

Metapopulation structure informs conservation management in a heavily exploited coastal shark (*Mustelus henlei*)

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Supplement. Mismatch distribution of pairwise sequence and population expansion analysis

Table S1. Results of analyses of historical demographic expansion. F_u 's F_s , τ , corresponding 95% CI, time since expansion ($t = \tau / 2\mu$) in millions of years ago (Mya), P values for model of demographic expansion (Exp P) and spatial expansion (Spt P), for (NP) North Coast, (SP) South Coast, (LG) Lower Gulf, (IG) Islands, (UG) Upper Gulf and (OP) Open Gulf, (PC) Pacific Coast, and (GC) Gulf of California.

	NP	SP	LG	IG	UG	PC	GC	Mh
Fu's F_s	-6.96	-2.51	-5.75	-3.37	-1.62	-6.44	-8.29	-11.26
P	0.00	0.01	0.00	0.02	0.23	0.00	0.01	0.01
τ	0.56	1.12	1.90	1.09	1.45	0.86	1.80	1.63
5%	0.00	0.25	0.84	0.54	0.88	0.38	1.37	1.23
95%	3.23	2.18	3.37	1.96	2.20	1.39	2.37	2.09
Time (Mya)	0.70	1.40	2.38	1.37	1.81	1.07	2.26	2.04
Exp P	0.81	0.38	0.55	0.79	0.03	0.69	0.12	0.09
Spt P	0.79	0.37	0.58	0.49	0.06	0.59	0.14	0.14

Table S2. Localities pairwise fixation indices. Below diagonal are Φ_{ST} based on mitochondrial DNA. Above diagonal are F_{ST} based on microsatellites. Significant values at 95% confidence level after sequential Bonferroni correction are in bold. Localities Popotla (Po), San Quintin (SQ), Laguna Manuel (LM), San Ignacio (SI), Todos Santos (TS), La Paz (LP), Mulege (ML), El Barril (EB), Bahia de los Angeles (BAN), San Felipe (SF) and Puerto Peñasco (PP).

	Po	SQ	LM	SI	TS	LP	ML	EB	BAN	SF	PP
Po		0.003	0.017	0.066	0.000	0.067	0.060	0.041	0.105	0.037	0.034
SQ	0.000		0.003	0.010	0.005	0.023	0.000	0.000	0.023	0.011	0.000
LM	0.034	0.000		0.000	0.000	0.000	0.000	0.000	0.054	0.023	0.021
SI	0.000	0.000	0.000		0.024	0.026	0.000	0.011	0.084	0.049	0.043
TS	0.023	0.000	0.000	0.000		0.011	0.018	0.000	0.049	0.010	0.020
LP	0.046	0.000	0.000	0.000	0.000		0.000	0.003	0.029	0.017	0.017
ML	0.125	0.000	0.000	0.059	0.000	0.000		0.000	0.001	0.001	0.000
EB	0.240	0.158	0.085	0.095	0.089	0.020	0.020		0.020	0.019	0.003
BAN	0.195	0.128	0.077	0.079	0.097	0.000	0.000	0.000		0.000	0.011
SF	0.180	0.100	0.087	0.078	0.108	0.007	0.009	0.000	0.000		0.006
PP	0.131	0.048	0.016	0.005	0.003	0.002	0.000	0.001	0.000	0.000	

Table S3. Bioregions and regions pairwise fixation indices. Below diagonal are Φ_{ST} based on mitochondrial DNA. Above diagonal are F_{ST} based on microsatellites. Significant values at 95% confidence level after sequential Bonferroni correction are in bold. Bioregions: North Pacific (NP), South Pacific (SP), lower gulf (LG), islands (IG), upper gulf (UG). Regions: Pacific Coast (PC) and Gulf of California (GC).

	NP	SP	LG	IG	UG	PC	GC
NP		0.000	0.016	0.017	0.012		
SP	0.000		0.011	0.022	0.021		
LG	0.023	0.011		0.007	0.011		
IG	0.144	0.143	0.028		0.001		
UG	0.091	0.087	0.010	0.000			
PC							0.006
UG						0.069	

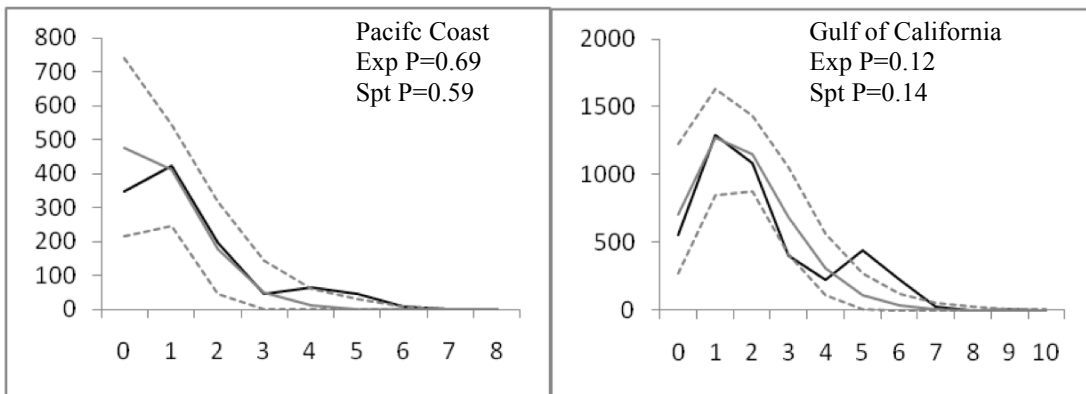


Fig S1. Mismatch distribution of pairwise sequence differences in *Mustelus henlei* from the Pacific Coast and the Gulf of California. Black solid lines are observed frequencies of nucleotide differences between pairs of samples, grey solid lines are the expected distributions under a model of demographic expansion, and the grey dashed lines represent the 99% confidence interval of 1,000 simulations. Harpending's Raggedness indices under significant demographic (Exp P) and spatial expansion (Spt P) models are also provided.

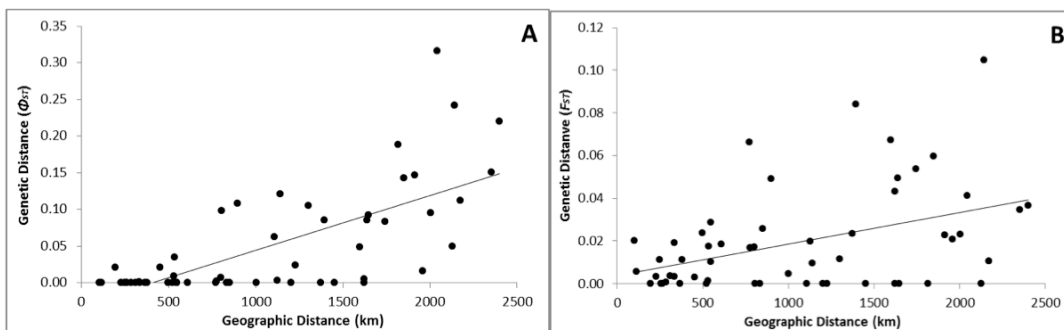


Fig S2 Plots of the linearized genetic distance versus the geographic distance. A) Mitochondrial DNA ($\Phi_{ST}/(1-\Phi_{ST})$). B) Microsatellites ($F_{ST}/(1-F_{ST})$).