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Marine and Freshwater Research

Supplementary Material

Evidence of mitochondrial capture in Australian glass shrimp (*Paratya australiensis*) in south-eastern Queensland

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Table S1. GenBank Accession numbers for all 39 individuals from Broken Bridge High (BBH) site

Individuals ID	Genbank Accession numbers
BBH29	MK312168
BBH27	MK312169
BBH 24	MK312170
BBH 4	MK312171
BBH 25	MK312172
BBH 6	MK312173
BBH 11	MK312174
BBH 20	MK312175
BBH 21	MK312176
BBH 3	MK312177
BBH 121	MK312178
BBH 132	MK312179
BBH 131	MK312180
BBH 127	MK312181
BBH 126	MK312182
BBH 133	MK312183
BBH 106	MK312184
BBH 136	MK312185
BBH 128	MK312186
BBH 23	MK312187
BBH 17	MK312188
BBH 13	MK312189
BBH 94	MK312190
BBH 87	MK312191
BBH 105	MK312192
BBH 48	MK312193
BBH 28	MK312194
BBH 12	MK312195
BBH 114	MK312196
BBH 99	MK312197
BBH 95	MK312198
BBH 110	MK312199
BBH 108	MK312200
BBH 129	MK312201
BBH 104	MK312202
BBH 85	MK312203
BBH 81	MK312204
BBH 123	MK312205
BBH 125	MK312206

Table S2. Microsatellite loci used to identify hybridisation among sympatric lineages of *P. australiensis* (taken from Wilson *et al.* 2016)

Locus	Primer Sequence (5'-3')	Repeat motif	Annealing temperature (°C)	Size range
Ion 09	F: TTCTGCCTTGAUTGCACCTT R: GGTGAGCATCGTGTGGACTT	AG	55	220–240
Ion 44	F: AGCAGCAATGAGGCACCTAGG R: ATCCTGGGCAAAGAACATA	AC	55	130–150
454-36	F: CCCTGAAAACCATGTGTATAACCC R: ATCCTGGGCAAAGAACATA	ACTG	58	130–180

Table S3. RFLP (with Pho-I and Tse-I restriction enzyme) results from all 6 sampling sites

Sites	L4		L6	
	Frequency	(%)	Frequency	(%)
BBH	40	33	80	67
BBL	30	100	0	0
OBH	30	100	0	0
OBL	30	100	0	0
BOH	30	100	0	0
BOL	30	100	0	0

Table S4. Haplotypes identified among the samples.

Hap 1	Hap 2	Hap 3	Hap 4	Hap 5	Hap 6
BBH11	BBH12	BBH6	BBH85	BBH 28	BBH128
BBH20	BBH13	BBH131	BBH94		
BBH21	BBH17		BBH104		
BBH24	BBH23		BBH110		
BBH25	BBH48		BBH114		
BBH27	BBH81		BBH125		
BBH29	BBH87		BBH99		
BBH3	BBH105				
BBH4	BBH108				
BBH106	BBH123				
BBH121	BBH129				
BBH126	BBH95				
BBH127					
BBH132					
BBH133					
BBH136					

Table S5: Genotype frequency of Broken Bridge High site individual based on allozyme and microsatellite marker (pure lineage 4 and 6 are taken from Wilson *et al.* 2016)

Marker	Locus	Genotype	Genotype frequency
Allozyme	AAT1	22	6
		23	20
		33	9
	AAT2	44	36
		23	8
		12	12
		22	12
		13	1
		11	2
		33	1
Microsatellite	Ion 9	234,234	15
		234,226	2
		226,226	Pure L4 (226,226)
		234,234	Pure L6 (234,234)
	Ion 44	138,138	5
		138,144	2
		133,144	4
		138,133	4
		133,133	2
		138, 138	Pure L4 (138,138)
		144,144	Pure L6 (144,144)
	454_36	144,144	4
		144,154	1
		144,170	3
		159,170	3
		170,170	1
		154,170	1
		154,154	1
		144,144	Pure L4 (144,144)
		170,170	Pure L6 (170,170)

Table S6: Showing summary statistics from HWE test based on allozyme and microsatellite data

Marker	Locus	Obs. Het	Exp. Het	P-value
Allozyme	Locus 1(AAT-1)	0.55556	0.50548	0.732646
	Locus 2(MPI)	0.58333	0.55516	0.63327
Microsatellite	Locus 1 (ion 9)	0.09091	0.08879	1.00000
	Locus 2 (ion 44)	0.50000	0.67143	0.17993
	Locus 3 (454_36)	0.59091	0.67759	0.40244

Reference

Wilson, J. D., Schmidt, D. J., and Hughes, J. M. (2016). Movement of a hybrid zone between lineages of the Australian glass shrimp (*Paratya australiensis*). *Journal of Heredity* **107**(5), 413-422.