

SUPPLEMENTARY MATERIALS

Contamination Acts as a Genotype-Dependent Barrier to Gene Flow, Causing Genetic Erosion and Fine-Grained Population Subdivision in Mussels from the Strait of Istanbul

Christopher W. Theodorakis^{1,2*}, Mary-Ann Meyer², Oya Okay³, Sevil Deniz Yakan³ and Karl-Werner Schramm^{4,5}

¹Department of Environmental Sciences, Southern Illinois University Edwardsville, Edwardsville, IL 62026-1099 USA.

²Department of Biological Sciences, Southern Illinois University Edwardsville, Edwardsville, IL 62026-1651 USA.

³ Faculty of Naval Architecture and Ocean Engineering, Istanbul Technical University, Maslak, Sarıyer, 34469 Istanbul, Turkey.

⁴Molecular EXposomics, Helmholtz Zentrum München, German Research Center for Environmental Health (GmbH), Ingolstädter Landstraße 1, 85764 Neuherberg, Germany.

⁵Department für Biowissenschaften, TUM, Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt, Weihenstephaner Steig 23, 85350 Freising, Germany.

*Corresponding author: ctheodo@siue.edu, ph +1 618-650-5235, fax +1 618-650-5102

I. Supplementary tables (next page)

Table S1 (cont')

[illegible]

Table S2 (cont')

[illegible]

Table S1 (cont')

	Nucleotide Position															
Haplotype	393	396	404	407	414	425	434	435	436	448	454	458	459	469	516	517
Hap_2	G	G	A	T	T	A	G	A	C	C	T	A	T	C	G	C
Hap_1	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_3	X	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_4	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_5	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_6	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_7	T	.	.	C	.	.	.	G	.	.	.	X	C	.	.	.
Hap_8	X	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_9	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_10	X	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.
Hap_11	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_12	X	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.
Hap_13	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_14	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_15	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_16	X	X	.	.	.	.	.	G	.	.	.	.	.	.	.	.
Hap_17	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_18	X	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_19	X	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_20	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	G
Hap_21	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_22	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	G
Hap_23	T	.	.	.	.	.	.	G	.	.	.	.	.	T	.	.
Hap_24	T	.	.	.	.	.	X	G	T	.	.	.	.	T	.	.
Hap_25	.	.	.	.	.	.	.	G	.	.	C	.	.	.	.	.
Hap_26	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_27	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_28	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_29	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.
Hap_30	.	.	.	.	.	.	.	.	.	.	.	.	.	.	T	.
Hap_31	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_32	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_33	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_34	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.
Hap_35	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
Hap_36	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.

^aNucleotides numbered starting from the 5' end of the PCR fragment relative to the reverse (R) PCR primer. A dot “.” represents a nucleotide identical to the one in Haplotype 2 at this position. An “X” represents a missing base (deletion) relative to haplotype 2. The typical convention is to represent deletions with a colon (“:”), but an “X” was used here to more easily distinguish it from a dot.

Table S2 – Frequencies of mitochondrial control region haplotypes in *Mytilus galloprovincialis* sampled from various sites along the Strait of Istanbul.

Haplotype:	Frequency							
	Site A	Site B	Site C	Site D	Site E	Site F	Site G	Site H
Hap_1	0.046	0.208	0.208	0	0.056	0.048	0.125	0.4
Hap_2	0.500	0.542	0.208	0.700	0.333	0.714	0.542	0.300
					0.055	0.047		
Hap_3	0.136	0	0	0	6	6	0	0
Hap_4	0.046	0	0	0	0	0	0	0
Hap_5	0	0.042	0	0	0	0	0	0
Hap_6	0.046	0.042	0.167	0	0.056	0.048	0.125	0.133
Hap_7	0.046	0	0.042	0.05	0	0.048	0	0
Hap_8	0.046	0	0.042	0.100	0.111	0	0	0
Hap_9	0.046	0	0	0	0	0	0	0
Hap_10	0.046	0	0	0	0	0	0	0
Hap_11	0.046	0	0	0	0	0	0	0
Hap_12	0	0.042	0	0	0	0	0	0
Hap_13	0	0	0.042	0	0	0	0	0
Hap_14	0	0	0.042	0	0	0	0	0
Hap_15	0	0	0.042	0	0	0	0	0
Hap_16	0	0	0.042	0	0	0	0	0
Hap_17	0	0	0	0.050	0	0	0	0
Hap_18	0	0	0	0.050	0	0	0.042	0
Hap_19	0	0	0	0	0.056	0	0	0.033
Hap_20	0	0	0	0	0.056	0	0	0.067
Hap_21	0	0	0	0	0	0	0.042	0
Hap_22	0	0	0	0	0	0	0.042	0
Hap_23	0	0	0	0	0	0	0.042	0
Hap_24	0	0	0	0	0	0	0	0.033
Hap_25	0	0	0	0	0	0	0	0.033
Hap_26	0	0.042	0.042	0	0.111	0	0	0
Hap_27	0	0.042	0	0	0	0	0	0
Hap_28	0	0.042	0	0	0	0	0	0
Hap_29	0	0	0.083	0	0.056	0	0	0
Hap_30	0	0	0.042	0	0	0	0	0
Hap_31	0	0	0	0.050	0	0	0	0
Hap_32	0	0	0	0	0.056	0	0	0
Hap_33	0	0	0	0	0.056	0	0	0
Hap_34	0	0	0	0	0	0.048	0	0
Hap_35	0	0	0	0	0	0.048	0	0
Hap_36	0	0	0	0	0	0	0.042	0

Table S3 – Sample size (N), number of polymorphic or segregating sites (S), total number of haplotypes (H), and number of unique haplotypes (Hu) for mitochondrial control region haplotypes in *Mytilus galloprovincialis* sampled from various sites along the Strait of Istanbul.

Sample Site	N	S	H	Hu
A	22	32	10	4
B	24	26	8	4
C	24	36	12	5
D	20	33	6	2
E	18	30	11	2
F	21	30	7	2
G	24	28	8	4
H	30	25	7	2
Total	183	55	36	25

Table S4 – Number of transversions, transitions, and their ratio using mitochondrial control region haplotypes in *Mytilus galloprovincialis* sampled from various sites along the Strait of Istanbul.

	Site A	Site B	Site C	Site D	Site E	Site F	Site G	Site H
No. of transitions	30	25	32	30	25	28	24	22
No. of transversions	3	1	5	4	5	2	4	3
Transversion/transition ratio	0.10	0.04	0.16	0.13	0.20	0.07	0.17	0.14

Table S5 – Results of an AMOVA analysis using mitochondrial control region haplotypes in *Mytilus galloprovincialis* sampled from various sites along the Strait of Istanbul.

Source of variation	d.f.	Sum of squares	Variance Components	Percentage
Among populations	7	403.879	1.98228	13.69
Within populations	175	2186.274	12.49299	86.31
Total	182	2590.153	14.47527	

II. Supplementary figures

1	TATAGGAAGG	GTTACCTTTT	ATGTAAATGA	ACATATTGTT	TGGTGATAGG
51	TTGTTAAGCG	TGGTAGATTT	CAGAGGAGTC	CTATGTAGCT	GGTTTAAAGC
101	AGGCTTTTTA	GTAAAAAAG	ACCTGCTGTT	GAGGAGGGTG	TGAGATACTT
151	TTCTTTCGCA	TAAAAATTCC	ATGTTTGGAA	TAGATGCAGG	AGATGGGGGC
201	TTATGTCAGG	GTGGAGAAGG	CGACGGTGCC	CAAGCACGTG	TTATTCCTGA
251	AGCTGTAGGG	GGTGGTGGAG	ACACAGCTGT	AAATGCGGGC	GCCGAAGCCG
301	CTCCTGATAA	TGCGGAGGAT	GCGGGCGCCG	AAGCCGCTCC	TGATAATGTG
351	GAGGGGGCGG	GGTGGAACGT	TGGAGACGGC	TATGCCCTTC	CGGTAGAAGA
401	AGTAGGTTGT	AGTTCAGTTG	AAGAAAGAGA	AAGGACTGTC	GCGGAGCCTG
451	AAGTTGTATC	TAGCGGTTCC	GAGCCGGTCG	AGCAGAGAGG	TGTGCTAATT
501	AGCGAAGCTA	GTGGTGCCAT	TAATGCTGGC	AAAGAAAGGT	TTAGTGATTG
551	TTAATGCCCA	GG			

Figure S1 – DNA sequence of Haplotype 2 from *Mytilus galloprovincialis* from the Strait of Istanbul.



Figure S2. Neighbor-joining tree of the Strait of Istanbul *M. galloprovincialis* mitochondrial control region haplotypes constructed using Nei's Dxy distances between consensus haplotype sequences. A. Tree with original topology. B. Tree with branch lengths artificially distorted to allow for placement of bootstrap values (numbers at the nodes or branch points).

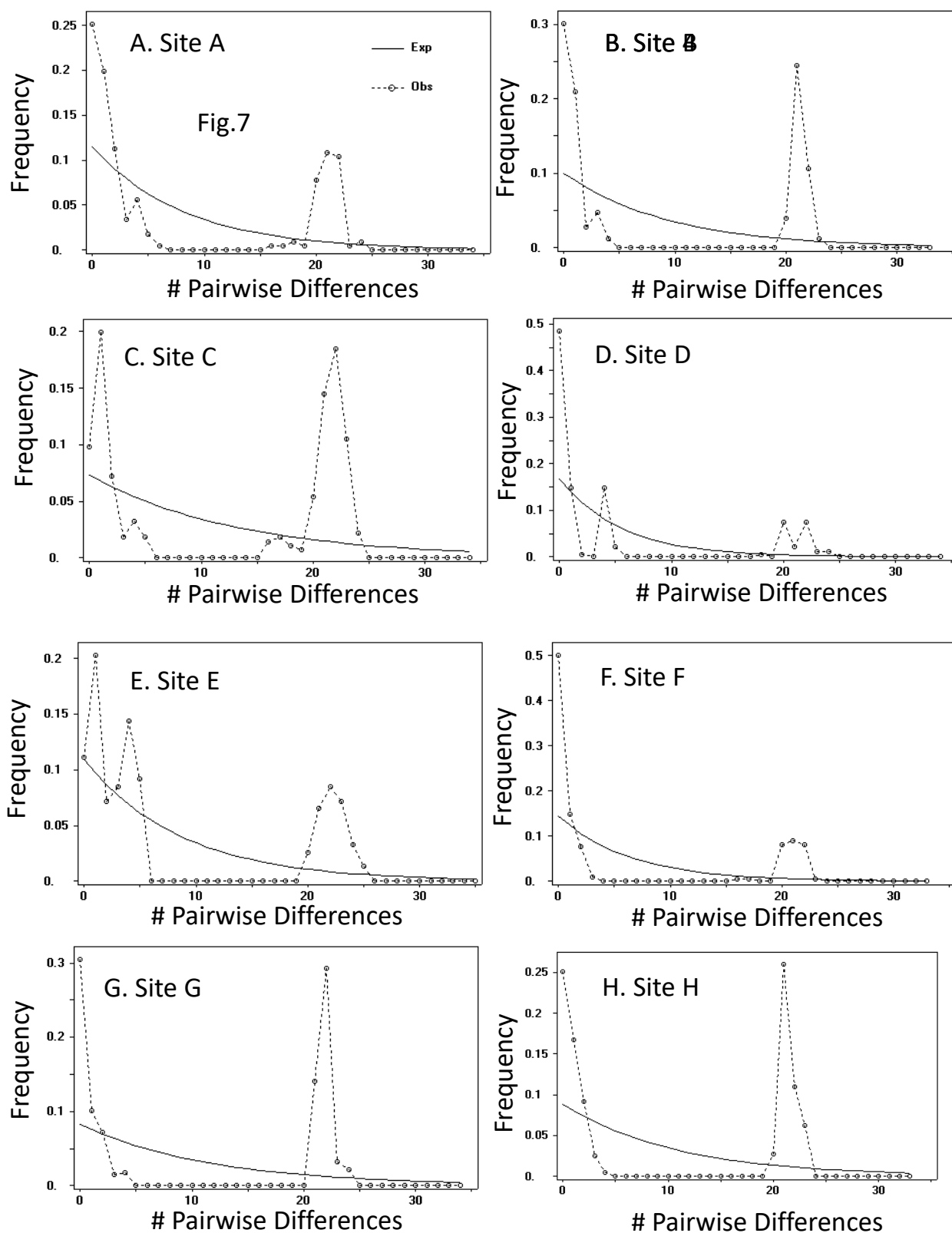


Figure S3. Mismatch distributions for mitochondrial control region haplotypes from *M. galloprovincialis* collected from each of eight sites along the Strait of Istanbul. The solid line represents an expected distribution based on a model of population expansion, the dashed line represents the actual distribution.

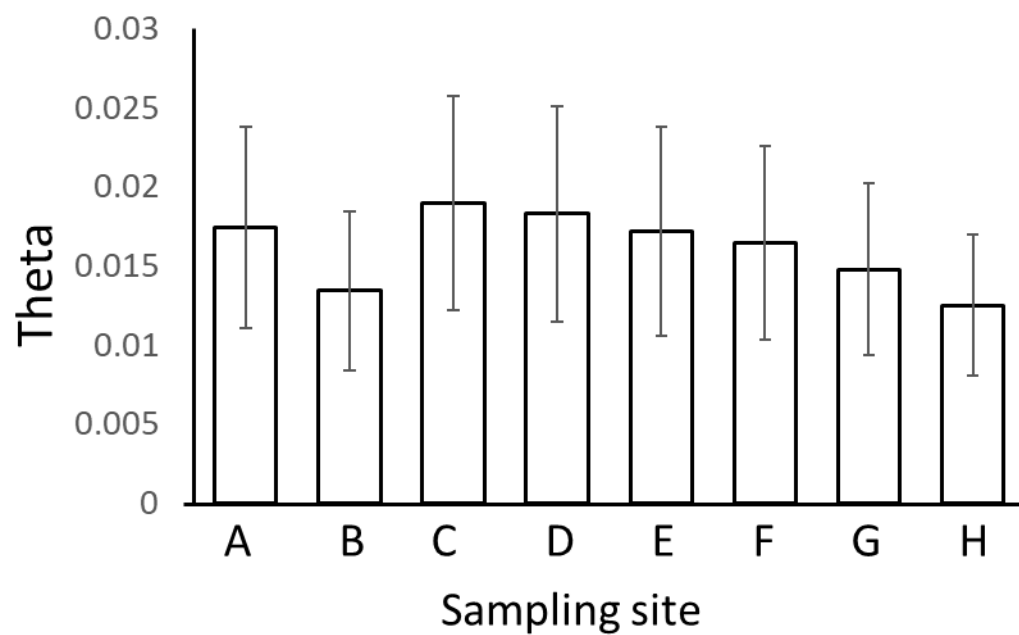


Figure S4. Maximum likelihood estimators of Θ for *Mytilus galloprovincialis* sampled from various sites in the Strait of Istanbul.