The following supplement accompanies the article

Genotypic diversity at multiple spatial scales in the foundation marsh species, *Spartina alterniflora*

A. Randall Hughes[1,*], Katie E. Lotterhos[2]

[1]**Northeastern University Marine Science Center, 430 Nahant Rd., Nahant, Massachusetts 01945, USA**
[2]**Department of Zoology, University of British Columbia, Vancouver, British Columbia V6T 1Z4, Canada**
[3]***Present address:*** **Biology Department, Wake Forest University, Box 7325 Reynolds Station, Winston-Salem, North Carolina 27109, USA**

*Corresponding author: rhughes@neu.edu

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Supplement. Statistical results for differences in diversity indicies between pairs of populations, linkage disequilibrium by site and locus, pairwise F_{ST} between sites, and model selection analyses.

Table S1. p-values for differences in diversity indices; div = Nei's (Simpson's) diversity index, shc = Shannon's diversity index corrected. Bootstrap tests for differences in clonal diversity between pairs of populations was implemented in Genodive with subsampling to match population sizes

Island-Island		div	div	shc	shc
pop A	pop B	p(A≥B)	p(A≤B)	p(A≥B)	p(A≤B)
I1	I10	0.765	0.237	0.794	0.207
I1	I2	0.786	0.215	0.936	0.065
I1	I3	1	**0.001**	1	**0.001**
I1	I4	0.195	0.806	0.999	0.002
I1	I5	0.041	0.96	**0.006**	0.995
I1	I6	0.913	0.088	0.999	**0.002**
I1	I8	**0.001**	1	**0.001**	1
I10	I2	0.494	0.509	0.775	0.226
I10	I3	1	**0.001**	1	**0.001**
I10	I4	0.103	0.898	0.987	**0.014**
I10	I5	0.017	0.984	**0.002**	0.999
I10	I6	0.745	0.256	0.993	**0.008**
I10	I8	**0.001**	1	**0.001**	1
I2	I3	1	**0.001**	1	**0.001**
I2	I4	0.097	0.904	0.929	0.072
I2	I5	0.009	0.992	**0.001**	1
I2	I6	0.766	0.236	0.929	0.072
I2	I8	**0.001**	1	**0.001**	1
I3	I4	0.003	0.998	**0.003**	0.998
I3	I5	0.001	1	**0.001**	1
I3	I6	0.006	0.995	**0.001**	1
I3	I8	**0.001**	1	**0.001**	1
I4	I5	0.35	0.651	**0.001**	1

I4	I6	0.946	0.055	0.362	0.639
I4	I8	**0.008**	0.993	**0.001**	1
I5	I6	0.998	**0.003**	1	**0.001**
I5	I8	**0.014**	0.987	**0.024**	0.977
I6	I8	**0.001**	1	**0.001**	1

Island-Mainland		div	div	shc	shc
pop A	pop B	p(A≥B)	p(A≤B)	p(A≥B)	p(A≤B)
I1	S1	**0.001**	1	**0.001**	1
I1	S2	1	**0.001**	1	**0.001**
I1	S3	1	**0.001**	1	**0.001**
I1	S4	1	**0.001**	1	**0.001**
I1	S5	1	**0.001**	1	**0.001**
I1	S6	1	**0.001**	1	**0.001**
I1	S7	1	**0.001**	1	**0.001**
I1	S8	**0.002**	0.999	0.216	0.785
I10	S1	**0.001**	1	**0.001**	1
I10	S2	0.989	**0.012**	1	**0.001**
I10	S3	1	**0.001**	1	**0.001**
I10	S4	1	**0.001**	1	**0.001**
I10	S5	1	**0.001**	1	**0.001**
I10	S6	1	**0.001**	1	**0.001**
I10	S7	1	**0.001**	1	**0.001**
I10	S8	**0.001**	1	**0.038**	0.963
I2	S1	**0.001**	1	**0.001**	1
I2	S2	0.999	**0.002**	1	**0.001**
I2	S3	1	**0.001**	1	**0.001**
I2	S4	1	**0.001**	1	**0.001**
I2	S5	1	**0.001**	1	**0.001**
I2	S6	1	**0.001**	1	**0.001**
I2	S7	1	**0.001**	1	**0.001**
I2	S8	**0.001**	1	**0.015**	0.986
I3	S1	**0.001**	1	**0.001**	1
I3	S2	0.257	0.744	0.522	0.479
I3	S3	0.993	**0.008**	1	**0.001**
I3	S4	0.982	**0.019**	0.999	**0.002**
I3	S5	0.957	**0.044**	0.871	0.13
I3	S6	0.78	0.222	1	**0.001**
I3	S7	0.95	**0.051**	1	**0.001**
I3	S8	**0.001**	1	**0.001**	1
I4	S1	**0.001**	1	**0.001**	1
I4	S2	0.996	**0.005**	0.999	**0.002**
I4	S3	1	**0.001**	1	**0.001**
I4	S4	1	**0.001**	1	**0.001**
I4	S5	1	**0.001**	1	**0.001**
I4	S6	1	**0.001**	1	**0.001**
I4	S7	1	**0.001**	1	**0.001**
I4	S8	**0.006**	0.995	**0.002**	0.999
I5	S1	**0.001**	1	**0.001**	1
I5	S2	1	**0.001**	1	**0.001**
I5	S3	1	**0.001**	1	**0.001**
I5	S4	1	**0.001**	1	**0.001**
I5	S5	1	**0.001**	1	**0.001**
I5	S6	1	**0.001**	1	**0.001**
I5	S7	1	**0.001**	1	**0.001**

I5	S8	**0.002**	0.999	0.402	0.599
I6	S1	**0.001**	1	**0.001**	1
I6	S2	0.984	**0.017**	1	**0.001**
I6	S3	1	**0.001**	1	**0.001**
I6	S4	1	**0.001**	1	**0.001**
I6	S5	1	**0.001**	1	**0.001**
I6	S6	0.998	**0.003**	1	**0.001**
I6	S7	1	**0.001**	1	**0.001**
I6	S8	**0.001**	1	**0.003**	0.998
I8	S1	**0.001**	1	**0.026**	0.975
I8	S2	1	**0.001**	1	**0.001**
I8	S3	1	**0.001**	1	**0.001**
I8	S4	1	**0.001**	1	**0.001**
I8	S5	1	**0.001**	1	**0.001**
I8	S6	1	**0.001**	1	**0.001**
I8	S7	1	**0.001**	1	**0.001**
I8	S8	0.189	0.812	0.953	**0.048**

Mainland-Mainland		div	div	shc	shc
pop A	pop B	p(A≥B)	p(A≤B)	p(A≥B)	p(A≤B)
S1	S2	1	**0.001**	1	**0.001**
S1	S3	1	**0.001**	1	**0.001**
S1	S4	1	**0.001**	1	**0.001**
S1	S5	1	**0.001**	1	**0.001**
S1	S6	1	**0.001**	1	**0.001**
S1	S7	1	**0.001**	1	**0.001**
S1	S8	0.994	**0.007**	0.999	**0.002**
S2	S3	0.997	**0.004**	1	**0.001**
S2	S4	0.988	**0.013**	0.995	**0.006**
S2	S5	0.959	**0.042**	0.805	0.196
S2	S6	0.843	0.158	1	**0.001**
S2	S7	0.973	**0.028**	1	**0.001**
S2	S8	**0.001**	1	**0.001**	1
S3	S4	0.163	0.838	**0.022**	0.979
S3	S5	**0.026**	0.975	**0.001**	1
S3	S6	0.061	0.94	0.967	**0.034**
S3	S7	0.078	0.923	0.182	0.819
S3	S8	**0.001**	1	**0.001**	1
S4	S5	0.163	0.839	0.016	0.985
S4	S6	0.127	0.875	1	**0.001**
S4	S7	0.238	0.763	0.824	0.177
S4	S8	**0.001**	1	**0.001**	1
S5	S6	0.237	0.764	1	**0.001**
S5	S7	0.432	0.57	0.998	**0.003**
S5	S8	**0.001**	1	**0.001**	1
S6	S7	0.747	0.254	**0.007**	0.994
S6	S8	**0.001**	1	**0.001**	1
S7	S8	**0.001**	1	**0.001**	1

Table S2. Linkage disequilibrium (LD) by site and locus. p-values shown are before correction for multiple tests. * indicates significance after Bonferroni correction. NA indicates sample sizes were too small to calculate LD because of missing data

Pop	Locus#1	Locus#2	p-value
I1	Spar2	Spar7	0.06314
I1	Spar2	Spar16	0.00061
I1	Spar7	Spar16	0.00107
I1	Spar2	Spar34	0.09662
I1	Spar7	Spar34	0.00015
I1	Spar16	Spar34	0.00195
I1	Spar2	Spar8	0.00351
I1	Spar7	Spar8	0.03932
I1	Spar16	Spar8	0.00995
I1	Spar34	Spar8	0.1275
I10	Spar2	Spar7	0.02165
I10	Spar2	Spar16	0.00163
I10	Spar7	Spar16	0.00016
I10	Spar2	Spar34	0.07366
I10	Spar7	Spar34	0.00077
I10	Spar16	Spar34	0.00135
I10	Spar2	Spar8	1
I10	Spar7	Spar8	0.30512
I10	Spar16	Spar8	0.10646
I10	Spar34	Spar8	0.19959
I2	Spar2	Spar7	0.04233
I2	Spar2	Spar16	0.17767
I2	Spar7	Spar16	0.00364
I2	Spar2	Spar34	1
I2	Spar7	Spar34	0.33245
I2	Spar16	Spar34	0.57666
I2	Spar2	Spar8	0.78639
I2	Spar7	Spar8	0.40452
I2	Spar16	Spar8	0.65919
I2	Spar34	Spar8	0.57125
I3	Spar2	Spar7	0
I3	Spar2	Spar16	0.02296
I3	Spar7	Spar16	0.05419
I3	Spar2	Spar34	0.00106
I3	Spar7	Spar34	0
I3	Spar16	Spar34	0.00018
I3	Spar2	Spar8	0.00356
I3	Spar7	Spar8	0.03436
I3	Spar16	Spar8	0.02492
I3	Spar34	Spar8	0.00004
I4	Spar2	Spar7	0.00163
I4	Spar2	Spar16	0.00053
I4	Spar7	Spar16	0.00957
I4	Spar2	Spar34	0.27012
I4	Spar7	Spar34	0.26958
I4	Spar16	Spar34	0.17011
I4	Spar2	Spar8	0.00363
I4	Spar7	Spar8	0.00644
I4	Spar16	Spar8	0.01621
I4	Spar34	Spar8	0.0528

I5	Spar2	Spar7	0.0082
I5	Spar2	Spar16	0.09146
I5	Spar7	Spar16	0.12448
I5	Spar2	Spar34	0.25433
I5	Spar7	Spar34	0.33841
I5	Spar16	Spar34	0.30012
I5	Spar2	Spar8	0.04844
I5	Spar7	Spar8	0.05551
I5	Spar16	Spar8	0.00621
I5	Spar34	Spar8	0.04817
I6	Spar2	Spar7	0.31991
I6	Spar2	Spar16	0.21964
I6	Spar7	Spar16	0.64591
I6	Spar2	Spar34	0.46881
I6	Spar7	Spar34	0.42143
I6	Spar16	Spar34	0.75826
I6	Spar2	Spar8	0.26673
I6	Spar7	Spar8	0.37445
I6	Spar16	Spar8	0.0376
I6	Spar34	Spar8	0.00622
I8	Spar2	Spar7	0.03371
I8	Spar2	Spar16	0.02324
I8	Spar7	Spar16	0.01378
I8	Spar2	Spar34	0.13426
I8	Spar7	Spar34	0.13849
I8	Spar16	Spar34	0.07248
I8	Spar2	Spar8	0.02526
I8	Spar7	Spar8	0.0307
I8	Spar16	Spar8	0.01397
I8	Spar34	Spar8	0.22022
S1	Spar2	Spar7	0.0276
S1	Spar2	Spar16	0.09207
S1	Spar7	Spar16	0.13078
S1	Spar2	Spar34	0.03349
S1	Spar7	Spar34	0.13024
S1	Spar16	Spar34	0.17177
S1	Spar2	Spar8	NA
S1	Spar7	Spar8	NA
S1	Spar16	Spar8	NA
S1	Spar34	Spar8	NA
S2	Spar2	Spar7	0.10459
S2	Spar2	Spar16	0.44547
S2	Spar7	Spar16	0.1723
S2	Spar2	Spar34	0.05342
S2	Spar7	Spar34	0.00129
S2	Spar16	Spar34	0.00173
S2	Spar2	Spar8	0.01476
S2	Spar7	Spar8	0.00882
S2	Spar16	Spar8	0
S2	Spar34	Spar8	0
S3	Spar2	Spar7	0.00566
S3	Spar2	Spar16	0.68513
S3	Spar7	Spar16	0
S3	Spar2	Spar34	0.17151
S3	Spar7	Spar34	0
S3	Spar16	Spar34	0.04612

S3	Spar2	Spar8	0.10752
S3	Spar7	Spar8	0
S3	Spar16	Spar8	0
S3	Spar34	Spar8	0.00037
S4	Spar2	Spar7	0.52399
S4	Spar2	Spar16	0.31075
S4	Spar7	Spar16	0.06997
S4	Spar2	Spar34	0.89534
S4	Spar7	Spar34	0.00434
S4	Spar16	Spar34	0
S4	Spar2	Spar8	0.82096
S4	Spar7	Spar8	0.10163
S4	Spar16	Spar8	0
S4	Spar34	Spar8	0.00029
S5	Spar2	Spar7	0.00164
S5	Spar2	Spar16	0.00591
S5	Spar7	Spar16	0.01449
S5	Spar2	Spar34	0.01801
S5	Spar7	Spar34	0
S5	Spar16	Spar34	0.00086
S5	Spar2	Spar8	0.23323
S5	Spar7	Spar8	0
S5	Spar16	Spar8	0.43728
S5	Spar34	Spar8	0.00825
S6	Spar2	Spar7	0
S6	Spar2	Spar16	0.03602
S6	Spar7	Spar16	0.01726
S6	Spar2	Spar34	0.00358
S6	Spar7	Spar34	0.00896
S6	Spar16	Spar34	0.00758
S6	Spar2	Spar8	0.24946
S6	Spar7	Spar8	0.00801
S6	Spar16	Spar8	0.00003
S6	Spar34	Spar8	0.01222
S7	Spar2	Spar7	0.72822
S7	Spar2	Spar16	0.17028
S7	Spar7	Spar16	0
S7	Spar2	Spar34	0.8771
S7	Spar7	Spar34	0.10364
S7	Spar16	Spar34	0.00046
S7	Spar2	Spar8	0.25984
S7	Spar7	Spar8	0
S7	Spar16	Spar8	0
S7	Spar34	Spar8	0.00909
S8	Spar2	Spar7	0.0023
S8	Spar2	Spar16	0.01122
S8	Spar7	Spar16	0.20035
S8	Spar2	Spar34	0.02618
S8	Spar7	Spar34	0.03932
S8	Spar16	Spar34	0.00253
S8	Spar2	Spar8	0.3385
S8	Spar7	Spar8	0.42094
S8	Spar16	Spar8	0.06457
S8	Spar34	Spar8	0.00952

Table S3. Pairwise F_{ST} between sites (lower left), and significance (upper right). Significance levels after Bonferroni correction (*p < 0.05, **p < 0.01, ***p < 0.001, NS = not significant)

pop	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1		***	NS	*	***	*	***	*	*	*	**	*	*	NS	*	*
2	0.04		NS	*	*	*	**	NS	*	**	*	*	*	NS	*	*
3	0.01	0.04		*	*	*	NS	NS	*	NS	NS	*	**	NS	**	*
4	0.16	0.14	0.12		*	*	*	*	*	*	*	*	*	*	*	*
5	0.04	0.09	0.07	0.16		*	*	*	*	*	*	*	*	*	*	*
6	0.15	0.21	0.11	0.21	0.17		*	*	*	*	*	*	*	*	*	*
7	0.05	0.10	0.02	0.15	0.06	0.11		*	*	*	NS	*	**	**	*	*
8	0.07	0.07	0.07	0.24	0.14	0.23	0.14		*	*	*	*	*	*	*	*
9	0.12	0.14	0.12	0.17	0.11	0.19	0.15	0.13		*	*	*	*	*	*	*
10	0.06	0.06	0.01	0.13	0.12	0.14	0.07	0.11	0.14		*	*	*	*	*	*
11	0.05	0.07	0.02	0.13	0.05	0.11	0.02	0.15	0.15	0.06		*	*	*	*	*
12	0.11	0.16	0.05	0.12	0.12	0.17	0.08	0.21	0.15	0.07	0.06		*	*	*	*
13	0.07	0.12	0.06	0.21	0.16	0.15	0.05	0.16	0.20	0.09	0.07	0.15		*	*	*
14	0.02	0.02	0.00	0.12	0.07	0.15	0.05	0.08	0.12	0.01	0.03	0.06	0.08		*	*
15	0.03	0.09	0.02	0.14	0.08	0.11	0.06	0.11	0.09	0.07	0.05	0.08	0.08	0.05		*
16	0.17	0.17	0.14	0.21	0.16	0.27	0.16	0.26	0.26	0.17	0.07	0.17	0.23	0.10	0.16	

Table S4. Results of nested linear mixed-effect models for the relationship between marsh type (mainland or island), spatial scale, and the *Spartina* genetic diversity. Models with interactions also include main effects of each factor. Bold indicates best model(s). Parentheses denotes random effect. ΔAIC is the difference between the AIC_c of a particular model compared to the lowest AIC_c observed. If ΔAIC is less than 2.0, models are considered equivalent. The Akaike weight is calculated as the model likelihood normalized by the sum of all model likelihoods; values close to 1.0 indicate greater confidence in the selection of a model.

Response variable	Model	df	ΔAIC	Weight
Genotypic richness	Genotypic richness = Intercept + (Site/Focal area) + (Marsh type/Site)	6	72.6	<0.001
	Genotypic richness = Marsh type + (Site/Focal area) + (Marsh type/Site)	7	70.3	<0.001
	Genotypic richness = Scale + (Site/Focal area) + (Marsh type/Site)	7	11.2	0.003
	Genotypic richness = Marsh type + Scale + (Site/Focal area) + (Marsh type/Site)	8	9.0	0.011
	Genotypic richness = Marsh type × Scale + (Site/Focal area) + (Marsh type/Site)	9	0.0	0.986

Genotypic diversity	Genotypic diversity = Intercept + (Site/Focal area) + (Marsh type/Site)	6	23.0	<0.001
	Genotypic diversity = Marsh type + (Site/Focal area) + (Marsh type/Site)	7	25.1	<0.001
	Genotypic diversity = Scale + (Site/Focal area) + (Marsh type/Site)	7	0.0	0.730
	Genotypic diversity = Marsh type + Scale + (Site/Focal area) + (Marsh type/Site)	8	2.2	0.245
	Genotypic diversity = Marsh type × Scale + (Site/Focal area) + (Marsh type/Site)	9	6.8	0.024
Genetic relatedness	**Relatedness = Intercept + (Site/Focal area) + (Marsh type/Site)**	6	0.0	0.824
	Relatedness = Marsh type + (Site/Focal area) + (Marsh type/Site)	7	4.8	0.073
	Relatedness = Scale + (Site/Focal area) + (Marsh type/Site)	7	4.3	0.093
	Relatedness = Marsh type + Scale + (Site/Focal area) + (Marsh type/Site)	8	9.2	0.008
	Relatedness = Marsh type × Scale + (Site/Focal area) + (Marsh type/Site)	9	16.7	<0.001
Plant species richness	Species richness = Intercept + (Site/Focal area) + (Marsh type/Site)	6	11.8	0.002
	Species richness = Marsh type + (Site/Focal area) + (Marsh type/Site)	7	10.3	0.003
	Species richness = Scale + (Site/Focal area) + (Marsh type/Site)	7	1.5	0.282
	Species richness = Marsh type + Scale + (Site/Focal area) + (Marsh type/Site)	8	0.0	0.592
	Species richness = Marsh type × Scale + (Site/Focal area) + (Marsh type/Site)	9	5.8	0.032
	Species richness = Genotypic richness + (Site/Focal area) + (Marsh type/Site)	7	7.4	0.014
	Species richness = Genotypic richness + Marsh type + (Site/Focal area) + (Marsh type/Site)	8	6.3	0.025
	Species richness = Genotypic richness + Scale + (Site/Focal area) + (Marsh type/Site)	8	7.2	0.016
	Species richness = Genotypic richness + Marsh type + Scale + (Site/Focal area) + (Marsh type/Site)	9	5.9	0.031
	Species richness = Genotypic richness + Marsh type × Scale + (Site/Focal area) + (Marsh type/Site)	10	11.9	0.001

Table S5. Results of nested linear models for the relationship between island area, distance to the mainland, and *Spartina* genetic diversity. Models with interactions also include main effects of each factor. Bold indicates best model(s). ΔAIC is the difference between the AIC_c of a particular model compared to the lowest AIC_c observed. If ΔAIC is less than 2.0, models are considered equivalent. The Akaike weight is calculated as the model likelihood normalized by the sum of all model likelihoods; values close to 1.0 indicate greater confidence in the selection of a model

Response variable	Model	df	ΔAIC	Weight
Genotypic richness	Genotypic richness = Distance to marsh	3	9.5	0.008
	Genotypic richness = Island area	3	0.0	0.900
	Genotypic richness = Distance to marsh + Island area	4	4.6	0.091
	Genotypic richness = Distance to marsh × Island area	5	17.4	< 0.001
Genotypic diversity	**Genotypic diversity = Distance to marsh**	3	0.0	0.640
	Genotypic diversity = Island area	3	1.5	0.300
	Genotypic diversity = Distance to marsh + Island area	4	4.9	0.050
	Genotypic diversity = Distance to marsh × Island area	5	23.5	<0.001
Genetic relatedness	**Relatedness = Distance to marsh**	3	0.0	0.624
	Relatedness = Island area	3	1.0	0.37
	Relatedness = Distance to marsh + Island area	4	9.2	0.006
	Relatedness = Distance to marsh × Island area	5	27.5	<0.001
Plant species richness	**Plant richness = Distance to marsh**	3	0.0	0.579
	Plant richness = Island area	3	0.7	0.407
	Plant richness = Distance to marsh + Island area	4	7.4	0.014
	Plant richness = Distance to marsh × Island area	5	23.5	<0.001