Stock structure of Atlantic herring Clupea harengus in the Norwegian Sea and adjacent waters

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Total number of authors: 13

Published in:
Marine Ecology - Progress Series

Link to article, DOI:
10.3354/meps11114

Publication date:
2015

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
The following supplement accompanies the article

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Christophe Pampoulie*, Aril Slotte, Guðmundur J. Óskarsson, Sarah J. Helyar, Ásbjörn Jónsson, Guðbjörg Ólafsdóttir, Sigurlaug Skirnisdóttir, Lisa Anne Libungan, Jan Arge Jacobsen, Hóraldur Joensen, Henrik Hauch Nielsen, Sindri Karl Sigurðsson, Anna Kristin Danielsdóttir

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Table S1. Characteristics of multiplexes for 24 microsatellite loci of Atlantic herring *Clupea harengus*. Tm stands for annealing temperature and μl for micro-litres of primer used. Genotyping quality reports the percentage of individuals which were correctly genotyped at a specific microsatellite locus. The forward primers were labelled with dye colors: 6-FAM (blue dye), NED (yellow dye), PET (red dye) and VIC (green dye).

<table>
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<tr>
<th>Multiplex</th>
<th>Loci</th>
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<th>Tm</th>
<th>Dye</th>
<th>Allele range</th>
<th>Genotyping quality</th>
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Values in bold indicate significant deviations from HWE (Exact tests, p < 0.05).
*Values remaining significant after Bonferroni correction (α = 0.05/168 = 0.0003).
Table S3. Results from Lositan outlier tests for the 24 microsatellite loci in 14 samples of Atlantic herring *Clupea harengus*. Expected heterozygosity ($H_e$) and $F_{ST}$ are given. The loci in bold were identified as 95% outliers, while one marked with an asterisk was identified as a significant outlier at a false discovery rate of 0.01.

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<thead>
<tr>
<th>Locus</th>
<th>Heterozygosity</th>
<th>$F_{ST}$</th>
<th>P (Simul $F_{ST} &lt; $ Sample $F_{ST}$)</th>
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<td>0.483</td>
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Table S4. Outlier tests performed in BAYESCAN for the 24 microsatellite loci in 14 samples of Atlantic herring *Clupea harengus*. The posterior probability for the model including selection (p), the log10 of the Posterior Odds for the model including selection (log10(PO)), and the estimated alpha coefficient indicating the strength and direction of selection (alpha; positive values indicate positive selection, while negative values indicate putative balancing selection) are given for each locus. It should be noted that the power to detect loci under putative balancing selection is low. The locus in bold was identified as a significant outlier under a false discovery rate of 0.05.

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<th>alpha</th>
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Table S5. Power of the 24 microsatellite loci in 10 samples of Atlantic herring *Clupea harengus*. The Norwegian local spring-spawning herring were excluded from the analysis. Estimations of the resolution power of the microsatellite loci were performed using POWSIM (Ryman & Palm 2006). \( N_e \): effective population size.

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<th>Fisher’s test</th>
<th>( N_e )</th>
<th>Generation (t)</th>
<th>Runs</th>
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The resolution power was assessed by simulating different expected levels of \( F_{ST} \) according to the effective population size \( (N_e) \) and generations \( (t) \) and to the Nei (1987) formula: \( F_{ST} = 1 – (1 – 1/2N_e)^t \). The significance, evaluated using Fisher’s exact tests as well as \( \chi^2 \) tests, reflects the power to detect any given level of differentiation (average \( F_{ST} \)) with the sampling design developed during our study. \( N_e \) values used during the test are based on estimates calculated from fisheries data. “Runs” denotes the number of simulations performed. The setting \( F_{ST} = 0 \) and \( t = 0 \) estimates \( \alpha \) (type I error; in the absence of genetic drift).
Table S6. Genetic differentiation among samples. Pairwise $F_{ST}$ (above diagonal) and p-values (below diagonal) among 14 samples of Atlantic herring *Clupea harengus* based on allelic frequencies at 24 microsatellite loci. See Table 1 in the main text for sample codes.

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Values in bold differ significantly from zero (Fisher’s exact test, p < 0.05).
* Values remaining significant after Bonferroni correction ($\alpha = 0.05/91 = 0.0005$).
Table S7. Genetic differentiation among samples. Pairwise $F_{ST}$ (above diagonal) and p-values (below diagonal) among 14 samples of Atlantic herring *Clupea harengus* based on allelic frequencies at Cpa111. See Table 1 in the main text for sample codes.

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Values in bold differ significantly from zero (Fisher’s exact test, \( p < 0.05 \)).

* Values remaining significant after Bonferroni correction (\( \alpha = 0.05 / 91 = 0.0005 \)).
Table S8. Results from the hierarchical Bayesian cluster analysis (STRUCTURE) based on all 24 microsatellite loci and all samples. STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 for the North Atlantic samples and from $K = 1$ to 4 for the local Norwegian fjords (samples 11, 12, 13 and 14). An admixture model with correlated allele frequencies without prior information on sample location was implemented. Bold values indicate the most likely number of clusters.

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<th>StDev LnP($K$)</th>
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Table S9. Results from the hierarchical Bayesian cluster analysis (STRUCTURE) based only on neutral microsatellite loci and all samples. STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 for the North Atlantic samples and from $K = 1$ to 3 for the local Norwegian fjords (samples 11, 13 and 14). An admixture model with correlated allele frequencies without prior information on sample location was implemented. Bold values indicate the most likely number of clusters.

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Fig. S1. Results of the Bayesian cluster analysis performed in STRUCTURE for all microsatellite loci and all samples. Two clusters were detected both at the $\text{LnP}(K)$ (left figure) and $\Delta K$ levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented.
Fig. S2. Results of the Bayesian cluster analysis performed in STRUCTURE for all microsatellite loci and the fjord samples. Two clusters were detected both at the LnP(K) (left figure) and ΔK levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for K = 1 to 5 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented.
Fig. S3. Results of the Bayesian cluster analysis performed in STRUCTURE for neutral microsatellite loci only and all samples. Three clusters were detected both at the LnP($K$) (left figure) and $\Delta K$ levels (right figure). STRUCTURE was run using 350,000 burn-in and 500,000 iterations for 10 independent runs for $K = 1$ to 10 using an admixture model with correlated allele frequencies. No prior information on sample location was implemented. No additional clusters were detected.