Negative genetic correlation between resistance against *Piscirickettsia salmonis* and harvest weight in coho salmon (*Oncorhynchus kisutch*)

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Introduction

- **Chile** is one of the main producers of salmonids in the world: *Atlantic salmon*, *rainbow trout* and *coho salmon*.

- Leading **coho salmon** (*Oncorhynchus kisutch*) production: about 90% of global production.

- One of the most economically important diseases affecting salmon production in Chile is **Piscirickettsia salmonis**

- Intracellular bacteria that causes the *Salmon Rickettsial Syndrome (SRS)* which generates high mortalities.

- **Genetic improvement** of disease resistance represents an alternative to face pathogens and increase the sanitary status in aquaculture.

*Piscirickettsia salmonis*

Fryer and Hedrick (2003)
**Piscirickettsia salmonis** resistance in Atlantic salmon

- We used different trait definitions: binary, day of death, test-day survival
- And several statistical models: linear, threshold, survival score, Cox and Weibull proportional hazards frailty models
- The estimated heritabilities for the different models ranged from 0.11 to 0.41
- The estimated the genetic correlation between *P. salmonis* resistance and body weight was negative but not significant (-0.19 ± 0.12)
Piscirickettsia salmonis resistance in salmonids

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SUSCEPTIBILITY AND ENDURANCE ARE SAME GENETIC TRAITS FOR RESISTANCE AGAINST Piscirickettsia salmonis IN ATLANTIC SALMON (Salmo salar)

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GENOME WIDE ASSOCIATION ANALYSIS FOR RESISTANCE TO Piscirickettsia salmonis IN ATLANTIC SALMON (Salmo Salar L.)


GENETIC PARAMETERS FOR RESISTANCE TO Caligus rogercresseyi, Piscirickettsia salmonis AND BODY WEIGHT IN RAINBOW TROUT (Oncorhynchus mykiss).

To determine levels of genetic co-variation between resistance against *Piscirickettsia salmonis* and harvest weight in coho salmon (*Oncorhynchus kisutch*)
Materials and methods

- Coho salmon breeding population established in 1997 (Puerto Montt, Chile)
- **Harvest weight (HW)** was recorded in 10,373 fish across 7 generations

**Challenge Test**

- **2,606** siblings from 108 maternal FS families (60 paternal HS), from the 2012 spawning year, were PIT-tagged and challenged against *P. salmonis* at Aquainnovo’s Research Station (Lenca River, Chile).
- Pathogenic strain of *P. salmonis* isolated in November 2012
- We used a dose of 0.2 ml of the LD\(^{50}\) inoculum (IP injection)
- Fish were divided and maintained in three different tanks with salt water (32 ppt) during the test period.
Materials and methods

We used a bi-variate linear animal model to analyze SRS and HW using ASREML (Gilmour et al., 2009)

\[
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix} =
\begin{bmatrix}
  X_1 & 0 \\
  0 & X_2
\end{bmatrix}
\begin{bmatrix}
  b_1 \\
  b_2
\end{bmatrix} +
\begin{bmatrix}
  Z_1 & 0 \\
  0 & Z_2
\end{bmatrix}
\begin{bmatrix}
  u_1 \\
  u_2
\end{bmatrix} +
\begin{bmatrix}
  W_1 & 0 \\
  0 & 0
\end{bmatrix}
\begin{bmatrix}
  c_1 \\
  0
\end{bmatrix} +
\begin{bmatrix}
  e_1 \\
  e_2
\end{bmatrix}
\]

\(y_1\) and \(y_2\) are vectors of observations for HW and SRS (day of death)

\(b_1\) is the vector of fixed effects for HW (sex, cage, year and age at harvest)

\(b_2\) is the vector of fixed effects for SRS (tank and weight at the end of the test)

\(u_i\) and \(e_i\) are vectors of random animal genetic and residual effects, respectively

\(c_1\) is the vector of random common environment effect for HW

\(X_i\) and \(Z_i\) are the design matrices linking fixed and random effects to observations

\(W_1\) is the design matrix for HW

Heritabilities and genetic correlations

\[h_i^2 = \frac{\sigma_{Gi}^2}{\sigma_{Gi}^2 + \sigma_{Ci}^2 + \sigma_{Ei}^2}\]

\[r_{HW,SRS} = \frac{\sigma_{aHW,aSRS}}{\sqrt{\sigma_{aHW}^2 \sigma_{aSRS}^2}}\]
Results

Kaplan–Meier survival curves of the best and the worst family and an average of the 108 families

Kaplan–Meier survival curves of the replicated tanks

Significant phenotypic variation for resistance against *P. salmonis* with cumulative survival rates ranging from 18% to 95%
Results

Variance components, heritabilities, genetic and phenotypic correlations for harvest weight (HW) and *Piscirickettsia salmonis* resistance (SRS). (± = Standard Error)

<table>
<thead>
<tr>
<th></th>
<th>HW</th>
<th>SRS</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\sigma^2_p$</td>
<td>0.56 ± 0.01</td>
<td>79.3 ± 2.46</td>
</tr>
<tr>
<td>$\sigma^2_a$</td>
<td>0.06 ± 0.002</td>
<td>11.1 ± 2.84</td>
</tr>
<tr>
<td>$\sigma^2_c$</td>
<td>0.05 ± 0.007</td>
<td>-</td>
</tr>
<tr>
<td>$\sigma^2_e$</td>
<td>0.44 ± 0.01</td>
<td>68.1 ± 2.56</td>
</tr>
<tr>
<td>$h^2$</td>
<td>0.12 ± 0.03</td>
<td>0.14 ± 0.03</td>
</tr>
<tr>
<td>$r_g$</td>
<td>HW</td>
<td>-0.50 ± 0.20</td>
</tr>
<tr>
<td>$r_p$</td>
<td>SRS</td>
<td>-0.06 ± 0.03</td>
</tr>
</tbody>
</table>
Conclusions

• Heritabilities for **HW** and **SRS** demonstrate the feasibility to improve these traits by selective breeding.

• The unfavorable genetic relationship between these traits must be accounted for when including them simultaneously into the breeding objective of coho salmon breeding programs (selecting for specific strains)
Future directions

Determining the genomic architecture of *P. salmonis* resistance in coho salmon and incorporating genomic information into the genetic evaluations to accelerate the genetic progress.
Thank you!

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