Temporal stability of a hybrid swarm between the migratory marine and estuarine fishes *Acanthopagrus australis* and *A. butcheri*

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Supplement. Information concerning the geographical distribution of black bream *Acanthopagrus butcheri* and yellowfin bream *A. australis,* as well as estimates of standard population genetic parameters for each contemporary and historical sample
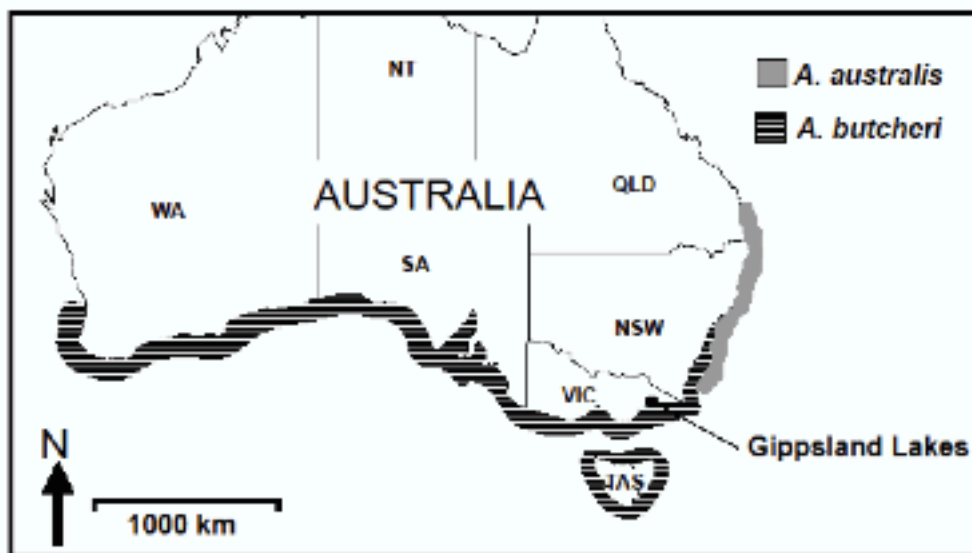

Fig. S1. *Acanthopagrus butcheri* and *A. australis*. Distribution of the estuary-restricted black bream *A. butcheri* and migratory marine yellowfin bream *A. australis* in Australia, and location of the Gippsland Lakes

Table S1. Number of alleles (A), allelic richness (A_R, alleles per locus, standardised to n = 42 ind.), number of private alleles (alleles unique to a particular collection) (P_A), observed heterozygosity (H_o), Nei's (1973) expected heterozygosity (H_e) and, the estimator f of the inbreeding coefficient, F_{IS} (Weir & Cockerham 1984), with corresponding statistical significance for departure from Hardy-Weinberg equilibria, for 2 historical and contemporary samples of *Acanthopagrus* spp. caught within the Gippsland Lakes in southeastern Australia, based on 6 microsatellite loci. The proportion of *Acanthopagrus australis* (Aa), *Acanthopagrus butcheri* (Ab) and hybrid (Hyb) fish in each collection and a comparison of the effect of varying the q-threshold (q_i = the average proportion of *A. butcheri* ancestry) used to distinguish pure species and hybrids is also shown. The specific-species status of each individual was determined using admixture analysis based on the 4 most diagnostic microsatellite loci (Roberts *et al.*, 2009). Estimates of ancestry ranging between 0 and 0.05, and 0.95 and 1.0 (i.e., in the case of q = 0.05) were used to classify each fish as either a pure *A. australis* or *A. butcher*, respectively, while fish with their estimate in between these values were classed as hybrid. Because estimates of the proportion of hybrids in a sample largely depend on the arbitrarily q-value threshold chosen to classify an individual as pure parental, we present the results for a range of q (q = 0.05 – 0.2). Significance: [NS] not significant, [a]p < 0.05, [b]p < 0.01, [c]p < 0.001

Year	Locus	A	A_R	P_A	H_o	H_e	f	q-threshold: proportion Aa/Ab/Hyb [*]
1941	*pAb2B7*	12	10.8	0	0.733	0.823	0.120[b]	
n = 91	*pAb2A5*	9	6.7	1	0.473	0.590	0.200[b]	q = 0.05: 0.00/0.01/0.99
	pAb2D1	7	6.1	1	0.685	0.626	−0.090[NS]	q = 0.10: 0.00/0.07/0.93
	Acs1[*]	7	6.5	0	0.615	0.739	0.173[c]	q = 0.20: 0.00/0.23/0.77
	Acs3[*]	9	7.4	2	0.635	0.698	0.096[a]	
	Acs6[*]	11	9.0	0	0.753	0.748	−0.001[NS]	
	Mean ± SE	9.2 ± 0.8	7.8 ± 0.7	0.7 ± 0.3	0.649 ± 0.042	0.704 ± 0.036	0.083 ± 0.045)[c]	
1943	*pAb2B7*	14	13.7	3	0.762	0.808	0.070[NS]	
n = 42	*pAb2A5*	6	6.0	0	0.357	0.601	0.415[c]	q = 0.05: 0.00/0.05/0.95
	pAb2D1	6	6.0	0	0.619	0.691	0.115[NS]	q = 0.10: 0.02/0.08/0.90
	Acs1[*]	7	7.0	0	0.561	0.716	0.229[a]	q = 0.20: 0.02/0.19/0.79
	Acs3[*]	8	8.0	0	0.575	0.679	0.166[c]	
	Acs6[*]	8	8.0	0	0.786	0.714	−0.089[NS]	
	Mean ± SE	8.2 ± 1.2	8.1 ± 1.2	0.5 ± 0.5	0.610 ± 0.064	0.702 ± 0.027	0.151 ± 0.069[c]	
1996	*pAb2B7*	15	13.7	1	0.704	0.840	0.171[c]	
n = 55	*pAb2A5*	5	4.7	0	0.455	0.489	0.080[a]	q = 0.05: 0.00/0.02/0.98
	pAb2D1	6	5.6	1	0.456	0.625	0.136[NS]	q = 0.10: 0.00/0.02/0.98
	Acs1[*]	8	7.7	1	0.615	0.756	0.196[c]	q = 0.20: 0.02/0.18/0.80
	Acs3[*]	8	7.7	0	0.604	0.690	0.135[a]	
	Acs6[*]	8	7.5	0	0.673	0.726	0.083[a]	
	Mean ± SE	8.3 ± 1.4	7.8 ± 1.3	0.5 ± 0.2	0.599 ± 0.037	0.687 ± 0.049	0.134 ± 0.019[c]	
2000	*pAb2B7*	13	12	1	0.684	0.815	0.169[b]	
n = 59	*pAb2A5*	10	8.0	1	0.407	0.500	0.195[c]	q = 0.05: 0.00/0.03/0.97
	pAb2D1	5	4.6	0	0.542	0.582	0.077[NS]	q = 0.10: 0.00/0.03/0.95
	Acs1[*]	7	6.3	0	0.655	0.685	0.052[NS]	q = 0.20: 0.02/0.29/0.69
	Acs3[*]	7	6.4	1	0.690	0.620	−0.104[NS]	
	Acs6[*]	8	7.4	0	0.755	0.732	−0.022[NS]	
	Mean ± SE	8.3 ± 1.1	7.4 ± 1.0	0.5 ± 0.2	0.622 ± 0.052	0.656 ± 0.046	0.061 ± 0.046[c]	

LITERATURE CITED

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