

The following supplement accompanies the article

Genetic evidence supports recolonisation by *Mya arenaria* of western Europe from North America

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Supplement 1

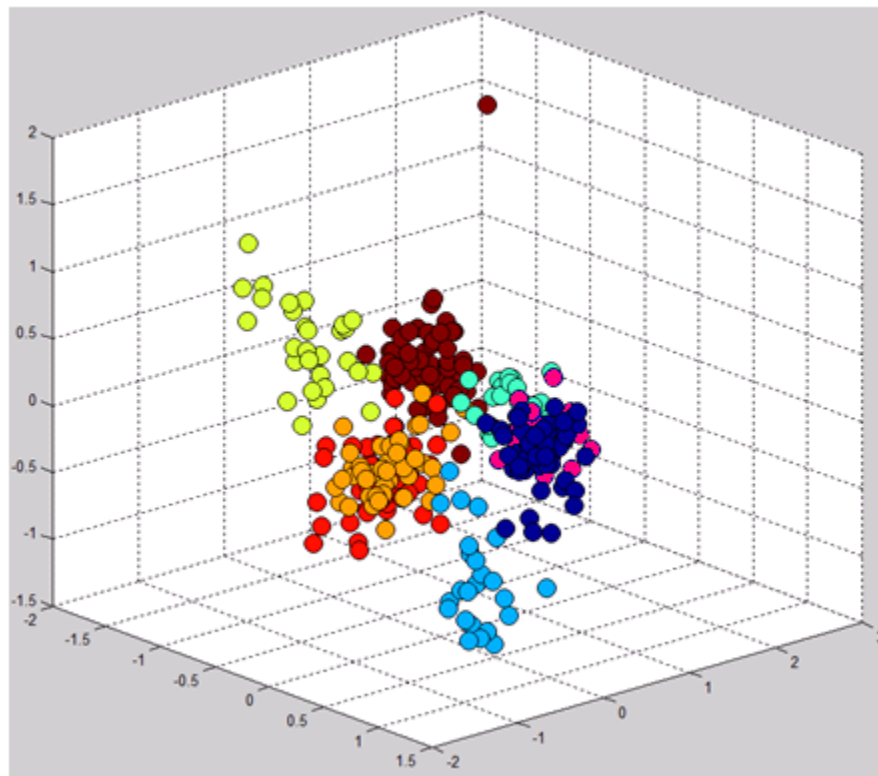


Fig. S1. Factorial Component Analysis of *M. arenaria* data from 10 microsatellite loci, showing population structure (All populations).

Table S1. Details (i.e. sequences and product sizes) of the ten microsatellite markers used in this study for the softshell clam *Mya arenaria* used in the present study (1= St-Onge et al., 2011, 2= Krappal et al., 2011, lower case letters indicate primer tails).

Primer Name	Product Size	Tail used	Primer Sequence (5'-3')	Universal dye label
Multiplex 1				
<i>Mar01</i> ¹	213-277	Hill	F: tgaccggcagcaaaattgAAGCCACGTCTCAAGCCTTA R: gtttcttATGCGTTCGTCCGTATGTG	FAM
<i>Mar06</i> ¹	243-247	Neo	F: aggtgagatgacaggagatcCAATGCCCAACCCACTAAAC R: gtttcttGCGATGTTGGTTGTGTTGAC	VIC
<i>Ma02</i> ²	270-370	M13	F: ggataacaatttcacacaggGGGCCCTATATACCCAGCAC R: gtttcttAAAACGGGTCAAAATAGGC	NED
<i>Ma06</i> ²	203-386	T3	F: aattaaccctcactaaagggCCTGACGGGAATAAAAACCA R: gtttcttCAGATGTAAATTGAGGCTTTGG	PET
<i>Ma11</i> ²	99-199	M13	F: ggataacaatttcacacaggTGGCTCAGACCATGTCAAAA R: gtttcttCGGCGAGCACACTGTACTAT	NED
Multiplex 2				
<i>Mar04</i> ¹	181-269	Neo	F: aggtgagatgacaggagatcTCAATGCCAAAACATTGGTTA R: gtttctyACCCCCAAGCCTTTACTAGC	VIC
<i>Mar07</i> ¹	183-215	M13	F: ggataacaatttcacacaggTTGCAGGCGATGTTTGTATC R: gtttcttATACGGCATTCTTGGTCAGG	NED
<i>Mar08</i> ¹	180-248	T3	F: aattaaccctcactaaagggCATGTGTGACGAAATGTTGATG R: gtttcttCAGAGTCATACACTGTCCATTGC	PET
<i>Ma14</i> ²	99-199	Hill	F: tgaccggcagcaaaattgCGCCTGAAAGGTAGTTTGACA R: gtttcttGAAAGTCCAGAGCAAGTATGAA	FAM
<i>Ma15</i> ²	253-353	Hill	F: tgaccggcagcaaaattgAAATTGCCAAGGGAGGGAGT R: gtttcttATTTAAAAGAGAAGCAAAAGCCACT	FAM

Table S2. Hierarchical analysis of molecular variance (AMOVA) for mtDNA *COX1* variation.

	d. f.	Variance components	Percentage of Variation	P value
Among regions	2	0.022	7.91	<0.001
Among populations				
Within regions	16	0.006	2.10	<0.050
Within populations	274	0.250	89.98	<0.001
Total	292	0.274	100	

Site abbreviations are given in Table 1. Total = number of individuals sampled.

Table S3. Summary statistics (n = number of individuals that amplified, a = number of alleles, R_s = allelic richness, a_s = allelic size range, H_e = expected heterozygosity, H_o = observed heterozygosity, HW = Hardy Weinberg test p-value) for ten microsatellite loci in *Mya arenaria* samples ('***' = $P < 0.001$, '**' = $P < 0.01$, '*' = $P < 0.05$).

Sample	Mar01	Mar04	Mar06	Mar07	Mar08	Ma02	Ma06	Ma11	Ma14	Ma15
Maryland(EB)										
<i>n</i>	41	41	43	42	42	31	36	42	42	27
<i>a</i>	19	29	10	14	24	18	33	28	26	21
R_s	10.686	13.084	5.381	8.048	11.254	10.816	14.484	13.123	12.185	12.373
a_s	227-303	212-302	243-277	220-258	215-269	325-361	335-421	148-201	137-221	322-390
H_e	0.917	0.946	0.682	0.865	0.907	0.915	0.960	0.948	0.937	0.934
H_o	0.902	0.927	0.837	0.714	0.976	0.839	0.694	0.905	0.857	0.333
HW	ns	ns	ns	ns	ns	***	***	ns	*	***
Maryland(MR)										
<i>n</i>	51	51	52	52	52	37	47	52	51	31
<i>a</i>	17	39	10	19	28	21	36	25	27	26
R_s	9.756	14.160	5.110	8.768	11.270	11.642	14.022	11.827	12.008	12.934
a_s	235-309	212-320	225-275	212-262	167-283	311-369	329-425	140-200	137-219	316-402
H_e	0.905	0.959	0.662	0.878	0.910	0.929	0.958	0.933	0.933	0.939
H_o	0.863	0.980	0.827	0.885	0.962	0.892	0.745	0.923	0.882	0.355
HW	ns	ns	ns	ns	ns	0.000	0.000	ns	ns	ns
Canadian										
<i>n</i>	30	30	30	30	28	11	27	30	25	9
<i>a</i>	16	27	7	10	12	8	21	19	18	8
R_s	10.324	12.443	4.622	6.702	7.367	7.556	12.003	10.863	10.251	8.000
a_s	227-309	206-292	247-289	222-250	229-267	343-361	335-401	136-206	149-215	328-368
H_e	0.911	0.926	0.655	0.791	0.747	0.826	0.931	0.901	0.892	0.858
H_o	0.900	0.967	0.800	0.900	0.821	0.455	0.704	0.933	0.880	0.111
HW	ns	ns	ns	ns	ns	0.000	0.000	ns	ns	0.000
Netherlands										
<i>n</i>	29	28	30	29	29	19	22	29	29	20
<i>a</i>	11	13	10	11	16	11	10	14	14	10
R_s	6.872	8.502	5.977	7.001	9.478	8.680	7.905	9.198	8.742	8.006
a_s	243-303	212-286	243-299	222-258	137-273	331-367	343-413	162-206	149-223	330-368
H_e	0.805	0.865	0.697	0.791	0.883	0.875	0.853	0.888	0.881	0.831
H_o	0.828	0.821	0.667	0.586	1.000	0.895	0.546	0.897	0.828	0.300
HW	ns	ns	ns	ns	ns	0.000	0.000	ns	ns	0.000

Sample	Locus									
	Mar01	Mar04	Mar06	Mar07	Mar08	Ma02	Ma06	Ma11	Ma14	Ma15
Bannow Bay										
<i>n</i>	39	41	44	45	43	19	19	44	46	23
<i>a</i>	9	11	7	9	11	5	9	11	9	8
<i>Rs</i>	6.448	6.146	4.608	5.066	6.487	4.806	7.640	7.140	5.093	6.540
<i>as</i>	247-269	198-274	269-297	220-252	221-265	341-367	331-395	160-206	149-195	330-382
<i>He</i>	0.835	0.744	0.687	0.692	0.795	0.702	0.841	0.842	0.584	0.802
<i>Ho</i>	0.821	0.854	0.727	0.889	0.884	0.368	0.368	0.909	0.652	0.304
<i>HW</i>	ns	0.404	0.058	0.259	0.559	0.002	0.000	0.885	0.419	0.000
Flaxfort										
<i>n</i>	30	27	31	31	31	21	17	31	31	12
<i>a</i>	10	11	6	6	11	9	11	10	8	7
<i>Rs</i>	7.158	6.921	4.224	4.307	7.356	6.683	8.221	7.019	3.945	6.239
<i>as</i>	243-269	212-274	263-289	220-254	137-265	331-367	349-413	160-192	137-209	330-388
<i>He</i>	0.821	0.790	0.545	0.632	0.833	0.781	0.822	0.830	0.495	0.778
<i>Ho</i>	0.667	0.963	0.677	0.774	0.807	0.714	0.412	1.000	0.516	0.333
<i>HW</i>	0.001	0.628	0.930	0.646	0.234	0.069	0.000	0.801	0.585	0.000
Wales										
<i>n</i>	24	19	22	24	24	12	18	25	23	17
<i>a</i>	10	10	5	7	6	6	8	10	6	4
<i>Rs</i>	7.353	7.686	3.725	5.088	5.454	5.685	5.892	7.532	4.688	3.397
<i>as</i>	241-269	212-286	253-273	220-250	221-265	339-353	331-395	156-192	149-195	334-364
<i>He</i>	0.831	0.835	0.471	0.760	0.777	0.778	0.711	0.844	0.655	0.393
<i>Ho</i>	0.833	1.000	0.364	0.792	0.917	0.917	0.667	0.960	0.783	0.353
<i>HW</i>	0.145	0.811	0.002	0.758	0.169	0.008	0.667	0.008	0.446	0.453
Oregon										
<i>n</i>	55	58	58	58	57	51	54	56	56	43
<i>a</i>	14	28	11	17	25	18	27	24	25	30
<i>Rs</i>	8.427	11.433	5.754	8.784	10.236	10.555	11.387	10.764	11.504	12.154
<i>as</i>	237-285	190-294	251-289	204-266	197-277	329-373	319-441	146-208	147-227	302-390
<i>He</i>	0.876	0.926	0.763	0.872	0.890	0.912	0.923	0.912	0.929	0.934
<i>Ho</i>	0.891	0.983	0.931	0.828	0.947	0.922	0.944	0.911	0.964	0.814
<i>HW</i>	0.131	0.834	0.106	0.054	0.319	0.000	0.548	0.333	0.609	0.014

Table S4. Unique microsatellite alleles specific to sampling areas.

	Sample size (n)	Percentage of unique alleles	Number of unique alleles
MLMR	53	28.6	26
MLEB	43	20.9	19
C	30	5.5	5
N	30	6.6	6
BB	48	3.3	3
FF	31	1.1	1
W	25	0	0
O	60	34.1	31
Total		100	91

Table S5. Hierarchical analysis of molecular variance (AMOVA) for microsatellite variation.

	d. f.	Variance components	Percentage of Variation	<i>P</i> value
Among regions	1	0.02448	5.4820	< 0.001
Among populations within regions	6	0.2782	6.2310	< 0.001
Within populations	282	3.9416	88.2870	< 0.001

Fixation Indices: $F_{SC} = 0.0659$, $F_{ST} = 0.1171$, $F_{CT} = 0.0548$.