

Genetic structure among spawning aggregations of the gulf coney *Hyporthodus acanthistius*

Ricardo Beldade^{1,2,3,4,*}, Alexis M. Jackson¹, Richard Cudney-Bueno^{5,6}, Peter T. Raimondi¹, Giacomo Bernardi¹

¹Department of Ecology and Evolutionary Biology, University of California Santa Cruz, 100 Shaffer Road, Santa Cruz, California 95060, USA

²USR 3278 CRILOBE, CNRS EPHE, CBETM de l'Université de Perpignan, 66860 Perpignan Cedex, France

³Laboratoire d'excellence 'Corail', USR 3278 CRILOBE CNRS-EPHE, 66860 Perpignan Cedex, France

⁴Universidade de Lisboa, Faculdade de Ciências, Centro de Oceanografia, Campo Grande, 1749-016 Lisboa, Portugal

⁵School of Natural Resources, University of Arizona, Biological Sciences East, Room 325, Tucson, Arizona 85721, USA

⁶Institute of Marine Sciences, University of California Santa Cruz, 100 Shaffer Road, Santa Cruz, California 95060, USA

*Corresponding author: rbeldade@gmail.com

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Supplement. Raw microsatellite diversity and HWE test results for each spawning aggregation; estimates of population size and number of migrants for three contrasting migration models; and skyline plots of $\log(\alpha)$ for the STRUCTURE analysis

Table S1. Diversity indices for 11 microsatellite loci amplified for specimens from 5 *Hyporthodus acanthistius* spawning aggregations in the Northern Gulf of California. Spawning aggregation site abbreviations are defined in Fig. 1; n = number of samples collected at each spawning location. Reported is the total number of alleles (nA), observed heterozygosity (H_o), expected heterozygosity (H_e) and respective p-values for Hardy-Weinberg equilibrium (HWE) tests after 10000 permutations. p-values in **bold** indicate significant deviations from HWE and presence of null alleles

Loci	PLI (n = 60)				PLO (n = 61)				STO (n = 24)				PPE (n = 59)				SLG (n = 42)			
	nA	H_o	H_e	p	nA	H_o	H_e	p	nA	H_o	H_e	p	nA	H_o	H_e	p	nA	H_o	H_e	p
EAC_C11	9	0.75	0.785	0.598	8	0.852	0.828	0.231	7	0.833	0.743	0.6	9	0.847	0.81	0.11	9	0.833	0.79	0.333
EAC_B03	11	0.717	0.785	0.23	12	0.836	0.833	0.147	10	0.792	0.824	0.83	11	0.847	0.824	0.586	12	0.643	0.782	0.103
EAC_D09	24	0.95	0.934	0.703	24	0.902	0.945	0.226	20	0.958	0.944	0.308	27	1	0.951	0.832	21	0.881	0.941	0.142
EAC_D08	7	0.433	0.462	0.319	10	0.541	0.551	0.151	6	0.417	0.451	0.465	8	0.475	0.487	0.549	6	0.452	0.507	0.469
EAC_A10	20	0.917	0.888	0.515	21	0.787	0.863	0.101	14	0.875	0.879	0.325	22	0.915	0.89	0.351	20	0.881	0.859	0.323
EAC_B10	6	0.567	0.57	0.312	6	0.541	0.459	0.042	4	0.625	0.532	0.614	8	0.559	0.508	0.472	8	0.595	0.604	0.936
EAC_B07	5	0.65	0.638	0.028	6	0.803	0.723	0.629	5	0.75	0.717	0.001	5	0.746	0.696	0.94	5	0.667	0.739	0.002
EAC_D02	10	0.767	0.763	0.321	13	0.754	0.773	0.439	13	0.792	0.816	0.932	16	0.831	0.86	0.459	14	0.881	0.845	0.498
EAC_A06	18	0.867	0.931	0.001	21	0.934	0.94	0.69	18	0.958	0.939	0.683	19	0.932	0.919	0.539	19	0.929	0.93	0.014
EAC_A03	20	0.8	0.92	0.003	22	0.918	0.921	0.593	16	0.833	0.926	0.104	24	0.881	0.924	0.55	19	0.738	0.923	0.002
EAC_C10	6	0.683	0.672	0.301	5	0.59	0.581	0.962	4	0.5	0.596	0.272	6	0.61	0.634	0.089	6	0.595	0.692	0.132

Table S2. Estimates of population size (θ) and number of migrants (Nm) for each of the 2 population groups considered; Puerto Libertad and the remaining aggregations nested into a second group. Autocorrelation and estimated sample size (ESS) values given were used to assess convergence during runs. Model 1 is an unconstrained migration model allowing for gene flow to follow any direction, Model 2 limits migration to an anticyclonic direction, and Model 3 allows for a cyclonic direction of gene flow (details can be found in the ‘Materials and methods’)

	Model 1	Autocorrelation	ESS
θ_1	10.78 [6.00 – 15.47]	0.264	171.648.73
θ_2	5.11 [1.47 – 8.67]	0.181	191.127.29
$Nm\ 1 \rightarrow 2$	4.73 [0 – 20.00]	0.215	191.315.56
$Nm\ 2 \rightarrow 1$	4.73 [0 – 20.00]	0.142	182.784.06
$\text{Ln}[\text{Prob}(D G)]$		0.794	20.318.71

	Model 2	Autocorrelation	ESS
θ_1	190.56 [181.07 – 200.00]	0.653	16.835.49
θ_2	1.68 [0 – 2.33]	0.659	18.489.17
$Nm\ 1 \rightarrow 2$	1.77 [0 – 5.67]	0.663	5664.54
$Nm\ 2 \rightarrow 1$	0	--	--
$\text{Ln}[\text{Prob}(D G)]$	--	0.894	2630

	Model 3	Autocorrelation	ESS
θ_1	2.01 [0 – 5.33]	0.213	33.180.99
θ_2	193.65 [187.06 – 195.53]	0.483	30.249.94
$Nm\ 1 \rightarrow 2$	0	--	--
$Nm\ 2 \rightarrow 1$	193.65 [187.07 – 195.53]	0.568	10.775.03
$\text{Ln}[\text{Prob}(D G)]$	--	0.702	6482.83

Fig. S1. Examples of skyline plots (1 replicate out of 10) for the behavior of $\log(\alpha)$ along 1500000 iterations (500000 of which were defined as the burn-in period)

