$\mathcal{F}=\mathcal{F}$

Spatio-temporal effects of stray hatchery-reared Atlantic salmon $\mathcal{S}_{\mathcal{S}}$ on population genetic structure within a 21 km-long Icelandic river system

Leó Alexander Gudmundsson Sigurdur Gudjónsson Gudrún Marteinsdóttir Dennis L. Scarnecchia Anna Kristín Daníelsdóttir Christophe Pampoulie

 \mathcal{R} December 2012 / Accepted: 24 July 2013 / Published online: 25 July 2013 / Publis \mathcal{L} Springer Science+Business Media Dordrecht 2013 \mathcal{R} Abstract $\ddot{\gamma}$, $\$ Salmo salar $\left(\begin{array}{ccc} 1 & 0 & 0 \\ 0 & 0 & 0 \end{array} \right)$ rivers and among tributaries with large river systems \mathbb{R}^2 and \mathbb{R}^2 systems systems systems. $(\sum_{i=1}^n k_i - k_i)^{-1}$ is \mathbb{F}_{n+1} is known is known is known in the set of \mathbb{F}_{n+1} about population structure with small river systems \mathcal{H}^2 and \mathcal{H}^2 small river systems systems. $\begin{pmatrix} 0 & k_1 & k_2 \end{pmatrix}$. In the present study, we investigate the present study, we investigate the \mathcal{N}_2 g_{α} ing of straying of straying of hatchery-reared salmon on ρ population structure and genetic composition within the \mathbf{m} river system, a small system, a small system, a small system, a small system (21 km total length)

 $\label{eq:2.1} \begin{array}{lllllllllll} \text{and} & \text{C2}_{\mathbf{F}} \leftarrow \cdots & \text{C1}_{\mathbf{F}} & \text{C1}_{\mathbf{F}} \leftarrow \cdots & \text{C2}_{\mathbf{F}} \leftarrow \mathbf{F} \leftarrow \$

 $D = \{x_1, x_2, y_1, y_2, y_3, y_4, y_5, y_6, y_7, y_8, y_9, y_9, y_{10}, y_{11}, y_{12}, y_{13}, y_{14}, y_{15}, y_{16}, y_{17}, y_{18}, y_{19}, y_{10}, y_{11}, y_{12}, y_{16}, y_{17}, y_{18}, y_{19}, y_{10}, y_{11}, y_{12}, y_{13}, y_{14}, y_{15}, y_{16}, y_{17}, y_{18}, y_{19}, y_{10}, y_{10}, y_{11}, y_{10}, y_{11}, y_{10}, y_{1$ $\mathbf{v} = \mathbf{v} \cdot \mathbf{F}$ ($\mathbf{w} = \mathbf{F}$ ($\mathbf{w} = \mathbf{F}$ $\mathbf{1}_{\mathcal{A}}$ using $\mathbf{1}_{\mathcal{A}}$ are $\mathbf{1}_{\mathcal{A}}$ and $\mathbf{1}_{\mathcal$ 2010 and significance assessed with 1000 permutations. \mathbf{G} and anong the wild samples wild samples were also were also were also were also were also \mathcal{L}_{\bullet} and \mathcal{R}_{\bullet} and \mathcal{R}_{\bullet} are constructed (NJ) trees constructed from D distances (Nei et al. [1983](#page-13-0)) using the software softw $P_{\text{max}} = \left(\frac{1}{L_{\text{H}}} \cos \theta \right) - \frac{1}{L_{\text{S}}} \cos \theta$ $W = \frac{S_{\text{max}}}{S_{\text{max}}}$ bootstrap replications over loc and the resulting tree was visualized in Tree was visualized in Tree was visualized in Tree was visualized in Tree W $T_s = \frac{1}{2} \sum_{i=1}^{n} \sigma_{i,i}$ is a generation of generation of generations contained in our samples, a Bayesian cluster analysis was perfor $\mathcal{L}(\mathcal{L})$ is $\mathcal{L}(\mathcal{L})$ and $\mathcal{L}(\mathcal{L})$ $-\frac{F_3^2}{100}$ ($\frac{5}{100}$). $\frac{5}{100}$ ($\frac{5}{100}$). Structure in the state same state in the state state in the stat $\sum_{i=1}^{\infty}$ for each individual to $\sum_{i=1}^{\infty}$ for each individual to K genetic clusters $\sum_{i=1}^{\infty}$ K genetic clusters $\sum_{i=1}^{\infty}$ K genetic clusters $\sum_{i=1}^{\infty}$ K genetic clusters $\sum_{i=1}^{\infty}$ K genetic and the log-likelihood (L_1, K_2) most likely number of clusters was inferred from log-likelihood and log-likelihood log-likelihood log-likelihood values and the additional the additional the additional the additional the additional the additional the $K_{\rm{max}}$, (Eq. [2005\)](#page-12-0), $\frac{1}{2}$ \mathcal{L}_1 in \mathcal{L}_2 in STRUCTURE HARVESTER voltage voltage \mathcal{L}_3

 $\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$

 $P_1 = 1$ structure and temporal structure and temporal structure and temporal structure and temporal structure among with P_1

 \mathbf{v} is a implemented and ALPHAPPOINT was set at \mathbf{v} $0.05, 0.05$ $t_1^{\nu+1}$ $\begin{pmatrix} 1 & 0 \ 0 & 0 \end{pmatrix}$ which considers sample in \mathcal{L} \mathcal{L}_{c} in formation on \mathcal{L}_{c} or time. This recently developed \mathcal{L}_{c} $m_{\nu}=\frac{1}{2}m_{\nu}$ et al. [2009](#page-12-0)) has been supported to perform $\frac{1}{2}m_{\nu}$ better than the traditional strategy of the traditional strategy $\mathcal{B}_\mathcal{A}$

$\left(\begin{array}{cc} 0 & 1 \end{array} \right) \left(\begin{array}{cc} 1 & 1 \end{array} \right) \left(\begin{array}{cc} 1 & 1 \end{array} \right) \left(\begin{array}{cc} 1 & 1 \end{array} \right) \left(\begin{array}{cc} \frac{2\sqrt{3}}{3} & 1 \end{array$

 \mathbf{h}^{c} indicated homogenization of the popular \mathcal{B}^{c}_n indicated \mathcal{B}^{c}_n is a popula- $\begin{bmatrix} 1 & 1 & 1 \end{bmatrix}$ ($\begin{bmatrix} 1 & 1 & 1 \end{bmatrix}$ [,](#page-6-0) $\begin{bmatrix} 1 & 1 & 1 \end{bmatrix}$, $\begin{bmatrix} 1 & 1 & 1 \end{bmatrix}$ generally supported reduced divergence between the Ellidaa`r samples and Hoolmsa' in $\left(\begin{array}{c} 1 \end{array}\right)$ $\left(\begin{array}{c} 1 \end{array}\right)$. This summary $\left(\begin{array}{c} 1 \end{array}\right)$. This summary H^{max} that factors of the than \mathcal{B}_max may have been important may have been important may have been important tant. Two non-mutually explanations can be possible explanations can be possible explanations can be possible explanations of λ be identified: $\frac{1}{4}$ identified: $\frac{1}{4}$ wild populations $\frac{1}{4}$ $\frac{1}{4$ and introduced satisfies of \mathcal{A} and \mathcal{B} are first possible possible. sible explanation, natural generation, might involve a source- \mathbb{R} sink system (e.g. Dias [1996\)](#page-11-0), where \mathbb{R} $f: \mathbb{R}^3$ high $f: \mathbb{R}^3$ in Ellidaa $f: \mathbb{R}^3$ in Ellidaa $f: \mathbb{R}^3$ in Ellidaa $f: \mathbb{R}^3$ in \mathbb{R}^3 in Ellidaa \mathbb{R}^3 $t\Delta^2 + Y = T\Delta^2 + T\Delta^3$ s scenario is supported by the observed differences in \mathcal{B}_s $\overline{\mathcal{C}}_{\mathbf{q}} = \mathcal{C}_{\mathbf{q}}$ with the system in $\overline{\mathcal{C}}_{\mathbf{q}}$ viewed by higher juveniles $\overline{\mathcal{C}}_{\mathbf{q}}$ density and growth rate in Ellidaa´r; Antonsson and A´ rnason \mathbf{C} 11). Also, source-sink metapopulation systems may be systems. \mathcal{C}_2 complexes, salmon population population complexes saling \mathcal{C}_1 is complexed by \mathcal{C}_2 composed of large and small populations (Hindar et al., θ et al., θ \mathcal{L}_{max}). However, source-sink dynamics may not explain the sink dynamics may n observed genetic pattern as the reduction in genetic diverse $\mathcal{B}_\mathbf{z}$ gence occurred after a period of population decline (Fig. a, β . Alternatively, it has been suggested that low density of $H = \mathbb{R}^2$. adult spawners may increase straying due to different straying du $f_{\rm eff}$ finding mates (Hindar [1992\)](#page-12-0). Although this possibility that $f_{\rm eff}$ cannot be ruled out in the tributaries, it was unlikely in \mathbf{v} in \mathbf{v} in Ellida $\mathcal{B}_{\text{c},1}$ given the relatively large population size. $A = \frac{1}{2} \sum_{i=1}^{n} A_{i} \sum_{i=1}^{n} A_{i}$ explanation for the observed terms of the observe $\mathcal{L}_{\mathcal{F}} = \mathcal{F} = \mathcal{F} = \sum_{i=1}^{N} \sum_{i=1}^{N} \sum_{j=1}^{N} \sum_{j=1}^{N} \sum_{j=1}^{N} \sum_{j=1}^{N} \mathcal{F}^{(j)}$ h^2 hatcher reared salmon. Although we did not find significant we did not find significant μ can be evidence of homogenization between the \mathbf{v}_1 - \mathbf{v}_2 h^2 , we found (\mathcal{F}_E) , we found the fig. $\frac{1}{2}$ hybridization between wild and hatchery-reared salmon \mathbf{r}_1 $(\underline{I}_{\mathbf{E}} | \mathbf{v}_1)$. \mathbf{P}_2 . This evidence was observed not only during the I $t_s^2 = \sum_{i=1}^N \sum_{i=1}^N \sum_{j=1}^N \sum_{j=1}^$ and \mathbf{y}_1 and \mathbf{y}_2 is \mathbf{y}_3 . Although hybrids of wild and hatcher \mathbf{y}_1 and \mathbf{y}_2 is \mathbf{y}_3 $\sum_{i=1}^n \sum_{i=1}^n \sum_{j=1}^n \sum_{j$ \mathcal{L}_{max}), our results indicated that some survived and some survived an reproduced in this small river system. For example, \mathbb{R}^2 $i = \frac{1}{0.5}$ in Ellis in Ellis in Ellis and were identified as hybrids as hybrids and \mathbf{w} could be a \mathbf{Y} and the later and t detected occurrence of hatchery-reared fish in the system W , and $199.$ We acknowledge that the level of divergence that the level of divergence \mathcal{L}_max between \mathbf{v}_1 and the hatcher real the hatcher reared strains was low for \mathbf{v}_1 and \mathbf{v}_2 hybrid analysis (e.g. $\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$). However, strong s assignment of the historical Ellidaa r sample collected prior r t to the influence of strategy t of support support support support saling support t to introduce the level of differentiation. Also, the level of differentiation was \mathbf{v}_i influenced by many hatchery individuals with intermediate q values of strong assignment to wild \mathbf{v}_1 (Fig. [\)](#page-8-0). In portantly, t_{max} individuals contribution individuals contribution individuals contribution in \mathcal{L} t_{max}^2 comparison of the Ranched Salmon of the Ranched salmon of the Ranched salmon of the Ranched salmon \mathcal{L}_max and overall a large proportion of the hatcher proportion of the hatchery-reared fished fished fished fished fish entering the system (F_1 [c](#page-3-0)). In addition, more introduced, more introduced, more introduced, more introduced,

 $W = \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix}$, $W = \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix}$ $\sum_{i=1}^n \sum_{i=1}^n \sum_{j=1}^n \sum_{j$ bers and for a longer period ($\mathcal{L}_{\mathbf{E}}$ $\mathcal{L}_{\mathbf{E}}$ $\mathcal{L}_{\mathbf{E}}$), but also because it is isomorphism. $\hbar = -\hbar^2 - \hbar^2 \hbar^2$, $\hbar = -\hbar = -\hbar = -\hbar = 0$ et al. [1996](#page-12-0)). Such potential differences likely reflect differences likely reflect differences likely reflect \mathbf{r} $f_{\mathbf{r}}=\left(\begin{array}{cccccc} \mathbf{b}_{1} & \mathbf{b}_{2} & \cdots & \mathbf{b}_{n} \end{array}\right)$ of the two types due to different of the to different of the two types due to different of the two types due to different of the two types due to different of the $r \in \mathbb{R}$ rearing techniques.

 ϕ conservation implications

 $\mathcal{F}(\mathcal{F}(\mathcal{C}_1,\mathcal{C}_2,\mathcal{C}_3)) = \mathcal{F}(\mathcal{F}(\mathcal{C}_1,\mathcal{C}_3,\mathcal{C}_4))$ $(\mathbf{y} \rightarrow (\mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y})$, $(\mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y})$, $(\mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y} \rightarrow \mathbf{y})$

 \mathbf{Y}_1 and reductions in \mathbf{Y}_2 and populations in fitness of wild salmon populations in \mathbf{Y}_3 $\left(\begin{matrix} 1 & 1 & 1 & 1 \end{matrix}\right)$ $\left(\begin{matrix} 2 & 1 & 1 \end{matrix}\right)$ $\left(\begin{matrix} 2 & 1 & 1 \end{matrix}\right)$ $\left(\begin{matrix} 2 & 1 & 1 \end{matrix}\right)$ $\sum_{i=1}^n$, $\sum_{i=1}^n$, $\sum_{i=1}^n$, $\sum_{i=1}^n$, $\sum_{i=1}^n$, $\sum_{i=1}^n$, $\sum_{i=1}^n$ decline in salmon numbers in the Ellidaa \mathcal{B}_{max} introgression from hatchery salmon. Although unfavourable conditions in the sea are likely one of the sea are likely one of the principal \mathcal{B}' f_{α} in the decline α (as has occurred elsewhere in Europe; $F = \mathbf{F} \mathbf{I} \cdot \mathbf{I} \cdot \mathbf{I} \cdot \mathbf{I} \cdot \mathbf{A} \cdot \mathbf{$ $E = \frac{1}{2}$ river system raises the possibility that the possibility that the possibility that the large- $\frac{1}{\sqrt{2}}$ straying of hatchery-reared salmon may partly be $\frac{1}{\sqrt{2}}$ responsible for the decline through genetic effects, equality \mathcal{R}_1 $\mathcal{U}_{\mathcal{A}}(j)$ interactions, or both $\mathcal{B}_{\mathcal{A}}(j)$

