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1 **Effects of fine-scale environmental heterogeneity on local genetic structure in *Macoma balthica***  
2 **from the Gulf of Gdańsk (southern Baltic Sea)**

3

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18

19 **Abstract**

20 It is increasingly recognized that populations of marine organisms with potential for large-scale  
21 dispersal may exhibit fine-scale genetic structure. The Gulf of Gdańsk (Poland) is an interesting  
22 setting to study fine-grained population structure in marine organisms as it is characterized by chronic  
23 anthropogenic pollution and strong salinity gradients. We investigated, at two nested spatial scales (35  
24 and 7 km), genetic structure among populations of the infaunal tellinid bivalve *Macoma balthica*. The  
25 COI mitochondrial marker revealed a likely mix of evolutionary lineages in the Gulf, with no  
26 detectable spatial structure. Seven microsatellite markers detected weak population structure,  
27 separating deep and shallow populations within short distances (7 km) and assignment tests suggested  
28 asymmetric gene flow among these populations, with no shallow recruits being detected in deep  
29 waters. Given the specific environmental conditions encountered at deeper depths in the Gulf  
30 (increased salinity, lower temperatures, oxygen depletion, hydrogen sulfide pollution), we suggest that  
31 deeper populations may be subjected to local adaptation.

32

33 **Keywords**

34 Population structure ; Vistula ; Asymmetric gene flow ; Local recruitment ; Depth stratification ;  
35 Microsatellites

36

## 37 **Introduction**

38 Many marine species are characterized by a high fecundity, large population sizes, long  
39 distance dispersal via a planktonic larval stage, and, very often, low geographic differentiation. As a  
40 consequence, the extent of small-scale genetic structure has long been neglected for marine organisms.  
41 However, many studies have shown that marine populations may exhibit strong genetic structure due  
42 to limited gene flow, genetic drift and unequal dispersion, caused by cryptic barriers or local  
43 adaptation in a heterogeneous environment (Koehn et al., 1980, Mitton, 1997, Powers & Schulte,  
44 1998, Schmidt & Rand, 2001, Riginos et al., 2002).

45 The Baltic Sea is a noteworthy system to study the impact of high environmental patchiness  
46 on the genetic structure of marine organisms. It is characterized by restricted water exchanges with  
47 other oceanic basins, shallow waters, and low salinities (3 to 7 PSU). Temperature and salinity are  
48 strongly stratified by depth, water below 20-50 m being colder and saltier (Rheinheimer, 1995).  
49 Moreover, oxygen concentration is often reduced, particularly in the bottom zone, due to an  
50 eutrophication-induced increase in primary production (Cederwall & Elmgren, 1980) and total  
51 particulate matter content (Maksymowska et al., 1997) along with a high sedimentation rate (of up to  
52 1-2 mm yr<sup>-1</sup>; Witkowski & Pempkowiak, 1995). In addition, the Baltic Sea suffers from chronic  
53 anthropogenic pollution. Southern waters are impacted by a constant input of heavy metals from the  
54 Vistula river (Gulf of Gdańsk, Sokolowski et al., 1998, 2002, 2007), which carries pollutant runoff  
55 from the industrial cities of Katowice, Kracow or Warsaw (Rainbow et al., 2004, Szefer, 2002).

56 The infaunal bivalve, *Macoma balthica* is a dominant species of the benthic macrofauna in  
57 the Baltic Sea (Rumohr et al., 1996), being present from the sub-littoral to the aphotic zone (Väinölä  
58 & Varvio, 1989). Populations from the Baltic Sea are genetically distinct from those of the Atlantic  
59 and the North Sea, resulting from a mixture of Atlantic and Pacific parental lineages that are  
60 maintained by a strong barrier to gene flow in the Kattegat straight (Nikula et al., 2008). Local genetic  
61 differentiation can be strong in this species, as evidenced by the sharp differences in allele frequencies  
62 recorded along a 60 m-long temperature gradient in the White Sea (allozymic locus Idh; Hummel et  
63 al., 1998). The contrasted environmental conditions in the Gulf of Gdańsk represent an ideal place to

64 study fine-scale genetic structure among *M. balthica* subpopulations. In this work, we therefore used  
65 one mitochondrial and seven microsatellite markers (Becquet et al., 2009) to determine whether local  
66 genetic structure could be detected in these southern Baltic populations. We aimed at identifying  
67 putative barriers to gene flow at two nested geographic scales: a regional one (the Gulf of Gdańsk) and  
68 a local one (along a depth gradient, away from the mouth of the Vistula River).

69

## 70 **Materials and methods**

71 Adult specimens of *M. balthica* were collected between 1997 and 1999 at 11 locations  
72 with various environmental conditions (Fig. 1 and Table 1). Puck lagoon (MW30) is characterized by  
73 strong eutrophication and anoxia. Three populations were sampled in the lee of the Hel Peninsula at 45  
74 m (HEL45), 60 m (HEL60) and 85 m (HEL85) depth. GN40 was sampled in the main seaway between  
75 the ports of Gdynia and Gdańsk. Finally, 6 populations were sampled at the mouth of the Vistula,  
76 along a gradient of increasing depth and various pollutant concentrations (SW5 to SW60). Specimens  
77 were stored in 95% ethanol until DNA extraction. Total DNA was purified from <15 mg of muscle  
78 using the Dneasy<sup>TM</sup> Tissue Kit (Qiagen, Germany).

79 Multiple mitochondrial lineages with distinct colonization histories can co-occur in the  
80 Baltic Sea (Luttikhuisen et al., 2003; Nikula et al., 2007, 2008). If specimens from multiple lineages  
81 are indiscriminately used, an older historical signal may mask a younger and weaker geographical  
82 signal. We therefore first tested for the presence of multiple mitochondrial lineages in our collection.  
83 313 bp of the COI gene were successfully sequenced for 232 individuals, as in Becquet et al. (2012).  
84 In addition to the mitochondrial data, seven microsatellite loci (Mb-mac4, Mb-mac19, Mb-mac10,  
85 Mb-mac17, Mb-mac40, Mb-mac84 and Mb-mac64) were genotyped for 165 individuals, according to  
86 Becquet et al. (2009). We have attempted to genotype all individuals for which a COI sequence was  
87 obtained. All individuals for whom more than 3 microsatellite loci failed to amplify were removed  
88 from the analysis (Table S1).

89 Phylogenetic analyses were performed on mitochondrial sequences with the Network  
90 software v.4.0.0.0 (Bandelt et al., 1999) that builds haplotype networks based on the median-joining

91 algorithm (Cassens et al., 2003). Pairwise linkage disequilibrium between microsatellite loci was  
92 tested using GENEPOP version 4.0.10 (Rousset, 2008), and the significance of each test was  
93 evaluated using a Markov-chain randomization procedure (MCMC) with 1000 dememorization steps,  
94 100 batches and 1000 iterations per batch. The numbers of alleles per population and locus ( $N_{\text{all}}$ ), and  
95 the observed ( $H_o$ ) and expected ( $H_e$ ) heterozygoties under Hardy-Weinberg equilibrium were  
96 calculated using Genetix 4.05.2. (Belkhir et al., 1996-2004). Allelic richness ( $R_{\text{all}}$ ) was computed  
97 using FSTAT 2.9.3.2 (Goudet, 2002) to account for differences in sampling sizes across populations.  
98 Fixation indices ( $F_{\text{IS}}$ ,  $F_{\text{IT}}$ ,  $F_{\text{ST}}$ ) were calculated using Genetix 4.05.2 according to Weir & Cockerham  
99 (1984). The significance of pairwise population differentiation, as measured by  $F_{\text{ST}}$ , was estimated  
100 based on 1000 permutations. Population self-assignment tests were conducted using GeneClass v2.0  
101 (Piry et al., 2004), based on the Bayesian method of Rannala & Mountain (1997), and incorporating  
102 the exclusion-simulation significance test of Cornuet et al. (1999). The level of statistical significance  
103 was set to  $\alpha = 0.05$ .

104           Spatial population structure was further explored using bayesian clustering analyses.  
105 These analyses were performed using the BYM admixture model implemented in TESS v.2.3 (Durand  
106 et al., 2009), using 12,000 MCMC steps and a burnin period of 2,000 steps. Based on the results of  
107 preliminary test runs, the presence of two to 4 genetic clusters was evaluated, with 10 replicate runs of  
108 each Kmax (spatial interaction parameter set to 0.6, linear degree of trend). The most likely Kmax was  
109 selected based on the Deviance Information Criterion (DIC), by minimizing its value and its variance,  
110 and by examining plots of individual membership probabilities. The most likely run among 10  
111 replicates was then selected based on DIC.

112

## 113 **Results**

114 A total of 32 COI haplotypes were detected among 232 individuals, 6 of which being putatively  
115 endemic to the Baltic Sea. Three closely-related clades were observed: clade 3, clade 4 and clade 8,  
116 separated by 1 to 3 mutations along the 313 bp examined (Fig. 1 and Fig. 2). clade 4, characterized by  
117 12 haplotypes, was the most prevalent group, with 123 individuals. clade 3 (12 haplotypes) and clade

118 8 (6 haplotypes) group 35 and 70 individuals, respectively. There was no spatial or bathymetric trend  
119 in the distribution of haplotypes (Fig. 1 and Fig. 2).

120 A multilocus nuclear genotype was obtained for 165 individuals collected at 11 sampling sites with  
121 seven microsatellite markers. No linkage disequilibrium was detected ( $p \geq 0.2$ ). Overall, the number of  
122 alleles ( $N_{\text{all}}$ ) ranged from 2.5 (SW40) to 6.8 (HEL60 and MW30) with a total of 11.2 over the whole  
123 dataset (Table 2). There was little variation in allele number between populations (mean =  $5.1 \pm 1.7$ ),  
124 as confirmed by the allelic richness analysis ( $R_{\text{all}}$ );  $R_{\text{all}}$  varied from 1.5 (SW40) to 1.6 (HEL45) even in  
125 the population with small number of individuals (HEL85, SW40, SW60, mean value =  $1.6 \pm 0.03$ ).  
126 The observed heterozygosity ( $H_o$ ) varied from 0.3 (SW5) to 0.5 (SW30) and the mean value obtained  
127 for the 11 populations was 0.4 (standard error = 0.1). The expected heterozygosity ( $H_e$ ) showed little  
128 variation across the whole dataset (mean and standard deviation across the 11 populations equals  
129  $0.538 \pm 0.048$ ) and the heterozygote deficiency was quite high for all populations (mean  $F_{\text{IS}}$  value and  
130 standard deviation equals  $0.334 \pm 0.135$ ).

131           At the regional scale, the overall structure observed ( $F_{\text{IT}} = 0.557$ ) was essentially due to  
132 the high heterozygote deficiency within populations ( $F_{\text{IS}} = 0.554$ ) as genetic differentiation between  
133 populations was quite low ( $F_{\text{ST}} = 0.007$ ,  $p = 0.27$ ). Pairwise differentiation between populations was  
134 globally non significant (data not shown). Nevertheless, the SW60 population was significantly  
135 divergent from HEL60, SW5, SW10, SW20, SW30, GN40 and MW30 ( $0.094 < F_{\text{ST}} < 0.186$ ).  
136 Bayesian assignment of individuals to populations highlighted a great rate of self-recruitment varying  
137 from 30% (MW30) to 87% (SW60) with a mean value of 57% (Fig. 3). Excluding HEL85 (50%), the  
138 self-recruitment rate was function of depth (Linear regression test between paired samples,  $R^2 = 0.65$ ,  $t$   
139 = 2.45,  $df = 8$ ,  $p = 0.039$ , Fig.4). This result was confirmed for the Vistula populations (SW5 to  
140 SW60) for which self-recruitment rate varied from 40% for SW5 to 87% for SW60 (Fig. 3 and Fig. 4).  
141 Furthermore, beyond 40 m depth, this rate was higher than 80% ( $40\% < \text{SW5-SW30} < 50\%$  and  $80\%$   
142  $< \text{SW40-SW60} < 87\%$ ). Thus, no individual from the shallowest sites were recruited in populations  
143 located between 30 and 60 m depth (Fig. 3).

144           Bayesian clustering analyses suggested the presence of four clusters among 165  
145 individuals examined. No spatial or bathymetric trend could be detected among these clusters.

146 Mapping clades 3, 4 and 8 onto these clusters revealed no association between multi-locus genotypes  
147 and haplotypes, suggesting strong introgression (Fig. S1).

148

149

## 150 **Discussion**

151

### 152 **1- Genetic structure at the regional scale: the Gulf of Gdańsk**

153

#### 154 **1-1 Large genetic diversity and depth stratification**

155 Populations in the Gulf of Gdańsk were characterized by a large gene diversity ( $0.440 < H_e < 0.591$ ).

156 These diversity levels were similar to that obtained by Becquet et al. (2012), who observed a mean  $H_e$

157 of 0.63 among 18 European populations sampled from France to Russia. As their European

158 counterparts, Baltic populations were heterozygote deficient ( $F_{IS} = 0.55$ ), as currently observed in

159 marine mollusks (Zouros & Foltz, 1984). However, populations were probably not subjected to

160 inbreeding, given their high genetic diversity. In comparison with European populations (mean  $R_{all} =$

161 4.39), the allelic richness in the Gulf of Gdańsk was reduced ( $1.53 < R_{all} < 1.62$ ). This result might

162 be due to the rarefaction method used to standardize allele counts (El Mousadik & Petit, 1996), which

163 is known to underestimate the allelic richness especially when there is a large difference in the sample

164 size among populations ( $5 < N < 30$ ).

165 No genetic structure was detected among shallow-water subpopulations. In addition to tests of

166 significance on fixation statistics, TESS runs confirmed the absence of genetic structuring. This result

167 was probably linked to the ability of *M. balthica* larvae to disperse over long distances (e.g. Günther et

168 al., 1998). Private alleles were not correlated with environmental factors (salinity, pollution...), but

169 gene flow was reduced between deep (40-50 m depth) and shallow stations. This pattern, concordant

170 with previous results (Hummel et al., 2000), is probably linked to the thermo-haline stratification of

171 water masses occurring in the Gulf of Gdańsk at around 40 meters (Cyberska et al., 1998,

172 Rheinheimer, 1995, Rumhor et al., 1996).

173



174 **1-2 Strong self-recruitment**

175 The assignment probability of individuals to each population highlights a great rate of self-recruitment  
176 (30 to 87%). It is now well accepted that panmixia is not the rule in the marine environment (Swearer  
177 et al., 2002, Hellberg et al., 2002). On the contrary, larvae may recruit locally, because (i) spatio-  
178 temporals movements of water masses influence larval trajectories (Gaines et al., 2003, Siegel et al.,  
179 2003), (ii) survival conditions vary in space and time (Gaines & Bertness, 1992, Morgan et al., 2000,  
180 Ellien et al., 2004) and (iii) reproductive success is random (Hedgecock, 1994a, 1994b). The thermo-  
181 halocline present in the Bay of Gdańsk might be a strong vertical barrier to larval exchange and might  
182 explain the different self-recruitment rate for populations living above or below this cline. The low  
183 self-recruitment rate recorded at HEL85 (50% compared to > 70% at other deep-water locations), does  
184 not contradict this hypothesis, and may be explained by the specific sea-floor morphological features  
185 found near the Hel Cape. Indeed, there is a relatively steep slope descending to a depth of 50+ m on  
186 the open-sea side of the cape (Rucinska-Zjadacz & Rudowski, 2009). Upwelling and downwelling  
187 events occur often in this region (Kowalewski & Ostrowski, 2005) and maybe responsible for cross-  
188 slope larval transport.

189

190 **2- Genetic structure at the local scale, among Vistula populations**

191

192 **2-1 Asymmetric gene flow**

193 Genetic connectivity among Vistula populations from different depths was asymmetric, as gene flow  
194 was stronger from deep to shallow stations (Fig. 3). Even if these populations are geographically close  
195 to each other (horizontal distance is about 7 km), they are located along a clear environmental gradient  
196 (Table 1). While shallower populations (SW5 and SW10) are directly impacted by the freshwater of  
197 the Vistula River, carrying heavy metal pollution (Sokolowski et al., 1998, 2002, 2007), deeper  
198 populations (> 20 m) are challenged by saltier waters from the open part of the Gulf of Gdańsk and  
199 impacted by the release of metallic elements from the upper sediment layer that might exert toxic  
200 effects on bivalves (Janas et al., 2004, Sokolowski et al., 2007). Moreover bivalves leaving in the

201 deeper parts of the Gulf of Gdańsk can be subjected to hypoxia or anoxia and even hydrogen sulphide  
202 (Janas et al., 2004), because of the strong eutrophication occurring in this zone (Laine, 2003).  
203 These heterogeneous environmental conditions might favor chaotic genetic patchiness (Johnson &  
204 Black, 1982). Indeed, we observed a greater genetic heterogeneity between close populations (e.g.  
205 Vistula populations), than between more distant populations (e.g. at the scale of the entire Gulf of  
206 Gdańsk populations, Fig. 3). The asymmetric gene flow in the Gulf of Gdańsk might be the result of  
207 natural selection impacting larval and/or recruit survival induced by environmental conditions (e.g.  
208 Johnson & Black, 1982, 1984, Watts et al., 1990, Hedgecock, 1994a, Edmands et al., 1996, David et  
209 al., 1997).

210 The gene flow from deep (30 to 60 m) to shallow populations is probably due to the specific water  
211 mass dynamics in the Vistula Estuary. In this salt wedge estuary, a sharp boundary exists between an  
212 upper layer of brackish water and an intruding wedge-shaped bottom layer of denser saltwater. Under  
213 the typical circulation for such estuary, low salinity surface water moves toward the open sea (flushing  
214 larvae away from the mouth of the estuary), whereas sea bottom water moves toward the land (and  
215 transporting larvae from deep to shallow). Moreover, the thermo-halocline may act as a physical  
216 barrier to larvae dispersal, leading to genetic differentiation at a microscale, as was already found in  
217 many marine organisms (e.g. Torrents et al., 2008, Bongaerts et al., 2010, Mokhtar-Jamai et al., 2011).  
218 Depth-dependent timing of gonadal development and reproductive period might also influence genetic  
219 differentiation. Between 0 and 25 m depth, spawning is regulated by the warming of surface waters  
220 following air temperatures changes (Wenne, 1985 and 1993), while at intermediate depths (25 – 35 m)  
221 the spawning period is extended because of the longer persistence of colder water temperatures. In the  
222 deeper waters (70 – 75 m), spawning is uncorrelated with surface water temperatures and often  
223 depends on food availability (Wenne, 1993 after Pierścieniak et al., 2010).

224

## 225 **2-2 Are SW60 populations subjected to local adaptation?**

226

227 Microsatellite markers revealed a significant genetic differentiation between the deepest SW  
228 population (SW60) and others (except with SW40). Moreover, the SW60 population has the highest

229 self-recruitment rate (87%), which further supports the idea of genetic isolation between this  
230 population and shallower ones. The fact that SW60 is also characterized by a great genetic diversity  
231 ( $H_e = 0.52$ ) suggests that this population is not declining, or suffering from source-sink dynamics or  
232 inbreeding.

233 The challenging environmental conditions recorded at the SW60 site, associated with the high genetic  
234 polymorphism and reduced connectivity observed with other sites, may promote local adaptation via  
235 divergent natural selection within this population (Hasting, 1983). However, populations in this region  
236 deal with many natural (salinity, temperature) and/or anthropogenic stressors (eutrophication, heavy  
237 metals contamination) that may have synergistic effects on population structure. It was therefore  
238 difficult to distinguish which processes are directly implicated in structuring this deep population, and  
239 a more thorough sampling may address this issue in the future. Thus, given the observed variation in  
240 spawning time and the existence of physical barriers to gamete and larval dispersal (limited cross  
241 fertilization), SW populations may be far from panmixia.

242

243

244

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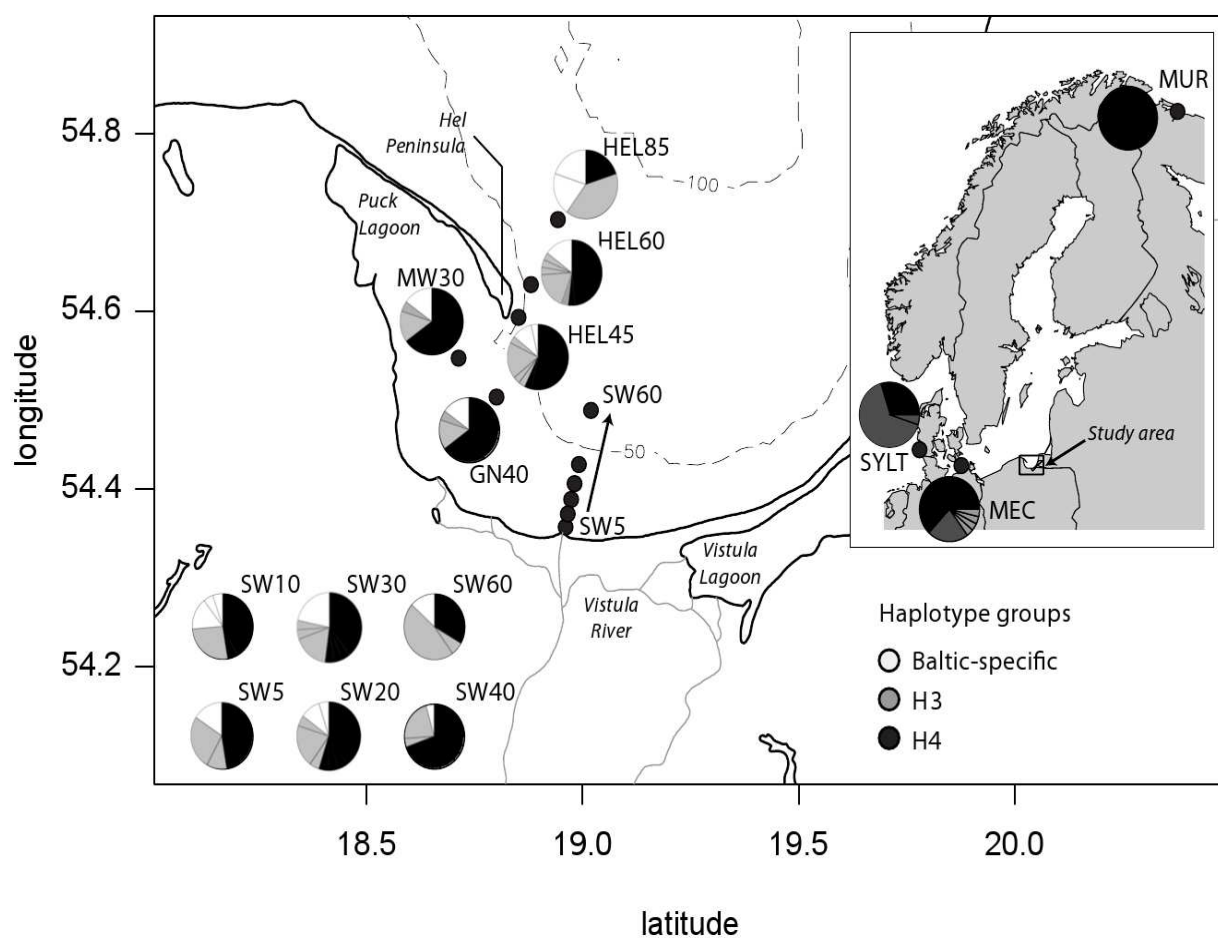
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1 Fig.1: Sampling locations and haplotype distribution in the Gulf of Gdańsk. HEL populations  
2 were collected close to the Hel Peninsula, MW30 in the Puck lagoon, GN40 in the main  
3 pathway of marine traffic and SW5 to SW60 in the Vistula mouth. Haplotype groups  
4 represents the most common haplotypes and their closest relatives (see haplotype network in  
5 Fig.2). Haplotypes H3 and H4 correspond to H3 and H4 of Becquet et al. 2012.

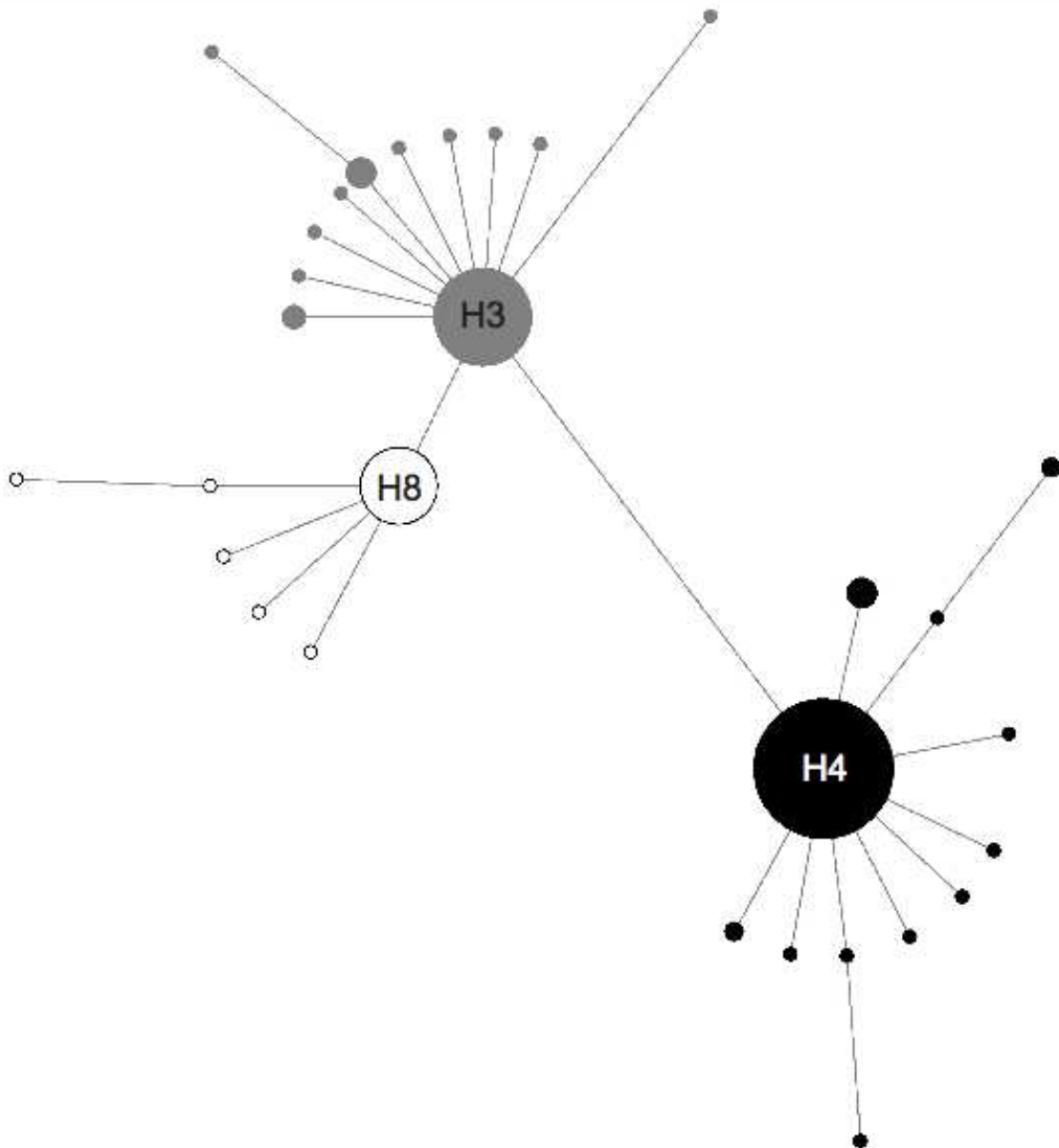
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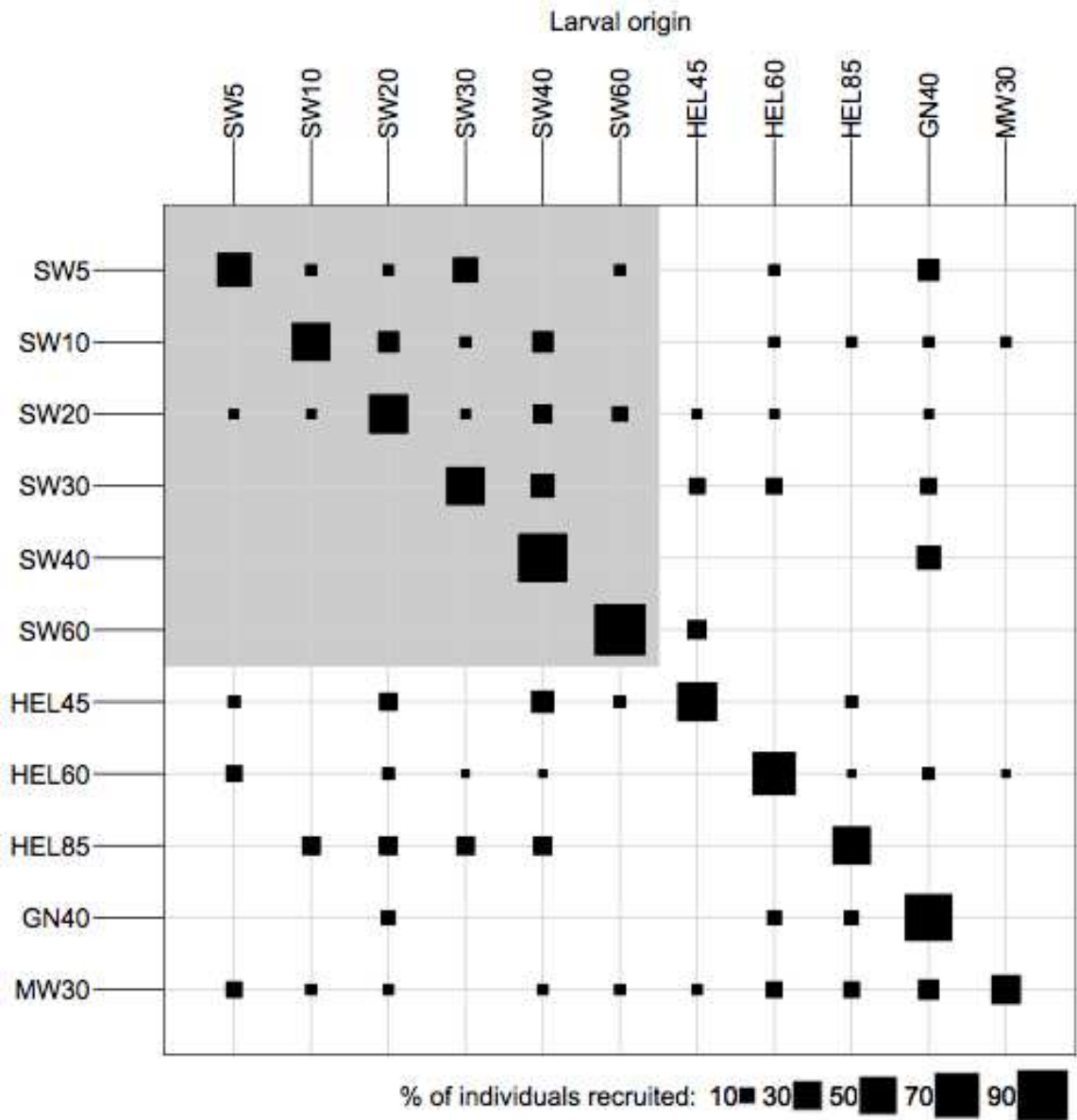
9 Fig.2: Minimum spanning network displaying mitochondrial variation along a 313 bp of the  
10 COI gene. Each circle represents a haplotype. Circle size is proportional to haplotype  
11 frequency (n = 30, 52, 106 for H8, H3, H4, respectively; rares haplotypes have a frequency  
12 between one and four). Each segment represents a single mutational event. H8 are  
13 characteristic of Baltic.



14

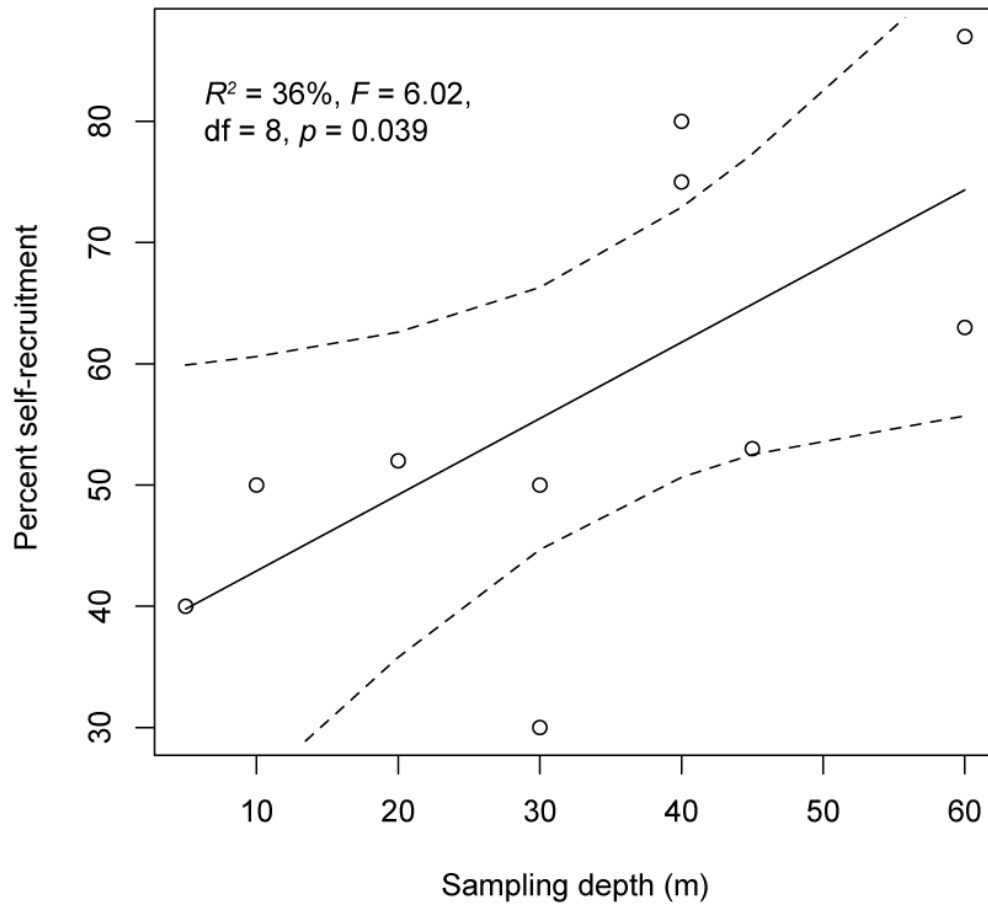
15 Fig.3: Assignment results. For each population, percentage of individuals was assigned to  
 16 each potential source (Larval origin) and represented by a square. Square size is a function of  
 17 a percentage of individuals.

18



19

20 Fig. 4: Relationship between sampling depth and the level of self-recruitment as estimated by  
21 GeneClass2. Top left corner: results of the linear regression analysis. R2 is adjusted for the  
22 number of variables used in the model.



23  
24

table

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- 1 Table 1: Physico-chemical characteristics of sampling locations in the Vistula river mouth. Data are presented as means. More detailed
- 2 information about metallic contamination can be found in Sokolowski 1999.

Population Code	Depth (m)	Salinity (PSU)	Temperature (°C)	Specific environmental features
SW60	60	9.6	5.1	Anoxia, hydrogen sulphide contamination, metallic pollutant release from sediments
SW40	40	8.2	13	Thermo-halocline
SW30	30	7.6	14.2	Intermediate zone
SW20	20	7.3	14.2	Vistula inflow
SW10	10	6.7	14.1	Vistula inflow
SW5	5	6.7	14.4	Vistula inflow

3 Table 2: Nuclear diversity for each sample site.  $N_{\text{nuc}}$ : number of individuals analyzed for  
4 microsatellite markers;  $N_{\text{all}}$ : allele number;  $R_{\text{all}}$ : allelic richness;  $H_o$ : observed heterozygosity;  
5  $H_s$ : gene diversity;  $F_{\text{IS}}$ : heterozygote deficiency.  $N_{\text{mito}}$  corresponds to the number of  
6 individuals for which a mitochondrial sequence was obtained. See also Table S1.

	$N_{\text{nuc}}$	$N_{\text{mito}}$	$N_{\text{all}}$	$R_{\text{all}}$	$H_o$	$H_s$	$F_{\text{IS}}$
<b>HEL85</b>	8	5	4.33	1.58	0.405	0.511	0.328
<b>HEL60</b>	26	28	6.83	1.59	0.408	0.578	0.315
<b>HEL45</b>	17	29	6.16	1.62	0.394	0.591	0.373
<b>GN40</b>	11	24	4.33	1.51	0.313	0.493	0.417
<b>MW30</b>	21	20	6.83	1.61	0.410	0.588	0.382
<b>SW5</b>	18	19	5.14	1.56	0.282	0.534	0.539
<b>SW10</b>	18	20	5.83	1.60	0.461	0.586	0.255
<b>SW20</b>	23	21	5.83	1.58	0.370	0.565	0.373
<b>SW30</b>	10	25	3.83	1.58	0.535	0.519	0.049
<b>SW40</b>	5	23	2.5	1.53	0.447	0.440	0.183
<b>SW60</b>	8	18	4.16	1.55	0.317	0.520	0.464
<b>Total</b>	165	232	11.16	1.61	0.281	0.600	0.558
<b>Mean</b>	15.45	21.09	5.07	1.57	0.394	0.538	0.334
<b>(S.D.)</b>	7.59	6.42	1.36	0.03	0.073	0.048	0.135

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