

Postglacial expansion routes and mitochondrial genetic diversification of freshwater pearl mussel in Europe and North America

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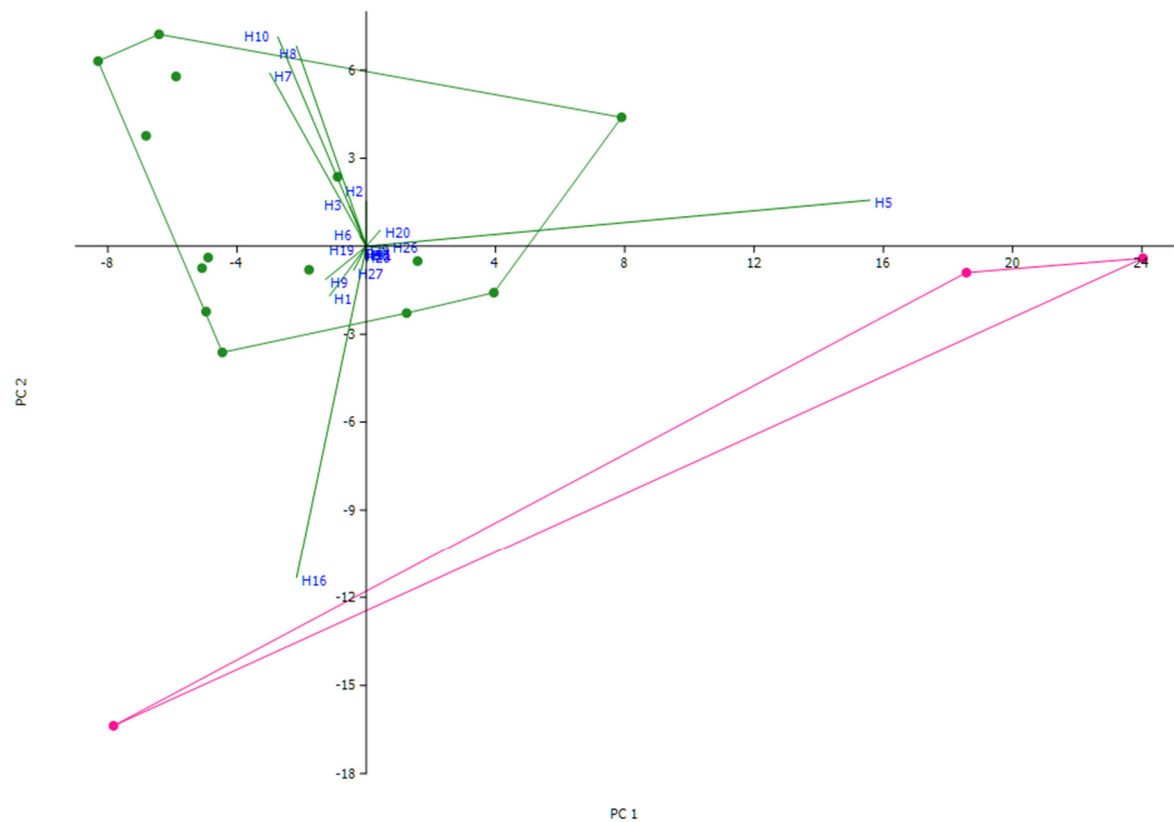


Figure S1. Principal component scores for the first two PC axes obtained by using PCA on matrix of haplotype frequencies in *Margaritifera margaritifera* populations. The green dots indicate pearl mussel populations belonging to the White Sea group (WS), and the pink dots indicate pearl mussel populations are belonged to the Baltic Sea group (BS). Biplot vectors indicate relative loadings of certain haplotypes in PCs. Convex hulls are shown for each group.

Supplementary Tables

Table S1. List of sequences used in this study, including the location, the haplotype numbers, NCBI’s GenBank accession numbers and references.
See the Excel file

Table S2. Distribution of *Margariitfera margaritifera* populations between factors for PCA and GLM analysis, and references with information about host fish.

River name	Factor “basin”	Factor “host”	Reference
Varzuga	WS	<i>S. salar</i>	[1]
Kozha	WS	<i>S. salar</i>	Our observation
Mutkajoki	WS	<i>S. trutta</i>	Our observation
Nuris	WS	<i>S. trutta</i>	Our observation
Tavajoki	WS	<i>S. trutta</i>	Our observation
Tuhka	WS	<i>S. trutta</i>	Our observation

Vozhma	WS	<i>S. salar</i>	Our observation
Ukhta	WS	<i>S. salar</i>	Our observation
Lopshenga	WS	<i>S. salar</i>	Our observation
Kem	WS	<i>S. salar</i>	Our observation
Vuokkijoki	WS	<i>S. salar</i>	[2]
Solza	WS	<i>S. salar</i>	Our observation
Maloshuika	WS	<i>S. trutta</i>	Our observation
Nimenga	WS	<i>S. trutta</i>	Our observation
Yanega	BS	<i>S. trutta</i>	[3]
Peypia	BS	<i>S. trutta</i>	[3]
Khorinka	BS	<i>S. trutta</i>	[4]

Table S3. Matrix of COI haplotype frequencies in populations of *Margaritifera margaritifera*.

	Kem	Khorinka	Kozha	Lopshenga	Maloshuika	Mutkajoki	Nimenga	Nuris	Peypia	Solza	Tavajoki	Tuhka	Ukhta	Varzuga	Vozhma	Vuokkijoki	Yanega
Hapl1	0	0	3	0	2	0	1	0	0	3	0	0	0	0	1	1	5
Hapl2	1	0	0	0	0	4	1	0	0	3	0	0	0	0	0	1	0
Hapl3	2	0	0	0	0	0	1	0	0	5	0	0	1	0	0	1	0
Hapl4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Hapl5	6	24	4	2	2	15	0	6	30	2	9	0	7	0	1	1	0
Hapl6	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Hapl7	5	0	3	14	6	0	8	0	0	2	0	0	1	0	4	1	0
Hapl8	1	0	0	0	15	10	9	1	0	5	2	0	4	2	4	5	2
Hapl9	1	0	0	0	0	0	2	0	0	0	0	0	0	3	3	8	2
Hapl10	6	0	3	9	5	4	7	0	0	13	0	0	0	1	0	1	1
Hapl16	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	20
Hapl19	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Hapl20	0	3	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0
Hapl25	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hapl26	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Hapl27	1	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0
Hapl28	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Hapl29	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Hapl30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Hapl31	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0

Table S4. Loading values of haplotypes to PC1 and PC2 obtained using matrix of haplotype frequencies in *Margaritifera margaritifera* populations.

Haplotype	PC 1	PC 2
H _{pop} 1	-0.0688	-0.1026
H _{pop} 2	-0.0002	0.0930
H _{pop} 3	-0.0317	0.0840
H _{pop} 4	-0.0038	-0.0016
H _{pop} 5	0.9438	0.0951
H _{pop} 6	-0.0121	0.0207
H _{pop} 7	-0.1808	0.3573
H _{pop} 8	-0.1309	0.4131
H _{pop} 9	-0.0763	-0.0685
H _{pop} 10	-0.1660	0.4326
H _{pop} 11	-0.1306	-0.6858
H _{pop} 12	-0.0073	-0.0097
H _{pop} 13	0.0263	0.0329
H _{pop} 14	-0.0013	-0.0017
H _{pop} 15	0.0411	-0.0059
H _{pop} 16	-0.0237	-0.0499
H _{pop} 17	-0.0033	-0.0079
H _{pop} 18	-0.0049	0.0094
H _{pop} 19	-0.0036	-0.0008
H _{pop} 20	0.0012	-0.0011

Table S5. Mismatch distribution verification tests for spatial population expansion and size population expansion assumptions for the WS group of *Margaritifera margaritifera* populations. Statistically significant values are marked in bold ($p < 0.05$)

Spatial expansion				Sudden expansion			
SSD	<i>p</i> -value	Raggedness	<i>p</i> -value	SSD	<i>p</i> -value	Raggedness	<i>p</i> -value
0.006	0.010	0.050	0.020	0.008	0.0001	0.040	0.0001

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