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

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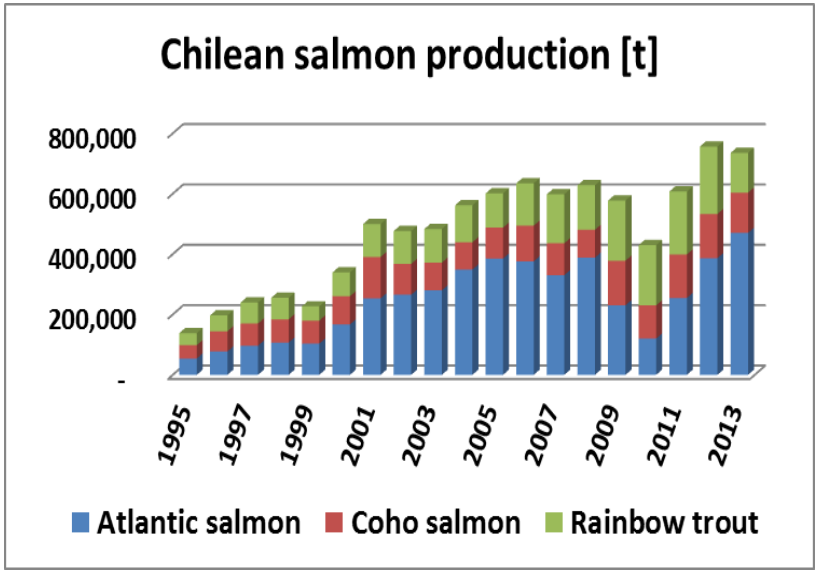
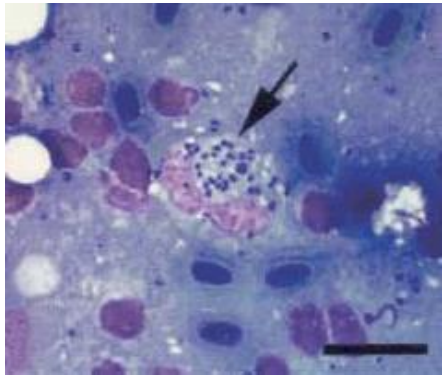
Introduction

- **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

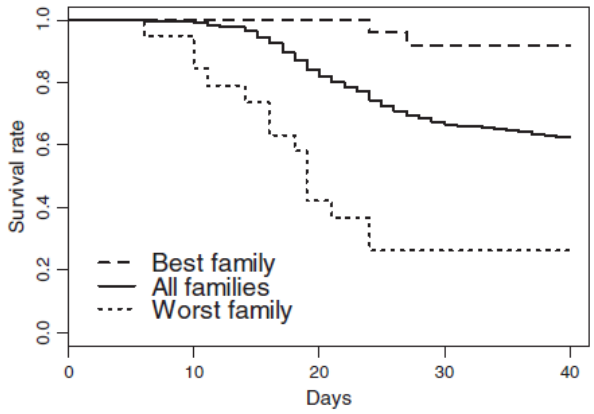


Fryer and Hedrick (2003)

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)

Phenotypic variation of **SRS resistance** across 118 FS families



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Quantitative genetic variation of resistance against *Piscirickettsia salmonis* in Atlantic salmon (*Salmo salar*)

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Genetic co-variation between resistance against both *Caligus rogercresseyi* and *Piscirickettsia salmonis*, and body weight in Atlantic salmon (*Salmo salar*)

José M. Yáñez [a,b,*], Jean P. Lhorente [b], Liane N. Bassini [b,c], Marcela Oyarzún [b], Roberto Neira [b,c], Scott Newman [d]

Piscirickettsia salmonis resistance in salmonids

The International Symposium on Genetics in Aquaculture XII 21st-27th June 2015 in Santiago de Compostela, Spain

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

R. Bangera [1,2] / J. P. Lhorente [1] / M. Oyarzun [1] / J.M. Yañez [1,3]

Rama Bangera

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

Correa K.[1,2] / Lhorente J.P.[2] / López M.E.[2,3] / Figueroa, R.[2] / Bassini L.[2,3] / Di Genova A.[4] / Maass A.[4] / Davidson W.[5] / Yáñez, J.M. [1,2]

Katharina Correa

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

Bassini N.L.[1,2] / Neira R.[2] / Yáñez J.M.[1,3] / Newman S.[4] / Oyarzún M.[1] / Erranz F.[1] / Figueroa R.[1] / Lhorente J.P.[1].

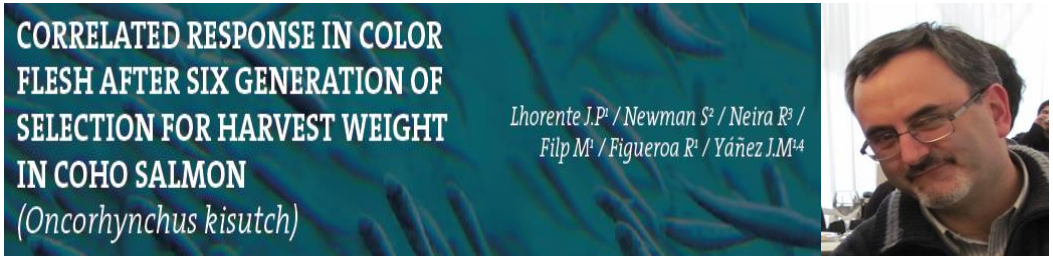
Liane Bassini

Objective

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)

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

$\mathbf{y_1}$ and $\mathbf{y_2}$ are vectors of observations for **HW** and **SRS** (day of death)

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

$\mathbf{b_2}$ is the vector of fixed effects for **SRS** (tank and weight at the end of the test)

$\mathbf{u_i}$ and $\mathbf{e_i}$ are vectors of random animal genetic and residual effects, respectively

$\mathbf{c_1}$ is the vector of random common environment effect for **HW**

$\mathbf{X_i}$ and $\mathbf{Z_i}$ are the design matrices linking fixed and random effects to observations

$\mathbf{W_1}$ is the design matrix for **HW**

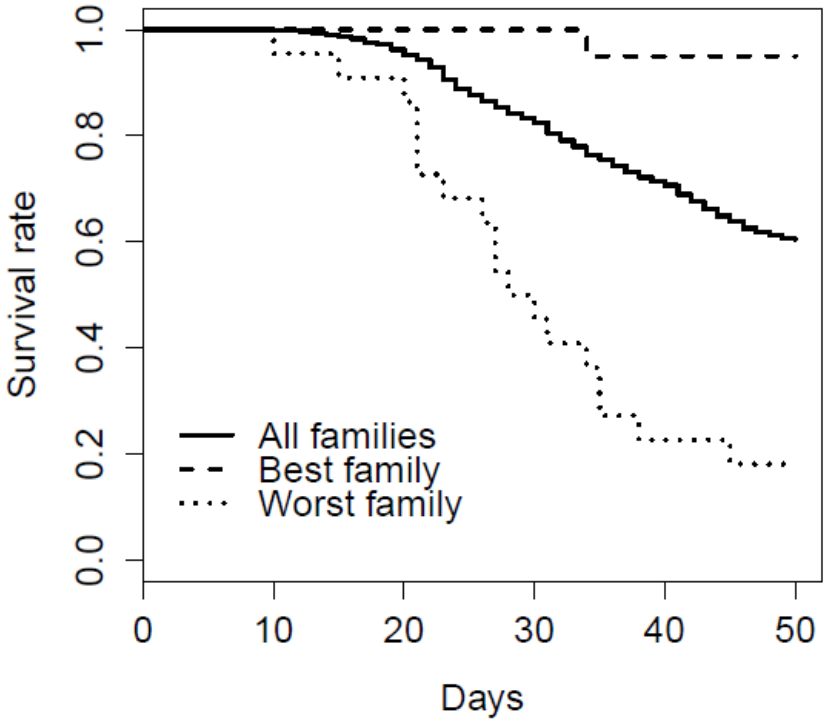
Heritabilities and genetic correlations

$$\boldsymbol{h_i^2} = \frac{\sigma_{Gi}^2}{\sigma_{Gi}^2 + \sigma_{Ci}^2 + \sigma_{Ei}^2}$$

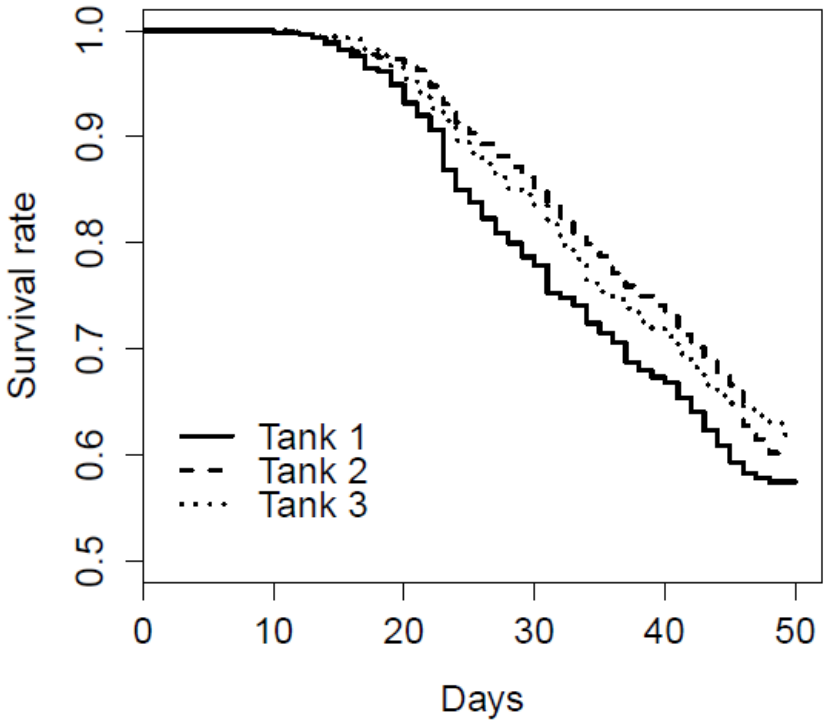
$$\boldsymbol{r_{HW,SRS}} = \frac{\sigma_{aHW,aSRS}}{\sqrt{\sigma_{aHW}^2 \ \sigma_{aSRS}^2}}$$

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)

		HW	SRS
	σ^2_p	0.56 ± 0.01	79.3 ± 2.46
	σ^2_a	0.06 ± 0.002	11.1 ± 2.84
	σ^2_c	0.05 ± 0.007	-
	σ^2_e	0.44 ± 0.01	68.1 ± 2.56
	h^2	**0.12 ± 0.03**	**0.14 ± 0.03**
r_g	**HW**	-	**-0.50 ± 0.20**
r_p	**SRS**	-0.06 ± 0.03	-

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.

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