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

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ABSTRACT

Infectious and parasitic diseases are recognized worldwide as primary causes of economic losses in salmon production. *Piscirickettsia salmonis* and *Caligus rogercresseyi* are the main diseases affecting the Chilean salmon aquaculture. In this study, we used data from experimental challenges against *P. salmonis* and *C. rogercresseyi* in full- and half-sibs from 118 families belonging to a *Salmo salar* breeding nucleus. Resistance against *P. salmonis* (SRS) was defined as the day of death of each fish and *C. rogercresseyi* resistance (CAL) was measured as the parasite load. We also measured body weight (BW) in full-sibs of the tested fish. We used a multi-trait animal model to estimate (co)variance components and to calculate genetic parameters. For BW we included contemporary group (sex*tank) as factor and age as a covariate. In addition, tank was included as a factor and weight at the end of test as a covariate for SRS and CAL. The estimated heritabilities for BW, SRS and CAL were 0.4 (±0.05), 0.18 (±0.03) and 0.1 (±0.03), respectively. The genetic correlations between BW–SRS, BW–CAL and SRS–CAL were −0.19 (±0.12), −0.32 (±0.14) and −0.02 (±0.17), respectively. The levels of genetic variation and the magnitude of the genetic correlations between resistance to *P. salmonis*, *C. rogercresseyi* and body weight found in the present study demonstrate the feasibility for the improvement of these traits simultaneously by means of selective breeding.

1. Introduction

Two of the main disease-causing agents affecting profitability of the Chilean salmon culture are *Piscirickettsia salmonis* and *Caligus rogercresseyi*. *P. salmonis* is an intracellular bacterium first isolated in Chile from coho salmon (*Oncorhynchus kisutch*) (Cvitanich et al., 1991). Currently, it has been found to be affecting several fish species, including Atlantic salmon (*Salmo salar*) (Fryer and Hedrick, 2003). The systemic infection caused by *P. salmonis*, also called Salmon Rickettsial Syndrome, is one of the main causes of mortality in seawater in the Chilean salmon farming (Rozas and Enríquez, 2014).

Caligidosis produced by *C. rogercresseyi* has generated annual losses over 170 million US dollars in the global salmon industry, mainly due to the cost of chemical drugs for controlling it and the loss of quality in the harvested product (Costello, 2009). *C. rogercresseyi* is a copepod ectoparasite, endemic to Chile, which has been transmitted to farmed salmon from native fish (Carvajal et al., 1998). It is the only louse species affecting fish in the grow-out stage in sea conditions in Chile (Boxshall and Bravo, 2000). *C. rogercresseyi* does not normally cause direct death, but rather produces chronic stress, reduces appetite, causes immunosuppression and damage to skin (Bravo et al., 2008).

Resistance to specific pathogens, together with other economically important traits (e.g. growth-related traits, which are typically measured as body weight), should be included in the breeding goal for economic and sustainability purposes (Gjedrem, 2000, 2012; Ødegård et al., 2011). Nevertheless, to include disease resistance traits into the breeding objective requires an understanding of the genetic (co)variation of these and other traits. There is considerable evidence showing that genetic variation for different diseases in salmonids exists (Ødegård et al., 2011; Yáñez and Martínez, 2010). Significant genetic variation has been demonstrated for both resistance against *C. rogercresseyi* (Lhorente et al., 2012) and *P. salmonis* (Yáñez et al., 2010, 2013). However, genetic correlations between resistance to these two specific diseases and other economically important traits, such as body weight, have not been assessed up to now in Atlantic salmon. The purpose of this study was to determine levels of genetic (co)variation for resistance against both *P. salmonis* and *C. rogercresseyi*, and body weight in Atlantic salmon using a multi-trait approach.

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2. Materials and methods

2.1. Fish

We used Atlantic salmon (*S. salar*) individuals belonging to 118 maternal full-sib families (40 paternal half-sib families) from the 2010 year–class of the breeding program of Salmones Chaicas (Puerto Montt, Chile). Each fish was tagged using PIT-tags (Passive Integrated Transponder) placed into the abdominal cavity, at an average weight of 13.1 (SD = 3.4) gm, for retaining genealogy traceability. A group of tagged fish was reared in a communal tank about 14 months before transfer to Aquainnovo's Research Station located in Lenca River, Xth Region, Chile, to perform experimental challenges. Another group of 9,280 tagged fish from the same 118 full-sib families was kept at an inland site located in Chaicas River, Xth Region, Chile. In these fish, body weight (BW) was recorded approximately 27 months after spawning (Table 1). In this case, the number of fish in tank 3C was lower than in tanks 1C and 2C because the former was smaller, thus we kept similar culture density between tanks during the grow-out period.

2.2. Challenge tests

The challenge test against *P. salmonis* was performed as described by Yáñez et al. (2013). Briefly, infection was induced in 2,601 fish through intra-peritoneal (IP) injection with 0.2 ml of a LD50 inoculum of *P. salmonis*. Post-injection, infected fish were distributed in three different tanks with salt water (31 ppt): 1A, 2A and 3A. The challenge test against *C. rogercresseyi* was carried out as described by Lhorente et al. (2012). Briefly, 2628 fish were randomly distributed in three tanks with salt water (31 ppt): 1B, 2B and 3B (876 fish per tank). The infestation with copepods in sessile stage (chalimus II and III) was performed using 21,000, 20,250 and 11,640 parasites (about 24, 23 and 13 copepods per fish) for tanks 1B, 2B and 3B, respectively. These differences were due to parasite availability at the day of infestation. During the infestation, we stopped the water flow of each tank and maintained a water temperature at 13 °C for a period of 6 h. Six days post-infestation the challenge was completed and pectoral, ventral, anal, caudal and dorsal fins of each fish were collected and fixed for further processing and counting. In both challenges a similar number of fish from each of the 118 full sib families were placed on each tank (Table 1).

2.3. Records and trait definitions

We defined resistance to *P. salmonis* (SRS) as day of death, which ranged from 1 to 40 depending on the day of mortality, thus the more survival time, the more resistant fish. *Caligus* resistance (CAL) was defined as the number of sessile lice per fish on all fins after six days of infestation, thus the lower CAL (parasite load), the more resistant fish. Body weight (BW) was measured in full-sibs of the challenged fish at an average of 1 kg.

2.4. Model

We used the following multi-trait linear animal model to estimate (co)variance components, heritabilities and genetic correlations for SRS ($\mathbf{y_1}$), CAL ($\mathbf{y_2}$) and BW ($\mathbf{y_3}$):

$$\begin{bmatrix}\mathbf{y}_1\\ \mathbf{y}_2\\ \mathbf{y}_3\end{bmatrix} = \begin{bmatrix}\mathbf{X}_1 & 0 & 0\\ 0 & \mathbf{X}_2 & 0\\ 0 & 0 & \mathbf{X}_3\end{bmatrix}\begin{bmatrix}\mathbf{b}_1\\ \mathbf{b}_2\\ \mathbf{b}_3\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_1 & 0 & 0\\ 0 & \mathbf{Z}_2 & 0\\ 0 & 0 & \mathbf{Z}_3\end{bmatrix}\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \mathbf{u}_3\end{bmatrix} + \begin{bmatrix}\mathbf{e}_1\\ \mathbf{e}_2\\ \mathbf{e}_3\end{bmatrix}$$

where $\mathbf{y_1}$, $\mathbf{y_2}$ and $\mathbf{y_3}$ are vectors of records for the fish measured for SRS, CAL and BW, respectively; $\mathbf{b_1}$ and $\mathbf{b_2}$ are vectors of fixed effects for SRS and CAL, respectively (tank as factor and weight at the end of test as a covariate); $\mathbf{b_3}$ is the vector of fixed effects for BW (contemporary group of sex*tank as factor and age at sampling time as a covariate); $\mathbf{u_i}$ and $\mathbf{e_i}$ are vectors of random animal genetic and residual effects, respectively, for trait i (= 1, 2, 3); and $\mathbf{X_i}$ and $\mathbf{Z_i}$ are the appropriate design matrices for trait i (= 1, 2, 3).

For all traits, both animal and residual effects were assumed random: $\mathbf{u} = [\mathbf{u}_1'\mathbf{u}_2'\mathbf{u}_3']' \sim N(\mathbf{0}, \mathbf{G_0} \otimes \mathbf{A})$, $\mathbf{e} = [\mathbf{e}_1'\mathbf{e}_2'\mathbf{e}_3']' \sim N(\mathbf{0}, \mathbf{R_0} \otimes \mathbf{I_N})$ where $\mathbf{A}$ is the additive genetic relationship matrix, $\mathbf{I}$ is an identity matrix with dimension N, and ⊗ represents the direct product operator. $\mathbf{G_0}$ and $\mathbf{R_0}$ represent the (co)variance matrices of animal additive genetic and residual effects, respectively. We excluded a random effect associated with common environment of full-sibs from the model because this effect was not significant ($P < 0.05$) based on a likelihood ratio test. The multi-trait model described above was fitted using ASREML software (Gilmour et al., 2009) to estimate (co)variance components.

2.5. Heritabilities and genetic correlations

For each trait i (= 1, 2 and 3) the heritability was calculated as

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

where σ_{Gi}^2 and σ_{Ei}^2 are the additive genetic and residual variances from $\mathbf{G_0}$ and $\mathbf{R_0}$ matrices, respectively. The genetic correlation (r_{xy}) between two traits x and y was defined as (Falconer and Mackay, 1996):

$$r_{xy} = \frac{\sigma_{ax,ay}}{\sqrt{\sigma_{ax}^2\sigma_{ay}^2}},$$

Table 1
Summary statistics for each trait: resistance against *Piscirickettsia salmonis*, resistance against *Caligus rogercresseyi* and body weight, by each replicated tank in Atlantic salmon (standard deviation in parenthesis).

Trait	Tank	n[a]	n/family	Mean	CV[b]	Min	Max	BW test[c]	Age[d]
Piscirickettsia salmonis resistance[e]	1A	860	7.3 (1.2)	32.9 (9.6)	29.3	1	40	0.323 (0.014)	–
	2A	867	7.3 (1.1)	33.7 (9.6)	28.6	3	40	0.321 (0.013)	–
	3A	874	7.4 (1.1)	32.9 (9.9)	30.2	4	40	0.323 (0.014)	–
Caligus rogercresseyi resistance[f]	1B	827	7.0 (1.2)	1.62 (1.5)	95.5	0	7	0.277 (0.009)	–
	2B	809	6.9 (1.3)	5.36 (3.6)	66.4	0	15	0.284 (0.009)	–
	3B	813	6.9 (1.2)	8.36 (4.8)	57.1	0	22	0.279 (0.009)	–
Body weight[g]	1C	3797	49.4 (1.3)	0.99 (0.3)	26.7	0.3	1.74	–	832.3 (13.15)
	2C	3888	49.3 (1.4)	1.00 (0.3)	25.9	0.31	1.74	–	831.9 (13.21)
	3C	1595	19.8 (0.5)	1.11 (0.3)	26.9	0.31	1.99	–	829.0 (12.02)

[a] Number of analyzed fish after filtering by interquartile range rule and removing missing values.
[b] Coefficient of variation.
[c] Body weight measured in kilograms at the end of the challenge test.
[d] Age at the recording time measured in days post fecundation.
[e] *P. salmonis* resistance measured as the day of death after 40 days of the experimental challenge.
[f] *C. rogercresseyi* resistance measured as the number of sessile lice per fish on all fins after six days of experimental infestation.
[g] Body weight measured in kilograms.