

Fine-scale genetic structure and relatedness in the eelgrass *Zostera marina*

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Supplement. PCR conditions and single locus statistics for the 5 microsatellite markers, as well as the pairwise F_{ST} -values among locations ($n = 21$) and the results from the cluster assignment analysis

Table S1. Microsatellite primer sequences and PCR conditions. PCR was performed as follows: 1 μ l DNA template in a 10 μ l reaction; 1 μ l of 10x reaction buffer (Promega); 0.6 μ l 1.5 mM $MgCl_2$; 0.2 μ l of each dNTP; 0.25 units of Taq polymerase; and 0.25 μ l of each primer. Accession numbers are for the European Molecular Biology Laboratory

Locus	Accession no.	Forward primer sequence	Reverse primer sequence
ZosmarCT-3	AJ009898	AAC AGC GAC GAA GGA TTT TG	GAC CCG TAA AGA TAC CAC CG
ZosmarCT-12	AJ249303	CGT TCA TCT TGT CCT CGT CC	TTT CAT TTC CAT TTC CCA CC
ZosmarCT-19	AJ249304	CCC AAG AAA TAT AAA ATC GGG G	CTT CTC CTT CCG CCG CTA C
ZosmarGA-2	AJ009900	AAC AGG CAA CAG CAC AAC TG	GCA AGA TCG GGA ACT GAA AC
ZosmarGA-3	AJ009901	GTG ACG GAT TGA TCG GAA TC	TTT CAT TTA TCC AAT AGT TTG CCT C

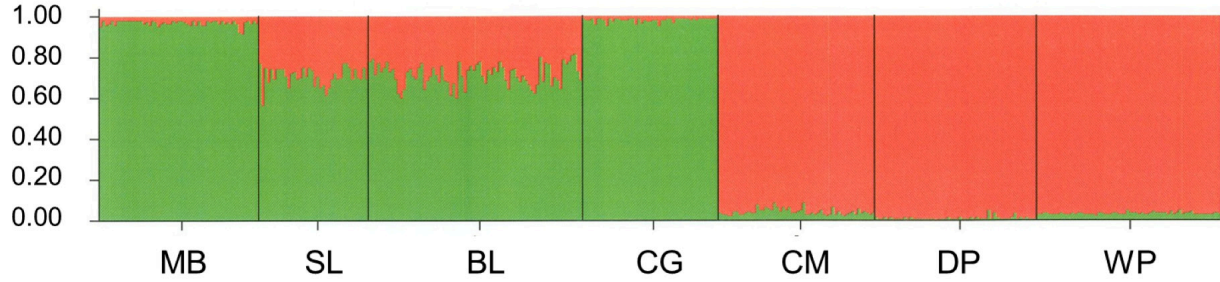
Table S2. Single locus statistics for the five microsatellites. Grey shading indicates a significant heterozygote excess and green shading indicates a significant heterozygote deficit at $p < 0.05$. H_o : observed heterozygosity, H_e : expected heterozygosity, F_{IS} : inbreeding coefficient

	Number of alleles	H_o	H_e	F_{IS}
Locus 1 (CT3)	13	0.544	0.639	0.149
Locus 2 (CT12)	11	0.591	0.632	0.025
Locus 3 (GA2)	10	0.612	0.718	0.005
Locus 4 (CT19)	7	0.674	0.693	0.029
Locus 5 (GA3)	8	0.626	0.559	-0.120
Mean	9.8	0.609	0.648	0.018

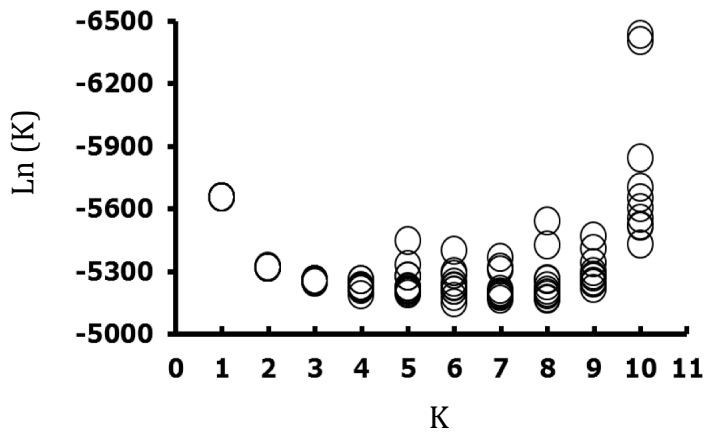
Table S3. Pairwise F_{ST} values among all tidal heights in Bodega Harbor and Tomales Bay ($n = 21$). Values that are not significantly different from zero are in **bold**. Pairs of tidal heights within the same bay are highlighted in grey. Significance testing of F_{ST} was based on 10,000 permutations. Column and row headings show site (MB: Marshall Beach, SL: Sacramento Landing, BL: Blake’s Landing, CG: Cypress Grove, CM: Channel Marker, DP: Doran Park, WP: Westside Park) plus tidal height (HI: high intertidal, LI: low intertidal, S: subtidal)

	MBHI	MBLI	MBS	SLHI	SLLI	SLS	BLHI	BLI	BLS	CGHI	CGLI	CGS	CMHI	CMLI	CMS	DPHI	DPLI	DPS	WPHI	WPLI	WPS	
MBHI	---																					
MBLI	0.070	---																				
MBS	0.050	0.026	---																			
SLHI	0.218	0.054	0.096	---																		
SLHI	0.139	0.023	0.059	0.011	---																	
SLS	0.144	0.024	0.073	0.012	0.055	---																
BLHI	0.224	0.138	0.084	0.147	0.104	0.198	---															
BLLI	0.240	0.113	0.170	0.043	0.095	0.099	0.193	---														
BLS	0.074	0.050	0.021	0.105	0.054	0.096	0.087	0.125	---													
CGHI	0.078	0.044	0.004	0.135	0.079	0.092	0.122	0.185	0.025	---												
CGLI	0.158	0.032	0.070	0.027	0.012	0.046	0.134	0.090	0.068	0.069	---											
CGS	0.033	0.007	0.007	0.085	0.045	0.052	0.162	0.159	0.037	0.007	0.068	---										
CMHI	0.315	0.207	0.205	0.161	0.175	0.176	0.221	0.121	0.142	0.226	0.146	0.269	---									
CMLI	0.253	0.138	0.139	0.101	0.129	0.117	0.132	0.109	0.125	0.161	0.113	0.197	0.028	---								
CMS	0.239	0.141	0.111	0.101	0.128	0.107	0.153	0.124	0.077	0.125	0.098	0.173	0.003	0.011	---							
DPHI	0.240	0.128	0.120	0.114	0.106	0.136	0.091	0.095	0.077	0.146	0.090	0.185	0.022	0.014	0.004	---						
DPLI	0.239	0.148	0.139	0.109	0.136	0.119	0.170	0.076	0.102	0.155	0.110	0.186	-0.004	0.022	0.000	0.021	---					
DPS	0.220	0.137	0.145	0.207	0.186	0.111	0.276	0.163	0.110	0.158	0.138	0.199	0.057	0.066	0.031	0.070	0.030	---				
WPHI																						
	0.276	0.160	0.148	0.102	0.156	0.107	0.171	0.130	0.140	0.164	0.135	0.201	0.048	0.010	0.007	0.049	0.027	0.067	---			
WPLI	0.197	0.092	0.102	0.053	0.095	0.069	0.126	0.064	0.089	0.117	0.083	0.134	0.041	0.009	0.022	0.033	0.017	0.065	0.021	---		
WPS																						
	0.232	0.161	0.136	0.154	0.177	0.138	0.182	0.145	0.093	0.156	0.141	0.193	0.045	0.056	0.012	0.018	0.037	0.045				

a)



(b)



(c)

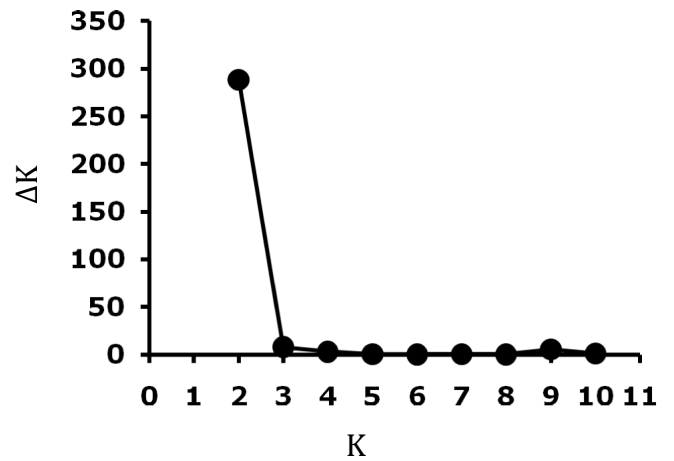


Fig. S1. STRUCTURE analysis of *Zostera marina* microsatellites. (a) The bars represent the probability of assignment to 1 of 2 empirically identified groups indicated by color (green: Tomales Bay; red: Bodega Harbor). (b) Log-likelihood scores up to $K = 10$, and (c) best-fit number of genotype clusters indicated by a model value of ΔK at $K = 2$ (Evanno et al. 2005)

LITERATURE CITED

Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol Ecol* 14:2611–2620