GENETIC VARIATION FOR CLIMATE CHANGE RESILIENCE IN GROWTH OF ATLANTIC SALMON

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Introduction

The presence genetic by environment interaction (GxE) tells that strains respond differently to changes in environmental/ climate parameters. Existence of such variation may hinder the optimal realization of genetic gain and affects the competitiveness of aquaculture industry. However, estimates of GxE are lacking for many economically important traits (Sae-Lim et al, 2016), and need to be assessed to enable optimization of breeding programs towards development of robust genetic material for future conditions. Climate changes and increased water temperature may cause higher risk for certain disease outbreaks in aquaculture (Towers, 2015, Khaw et al., 2019), and consequently selective breeding for better robustness is of interest. The aim of this work is to assess the genetic variation for climate resilience in growth traits in A. salmon.

Materials and Methods

Two parallel experiments were conducted at Austevoll, Institute of Marine Research (as SOUTH station) and Sauaneset locality of Gildeskål Research station, GIFAS, (as NORTH station). A total of 2,190 PIT tagged fish from 75 families from Benchmark Genetics Norway population yearcalss 2019 were transported to the experiment stations at the end of October 2019 and transferred to sea cages. There were two cages at each experiment station and the fish were fed the same 'conventional' fish diet. Environmental parameters such as temperature, salinity and oxygen, mortality, lice count, and wound were recorded weekly during the experiment period. Experiment at the SOUTH station was terminated at mid May 2020 and the NORTH station was terminated at early August 2020. At termination, body weight, length, wound and deformities, and sexual maturity were recorded.

In addition to body weight, thermal growth coefficient (TGC = [(end_weight^1/3) – (initial_weight^1/3)]/day*degree) was calculated and used as phenotypes. Multivariate model treating phenotypes at each experiment location as different traits was fitted to estimate the genetic parameters using restricted maximum likelihood in BLUPF90 (Misztal et al., 2018). Genomic relationship matrix was used in the estimation.

Results and Discussion

The mortality rate and average body weight at termination were 19.4% and 965g at the SOUTH station, and 18.6% and 1580g for the NORTH station, respectively. The monthly temperature variation at each station during the experiment are presented in Figure 1.

Heritability estimates for body weight at the different location ranged from moderate to high (0.39 – 0.62, Table 1). These estimate for the thermal growth rate (TGC) were also ranged form moderate to high (Table 1). Full-sib group effect (c^2) were not significant for any of the traits and not presented here. Genetic correlation estimate was very high between body weight measured at the two locations (0.99, Table 1). The genetic correlation for TGC was also very high but lower than that of end weight (0.88, Table 1)

The results showed there is limited re-ranking for growth, which indicates that either there exits limited genetic variation in climate change resilience, or the current breeding population is robust towards climate change.
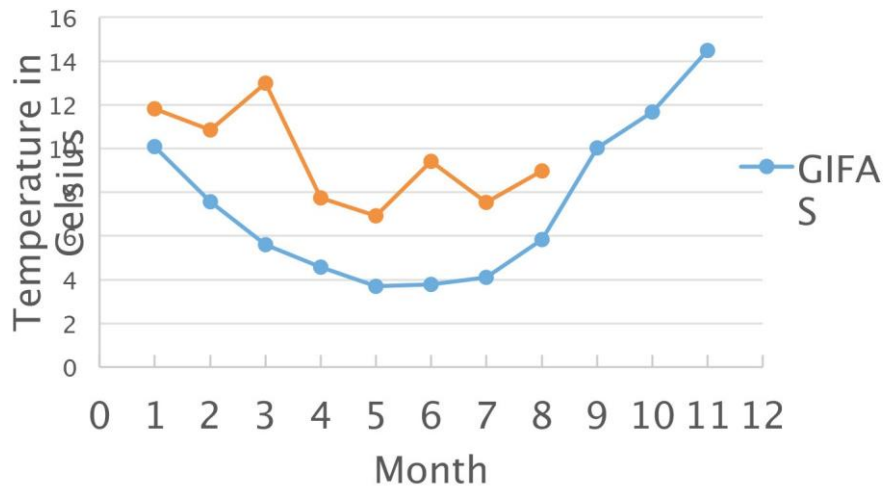
Figure 1:Average monthly temperature measurements in °C at the experimental locations. GIFAS is the NORTH location and IMR is the SOUTH location.

Table 1: Heritabilities and genetic correlations for end weight (EW) and TGC measured at different locations.

Traits	End weight (EW)		TGC	
	SOUTH	NORTH	SOUTH	NORTH
SOUTH	0.62±0.03		0.60±0.04	
NORTH	0.99±0.06	0.39±0.02	0.88±0.08	0.49±0.03

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