172	193	195	195	199	200	208	246	246	206	206	0	0
M7902	9	114	126	135	139	130	140	116	140	139	151	157	159	124	168	171	183	166	168	160	184	185	193	195	203	198	200	218	248	198	198	112	152
M8825	9	112	114	135	139	140	140	140	144	151	151	155	159	152	164	167	171	164	172	160	184	193	197	195	211	200	200	246	246	198	208	0	0
M9011	9	112	114	115	135	140	140	140	144	154	157	159	159	140	140	187	199	168	180	160	172	189	193	195	195	200	208	246	248	202	206	120	120

F225B	7	114	114	139	143	140	140	128	152	151	151	159	159	152	152	171	183	164	180	160	172	189	193	195	195	198	200	246	248	192	192	104	130
F41	7	114	120	131	131	138	140	140	152	142	154	155	159	152	152	199	199	174	180	160	184	193	193	195	199	200	200	218	246	198	204	112	152
M1D65	7	114	128	115	115	116	130	148	152	142	148	157	159	124	152	171	247	164	170	176	176	189	193	199	207	198	208	214	246	204	204	120	120
MB3A3	7	128	128	135	139	140	140	128	148	154	154	159	163	124	124	171	171	166	168	172	172	187	189	207	207	200	208	246	246	206	208	104	120
ME7F5	7	122	126	131	139	116	140	140	152	151	151	157	163	124	128	247	263	164	164	172	184	189	195	195	211	200	200	246	246	204	208	104	120
M10	10	126	128	135	139	128	140	144	144	154	157	155	159	124	124	199	247	168	168	172	184	189	195	195	195	200	200	246	246	204	204	120	128
M70	10	114	126	115	139	130	140	128	144	142	154	155	159	0	0	167	167	164	176	160	184	189	193	207	211	200	200	246	248	204	210	104	144
FBC5F	10	114	114	135	139	130	140	140	144	151	157	159	159	124	152	171	183	164	164	160	184	189	189	207	207	200	200	248	278	204	204	104	112
FA8A7	10	126	128	115	139	130	140	128	144	148	151	157	159	132	164	183	247	164	164	176	176	183	189	195	195	198	208	248	248	204	204	104	104
M9618	11	114	128	135	139	140	140	128	140	151	157	155	159	124	152	187	199	164	176	160	184	189	197	195	211	200	208	214	246	198	202	104	112
M21	11	114	126	135	139	140	140	148	152	139	151	155	163	152	152	183	183	164	168	172	172	187	189	195	211	200	200	246	246	198	204	0	0
M26	11	114	114	139	139	140	140	120	152	139	154	159	159	124	124	171	187	164	176	160	160	189	189	199	203	200	200	218	246	198	208	120	120
M988A	11	114	120	115	115	116	140	120	152	148	154	157	159	124	140	167	167	168	172	160	172	183	189	195	211	200	200	214	246	198	202	112	130
M47	11	126	128	115	135	140	140	144	144	139	157	159	159	152	152	247	263	172	176	160	172	183	189	211	211	198	200	214	246	198	204	104	120
M44A1	11	114	114	135	139	140	140	144	152	139	151	155	159	152	152	183	187	164	164	172	176	189	193	195	199	200	208	246	246	198	198	104	104
M72	11	112	114	115	135	140	140	152	152	151	151	155	159	152	152	171	187	164	168	160	184	189	189	195	195	200	208	214	246	198	204	104	112
MD051	11	114	128	139	139	140	140	128	144	151	157	159	167	152	164	247	247	164	164	160	172	183	189	207	211	200	208	214	214	198	204	112	120
FC03A	11	112	114	115	115	128	140	128	140	139	157	159	159	124	124	167	183	168	176	172	176	189	189	195	195	200	200	0	0	204	208	104	110
M6009	11	114	126	135	135	140	140	148	152	151	154	155	159	124	152	183	187	164	170	160	184	189	195	199	211	200	208	218	218	198	206	104	112
F8632	11	112	114	135	139	116	140	116	152	151	154	157	159	124	124	183	199	164	166	172	172	183	185	195	195	200	208	214	248	198	208	104	120
M20	4	112	114	115	135	130	140	144	148	151	151	155	159	124	152	167	183	164	180	160	184	189	193	207	211	194	200	246	248	198	198	104	122
F60	4	126	128	115	135	118	140	116	144	151	157	159	163	132	152	167	199	164	168	160	172	183	195	211	211	200	200	246	246	204	204	104	104
M01	1	114	114	135	135	128	130	148	152	142	154	155	157	124	164	183	187	164	180	160	160	193	195	195	195	200	200	246	248	206	208	112	120
M12	1	112	126	139	139	130	140	120	140	154	157	157	159	152	152	199	247	180	180	160	160	189	195	195	211	198	200	246	248	190	204	120	138
F7B00	1	114	114	139	143	116	130	120	148	151	154	157	159	136	152	183	187	164	180	176	184	189	195	203	203	200	208	246	246	190	198	104	112
M6428	1	114	120	135	139	140	140	128	144	139	157	155	155	124	124	183	187	164	164	172	172	187	193	195	211	198	200	246	246	198	204	112	112
F7030	1	112	114	135	139	140	140	140	144	151	154	159	159	124	124	171	183	164	168	176	184	189	195	203	203	200	200	214	246	190	198	104	104
F7FAD	1	114	124	131	135	116	130	144	152	139	157	155	159	124	152	171	263	164	168	160	184	189	189	199	211	198	200	246	248	198	204	104	104
M26F6	1	114	126	115	135	116	128	140	144	142	142	155	159	124	164	171	183	164	180	160	172	183	189	195	207	198	200	214	246	198	208	104	112

M9AFC	1	112	126	115	139	130	140	120	144	151	157	159	159	124	124	187	247	164	168	172	172	189	189	195	195	194	198	214	246	202	206	120	120
MDFD3	1	126	128	131	139	116	140	140	140	154	154	155	157	124	124	167	247	164	180	160	172	185	189	195	211	200	200	224	246	204	208	104	120
MDT	1	114	122	135	139	140	140	128	152	139	154	159	159	152	164	175	247	164	172	172	176	189	193	195	195	198	200	0	0	204	204	104	122
FC11C	1	114	128	115	135	138	140	140	148	139	157	155	159	124	168	187	247	164	180	160	184	183	195	195	211	198	198	214	248	198	198	104	120
M8471	1	114	114	115	131	130	144	140	152	151	154	155	159	152	152	167	203	164	164	160	176	187	189	195	195	200	200	214	246	204	206	104	112
M08	2	114	114	135	139	140	140	144	152	157	157	155	159	124	124	167	171	164	164	172	172	187	189	199	203	200	200	214	246	204	206	104	104
F4AD3	2	112	126	131	143	138	140	152	152	151	151	157	159	124	164	171	263	164	180	160	172	189	195	195	211	190	200	218	246	204	204	104	120
F5C24	2	114	126	115	131	130	140	120	140	151	154	159	159	140	152	167	263	164	172	172	172	189	189	195	211	200	200	246	246	198	208	104	112
M6737	2	114	128	139	139	116	144	140	152	151	151	159	159	124	168	183	183	164	164	172	172	189	189	207	207	200	208	218	218	198	206	112	112
F70	2	112	128	115	115	130	140	120	140	157	157	159	159	124	140	171	187	164	180	172	176	189	189	195	195	194	236	246	248	202	210	120	120
M7719	2	114	126	135	139	140	140	140	140	142	154	155	159	124	152	171	171	164	176	160	172	189	197	203	207	200	200	218	246	198	208	120	120
M304B	2	114	114	135	139	140	140	140	148	151	154	157	159	124	152	183	247	164	172	160	176	189	195	195	211	198	220	224	248	206	206	112	112
MD060	2	124	128	115	135	116	130	144	152	151	157	155	155	0	0	187	247	168	180	160	172	189	189	195	199	200	208	246	246	198	208	0	0
M03	6	114	124	131	139	130	140	140	148	142	154	155	155	124	164	203	247	164	166	172	176	189	195	195	199	194	200	214	248	204	204	112	120
F05	6	114	126	115	139	138	138	144	148	148	151	155	155	124	124	183	247	164	168	160	184	189	189	211	211	198	200	246	248	204	204	104	130
F8873	6	114	114	115	139	130	140	128	148	151	151	159	163	124	140	171	183	164	164	172	184	189	189	195	203	200	200	216	246	198	204	104	120
F829B	6	114	114	135	139	138	140	120	152	148	151	155	159	124	140	167	171	164	164	172	172	189	195	207	211	198	200	214	214	198	206	104	122
F14	6	112	124	115	139	130	138	128	144	148	154	159	159	132	164	199	247	164	164	160	184	0	0	199	211	198	200	246	248	206	208	104	104
M2716	6	114	114	131	139	136	140	120	148	151	154	157	159	152	152	247	263	164	170	160	184	189	195	195	211	200	200	246	246	206	206	112	120
F5A8C	6	114	114	139	139	138	140	140	144	142	148	155	155	124	124	183	203	164	166	176	184	189	189	199	199	194	200	214	246	204	204	104	120
F22	6	126	128	139	143	138	140	120	152	148	157	159	159	124	140	183	183	164	168	176	184	189	189	195	195	200	208	246	248	198	206	120	130
M44	6	0	0	115	139	130	140	152	152	151	151	155	155	124	152	187	203	164	168	160	172	193	195	195	195	200	200	214	246	204	206	104	104
FC8BA	6	114	124	139	139	128	140	128	140	139	151	159	163	124	152	171	247	164	168	160	184	189	189	203	211	198	200	214	248	206	206	104	104
M8838	6	112	126	139	143	130	140	120	140	142	148	155	157	0	0	171	247	164	172	160	176	193	195	203	211	198	208	218	246	198	204	104	120
M3ED7	6	114	128	135	135	140	140	140	140	151	151	155	159	164	164	183	187	164	164	172	184	193	195	195	199	200	200	246	246	204	206	120	120
MC7E6	6	126	128	135	143	130	140	144	152	139	151	159	159	132	164	199	199	164	168	160	172	189	189	195	211	198	200	246	248	202	208	104	120
F63D4	6	112	114	115	135	130	140	120	148	154	157	159	163	152	152	183	187	168	180	160	184	189	189	195	199	198	200	214	246	190	206	112	120

Supp Table S2

GenBank accession number for each haplotype identified from the broad-scale genetic study of *S. psammophila*. The number of samples identified for each haplotype, the location of the samples and the sample ID which corresponds to the neighbour joining phenogram (Supplementary Fig S1) are provided. Samples were collected from three populations; Eyre Peninsula, South Australia, Yellabinna Regional Reserve, South Australia, and south-western Great Victoria Desert, Western Australia.

Haplotype no.	GenBank Accession No.	No. of samples	Location	Sample ID
h1	MK491897	17	Ironstone Hill CP and Secret Rocks, Eyre Peninsula, SA	F12
h2	MK491898	1	Pinkiwillini CP, Eyre Peninsula, SA	FPINKI
h3	MK491899	7	Yellabinna Regional Reserve, SA	MC63D
h3	MK491899	2	South-west Great Victoria Desert, WA	325
h4	MK491900	2	Yellabinna Regional Reserve, SA	02 049/ ABTC64218
h5	MK491901	1	South-west Great Victoria Desert, WA	004
h6	MK491902	2	South-west Great Victoria Desert, WA	003
h7	MK491903	1	South-west Great Victoria Desert, WA	002
h8	MK491904	1	Yellabinna Regional Reserve, SA	M1C9D
h9	MK491905	7	Hinks CP and Middleback Ranges, Eyre Peninsula, SA	M72
h10	MK491906	15	Yellabinna Regional Reserve, SA	MBE1E

Supp Table S3

Genetic diversity parameters calculated from 16 microsatellite loci across 10 sites (Site 4 was excluded due to small sample size, $n = 2$) within the Middleback Ranges region. Parameters reported include sample size (n) allelic diversity (AD), observed (H_O) and expected (H_E) heterozygosity, allelic richness (A_R) based on three diploid individuals and inbreeding coefficient (F_{IS}). Differences in mean genetic diversity parameters among sites were tested for using Kruskal-Wallis rank sum test, however no parameter means were found to differ

among sites ($P < 0.05$). Site numbers are as shown in Fig 1B, and F_{IS} did not differ significantly from zero at any site.

Site	n	AD	H_O	H_E	A_R	F_{IS}
1	13	5.250	0.763	0.725	3.320	-0.054
2	8	4.750	0.656	0.706	3.278	0.060
3	15	5.438	0.646	0.722	3.296	0.113
5	10	4.625	0.670	0.676	3.128	0.014
6	13	5.188	0.737	0.717	3.293	-0.028
7	5	4.313	0.650	0.750	3.463	0.135
8	4	3.938	0.672	0.714	3.404	0.059
9	22	5.750	0.646	0.698	3.214	0.079
10	4	3.313	0.688	0.678	3.011	-0.029
11	11	4.688	0.649	0.667	3.075	0.014

Supp Table S4

Analysis methods used to identify the correct number of genetic clusters from the STRUCTURE analysis for the three populations, Eyre Peninsula, South Australia, Yellabinna Regional Reserve, South Australia, and south-western Great Victoria Desert, Western Australia. Two scenarios were tested in STRUCTURE; allele frequencies correlated and allele frequencies independent.

Method	Allele frequencies	Value	Number of clusters (K)
Evanno	Correlated	Delta K	3
Pritchard	Correlated	Ln Pr($X K$)	3
Puechmaille	Correlated	MedMedK	3
		MedMeaK	3
		MaxMedK	3
		MaxMeaK	3
		Delta K	2
Pritchard	Independent	Ln Pr($X K$)	3
Puechmaille	Independent	MedMedK	3
		MedMeaK	3
		MaxMedK	3
		MaxMeaK	3
		Delta K	3

Supp Table S5

Population differentiation calculated from 16 polymorphic microsatellite loci across 10 *S.*

psammophila sites (Site 4 was removed due to low sample size, $n = 2$) within the Middleback Ranges region (Middleback). Mean pairwise F_{ST} is reported below the diagonal and pairwise D_{est} above the diagonal.

*** $P < 0.001$ significant pairwise comparison after Bonferroni correction.

	1	2	3	5	6	7	8	9	10	11
1		-0.029	-0.001	0.030	0.008	0.002	-0.029	-0.010	-0.022	0.009
2	-0.006		0.009	0.056	0.003	-0.057	0.010	-0.008	0.027	-0.009
3	0.001	0.015		0.014	0.002	0.017	-0.023	-0.013	-0.008	0.011
5	0.011	0.024	0.011		0.061	0.030	-0.015	0.024	0.056	0.048
6	0.004	0.004	-0.002	0.021		-0.007	-0.053	0.001	-0.029	0.046
7	0.000	-0.014	0.005	0.013	0.003		-0.010	-0.009	0.002	0.027
8	-0.005	0.007	-0.007	-0.014	-0.012	-0.002		-0.010	0.049	-0.033
9	-0.001	0.003	-0.003	0.009	0.001	-0.001	-0.008		-0.019	0.004
10	0.008	0.027	0.010	0.035	0.001	0.013	0.028	0.003		0.047
11	0.015	0.001	0.016	0.027	0.028***	0.013	-0.009	0.011	0.045	

Supp Table S6

Results of heterogeneity test between adult male and female *S. psammophila* west of the Middleback Ranges (Middleback) showing the squared paired-sample t-test statistic (T2) for each distance class and the corresponding P-value.

Distance class (Km)	T2	P-value
1	0.543	0.480
3	0.195	0.657
8	0.128	0.775
12	0.147	0.775
22	0.097	0.763

Supp Table S7

Results of the BOTTLENECK analysis for *S. psammophila* in Middleback.

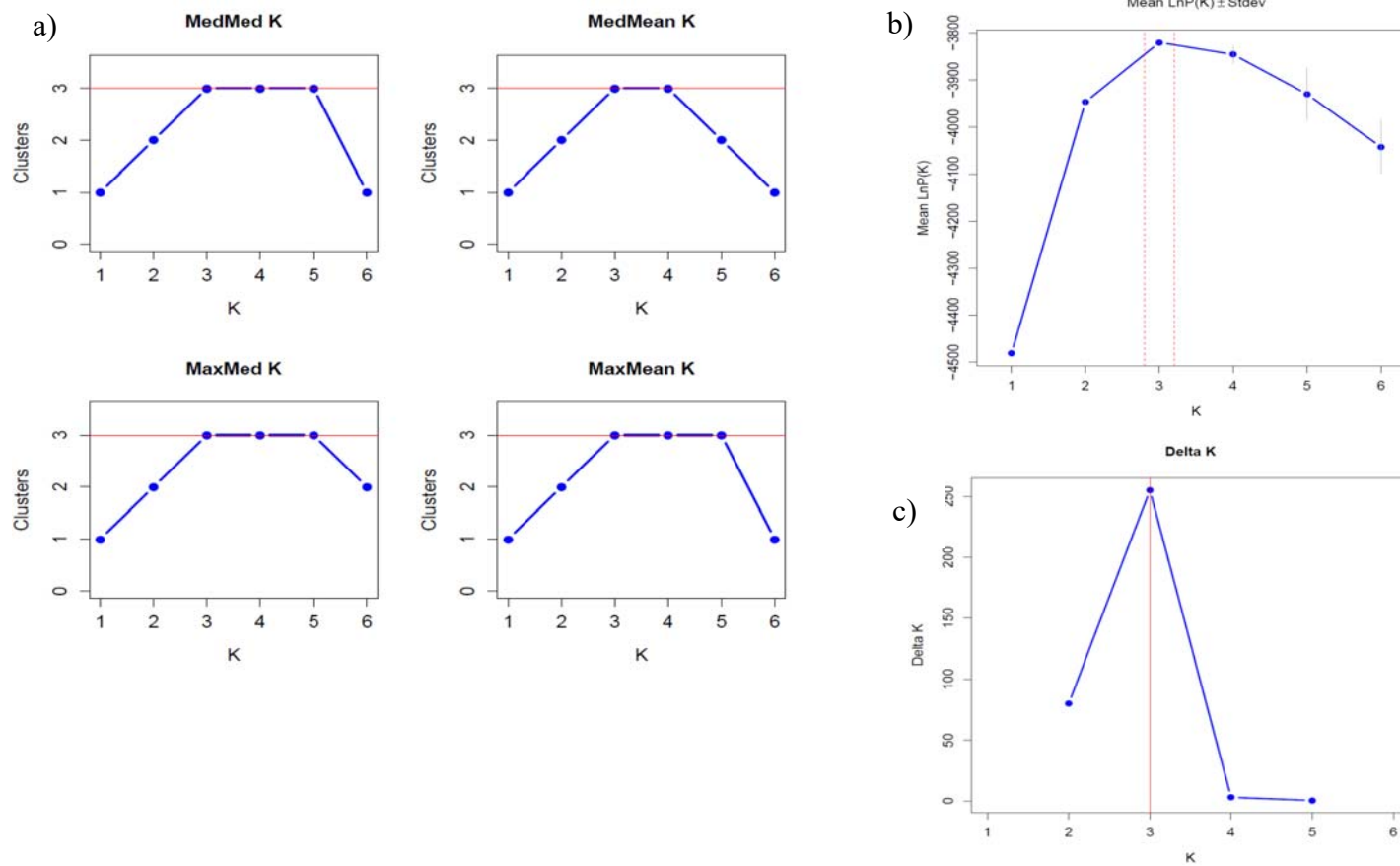
*12 % variance as per Piry *et al.* (1999)

Mutation Model	Heterozygosity excess
SMM	0.97467
TMP*	0.90359

Supp. Fig S1. Neighbour Joining phenogram of control region sequence data from *Sminthopsis psammophila*.



Supp Fig S2. Results of the STRUCTURE analysis for determining the number of genetic clusters (K) when allele frequencies were correlated for the three populations, Eyre Peninsula, South Australia, Yellabinna Regional Reserve, South Australia, and south-western Great Victoria Desert, Western Australia. a) The Puechmaille method, b) the Pritchard method, Mean LnP(K) c) the Evanno method, delta K. Graphs taken from output of STRUCTURESELECTOR (Li and Liu 2017).



Supp Fig S3

Results of the STRUCTURE analysis for determining the number of genetic clusters (K) when allele frequencies were correlated for the Middleback population. a) The Puechmaille method, b) the Pritchard method, c) the Evanno method, delta K . Graphs taken from output of STRUCTURESELECTOR (Li and Liu 2017).

