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Phylogeographic structure of a freshwater crayfish (Decapoda : Parastacidae : *Cherax preissii*) in south-western Australia

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Abstract. Although phylogeographic patterns of freshwater decapods elsewhere in Australia are well documented, little is known of the phylogeography and biogeography of the endemic freshwater fauna of south-western Australia. Here, the phylogeographic structure of a freshwater crayfish, *Cherax preissii* Erichson, 1846, was investigated to determine contemporary and historical patterns of gene flow and to examined evolutionary and biogeographical scenarios. Allozyme and cytochrome *c* oxidase subunit I mitochondrial DNA data were collected from 15 populations, sampled across the known *C. preissii* distribution. Both markers revealed a clear distinction and separation among populations occurring in the north-western and southern portions of the distribution. Inferences of allopatric fragmentation and molecular dating attributed the divergence of the aquatic fauna of these regions to periods of Pliocene–Pleistocene aridity. Connectivity appeared to be greater within each of these regions. Evidence suggested contemporary, but not ongoing, gene flow, particularly within the southern region. This was possibly facilitated by dispersal during pluvial Pleistocene periods or drainage connectivity during episodic marine regressions. The divergence and distributions of these lineages parallels patterns seen in other freshwater crayfish of the region. More explicit investigation of these and further fine-scale phylogeographic studies may contribute to the understanding of biogeography and evolution in the south-west, and may further refine currently recognised biogeographical regions.

Table 1. Allele frequencies at the six polymorphic loci for the 14 populations of *Cherax preissii* studied

Numbers directly below the population names denote the range of sample sizes at each of the 11 examined loci for each population

Locus	Allele	Populations													
		Norm	Good	Chel	Napi	Orup	Stir	Will	UHay	Litt	Styx	Dogg	Hill	Duns	Bota
		7–18	10	11–15	10–15	27–35	11–16	15–23	15	3	8–18	4–5	19–25	9–11	3
Gpi	.94	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	1.000	1.000
	.83	1.000	1.000	1.000	0.933	1.000	1.000	0.913	1.000	1.000	1.000	1.000	0.000	0.000	0.000
	.70	0.000	0.000	0.000	0.067	0.000	0.000	0.087	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LGG	1.04	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.000	0.000	0.000	0.000
	1.00	1.000	0.850	1.000	1.000	0.574	0.773	0.848	0.967	0.667	0.875	1.000	1.000	1.000	0.833
	.95	0.000	0.150	0.000	0.000	0.426	0.227	0.152	0.033	0.333	0.000	0.000	0.000	0.000	0.167
LT-1	1.12	0.167	0.000	0.000	0.000	0.286	0.219	0.000	0.000	0.667	0.100	0.000	0.000	0.000	0.000
	1.00	0.833	0.950	0.955	1.000	0.714	0.781	1.000	1.000	0.333	0.900	1.000	1.000	1.000	1.000
	.94	0.000	0.050	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LT-2	1.13	0.000	0.000	0.000	0.000	0.243	0.000	0.087	0.000	0.000	0.000	0.300	0.079	0.727	0.000
	1.00	1.000	1.000	1.000	1.000	0.757	1.000	0.913	1.000	1.000	1.000	0.700	0.921	0.273	1.000
Mdh-1	1.35	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	1.21	1.000	1.000	0.900	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Pgm	1.09	0.028	0.000	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000	0.100	0.000	0.000	0.000
	1.00	0.972	1.000	1.000	0.857	1.000	1.000	0.900	1.000	1.000	1.000	0.900	1.000	1.000	1.000
	.83	0.000	0.000	0.000	0.143	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table 2. Nei's (1978) genetic distances (*D*; below diagonal) obtained in pair-wise comparisons among populations, and Weir and Cockerham's (1984) estimates (θ; above diagonal) of population differentiation among the 14 *Cherax preissii* populations included in the allozyme analyses

Significant ($P < 0.05$) estimates of differentiation are indicated in bold font

	Populations													
	Norm	Good	Chel	Napi	Orup	Stir	Will	UHay	Litt	Styx	Dogg	Hill	Duns	Bota
Norm	–	0.032	0.051	0.078	0.169	0.039	0.070	0.072	0.361	0.000	0.167	**0.814**	**0.803**	0.715
Good	0.003	–	0.049	0.047	0.126	0.020	–0.002	0.028	0.407	–0.006	0.132	0.821	**0.788**	0.717
Chel	0.002	0.002	–	0.063	**0.226**	0.140	0.068	0.045	0.537	0.056	0.186	**0.845**	**0.817**	0.783
Napi	0.004	0.003	0.002	–	**0.227**	0.133	0.021	0.055	0.483	0.076	0.118	**0.809**	**0.781**	0.694
Orup	0.023	0.017	0.029	0.032	–	0.054	**0.138**	**0.227**	0.043	0.155	0.131	**0.599**	**0.574**	**0.463**
Stir	0.003	0.002	0.008	0.010	0.008	–	0.062	0.156	0.127	0.036	0.165	**0.749**	**0.734**	0.590
Will	0.005	0.000	0.004	0.002	0.018	0.005	–	0.044	0.341	0.048	0.035	**0.671**	**0.666**	0.541
UHay	0.002	0.000	0.001	0.002	0.026	0.006	0.002	–	0.701	0.051	0.281	**0.898**	**0.874**	**0.905**
Litt	0.026	0.034	0.043	0.048	0.012	0.011	0.041	0.042	–	0.378	0.364	0.856	0.778	0.635
Styx	0.001	0.001	0.002	0.003	0.021	0.003	0.003	0.001	0.030	–	0.158	0.817	0.796	0.699
Dogg	0.008	0.008	0.007	0.007	0.023	0.015	0.004	0.006	0.054	0.008	–	**0.807**	0.689	0.640
Hill	0.100	0.100	0.098	0.093	0.131	0.109	0.093	0.097	0.152	0.100	0.101	–	0.618	0.050
Duns	0.157	0.156	0.155	0.149	0.156	0.167	0.138	0.152	0.215	0.157	0.116	0.039	–	0.539
Bota	0.101	0.095	0.099	0.094	0.121	0.101	0.090	0.096	0.140	0.098	0.107	0.000	0.050	–

Table 3. Mitochondrial DNA differentiation among the 15 individual populations of *Cherax preissii* examined

Values of Φ_{ST} are presented below the diagonal, with values determined to be significant ($P < 0.05$) indicated in bold typeface. *P*-values from exact tests of differentiation are presented above the diagonal, with non-significant differentiation indicated by n.s.

	Populations														
	Norm	Good	Chel	Napi	Orup	Stir	Will	UHay	Litt	Styx	Dogg	Hill	Duns	Bota	Karr
Norm	–	0.048	0.015	0.008	0.008	0.008	n.s.	0.009	0.029	0.008	n.s.	0.041	0.007	n.s.	n.s.
Good	**0.520**	–	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	0.023	0.007	0.002	0.017	n.s.
Chel	**0.635**	0.003	–	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	0.009	0.004	0.001	0.013	n.s.
Napi	**0.706**	**0.000**	−0.034	–	n.s.	n.s.	n.s.	n.s.	n.s.	n.s.	0.008	0.008	0.001	0.019	n.s.
Orup	**0.706**	**0.000**	−0.034	0.000	–	n.s.	n.s.	n.s.	n.s.	n.s.	0.009	0.008	0.001	0.017	n.s.
Stir	**0.706**	**0.000**	−0.034	0.000	0.000	–	n.s.	n.s.	n.s.	n.s.	0.009	0.008	0.001	0.020	n.s.
Will	**0.583**	0.006	0.019	0.063	0.063	0.063	–	n.s.	n.s.	n.s.	n.s.	0.016	0.005	n.s.	n.s.
UHay	**0.706**	**0.000**	−0.034	0.000	0.000	0.000	0.063	–	n.s.	n.s.	0.008	0.008	0.001	0.018	n.s.
Litt	**0.667**	−0.053	−0.081	0.000	0.000	0.000	0.000	0.000	–	n.s.	0.028	0.009	0.002	0.029	n.s.
Styx	**0.706**	**0.000**	−0.034	0.000	0.000	0.000	0.063	0.000	0.000	–	0.008	0.009	0.001	0.018	n.s.
Dogg	**0.771**	**0.796**	**0.817**	**0.826**	**0.826**	**0.826**	**0.769**	**0.826**	**0.800**	**0.826**	–	0.015	0.005	n.s.	n.s.
Hill	**0.917**	**0.942**	**0.947**	**0.964**	**0.964**	**0.964**	**0.936**	**0.964**	**0.959**	**0.964**	**0.785**	–	0.002	0.033	n.s.
Duns	**0.914**	**0.927**	**0.933**	**0.937**	**0.937**	**0.937**	**0.922**	**0.937**	**0.931**	**0.937**	**0.900**	**0.941**	–	0.010	n.s.
Bota	**0.958**	**0.984**	**0.986**	**1.000**	**1.000**	**1.000**	**0.983**	**1.000**	**1.000**	**1.000**	**0.923**	**0.981**	**0.839**	–	n.s.
Karr	0.921	0.970	0.975	1.000	1.000	1.000	0.962	1.000	1.000	1.000	0.844	0.966	0.540	1.000	–