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GENOTYPE-BY-ENVIRONMENT INTERACTIONS IN YELLOWTAIL KINGFISH: IMPLICATIONS FOR GENETIC IMPROVEMENT

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SUMMARY

New Zealand's National Institute of Water and Atmospheric Research (NIWA) supports a genomics-based genetic improvement programme for *Seriola lalandi* (Yellowtail Kingfish or Haku in te reo Māori). Supplying genetically elite larvae, fry, and broodstock to diverse production systems, requires an understanding of potential genotype-by-environment (GxE) interactions and influence the configuration and design of the programme. We raised genetically related groups of progeny in tanks configured for either flow-through (FT) or recirculation (RAS) and estimated the between-environment genetic correlations for harvest length (HL) and harvest weight (HW). The genetic correlation estimates were modest (0.46 – 0.57) suggesting that GxE is quite strong and should be taken into consideration in the programme design.

INTRODUCTION

New Zealand's National Institute of Water and Atmospheric Research (NIWA) has recently initiated a genomics-based genetic improvement programme to improve production traits in *Seriola lalandi* (Yellowtail Kingfish or Haku in te reo Māori). The programme aims to supply genetically elite larvae, fry, and broodstock to the rapidly growing, global kingfish industry, which currently uses several growout systems. Consequently, the configuration and design of the programme must consider the potential for genotype-by-environment (GxE) interactions. If different genotypes are favoured in different systems, we could either select for generalist genotypes, potentially at the expense of performance in specific systems, or for specialist genotypes for specific systems.

GxE interactions are quantified using multi-trait genetic analyses with the same phenotype in different environments/systems treated as different traits (Falconer and Mackay 1996). High favourable between-environment genetic correlations indicate similar genetic architectures and responses to selection. High unfavourable genetic correlations imply that "winners" in one environment are "losers" in others because many genetic variants have opposite effects in different environments. Near zero genetic correlations suggest that different genes control variation in the same trait in the different environments.

In this paper, we report the between-environment genetic correlations between harvest weight (HW) and harvest length (HL) in a research-scale high density recirculating aquaculture system (RAS) and, because there is no sea cage production in New Zealand and biosecurity considerations prohibited exporting live juveniles, an identical system configured for single-pass flow-through (FT) and lower density as an admittedly rough proxy for alternative systems such as sea cages.

MATERIALS AND METHODS

Because it is impractical to strip spawn Haku for designed mating plans, we used group spawning in six large spawning tanks to produce our experimental fish. Between 15 October and 19 November 2020, we collected fertilised eggs from 13 spawning events and pooled them into five larger

temporal groups for larval rearing in RAS. We reared the later-spawning groups at a slightly higher temperature for a shorter time to equalise sizes at the tagging stage (~165g after an average of 187 and 160 days of growth), after which we combined and distributed them randomly but unevenly into the RAS and FT systems to mimic commercial densities. The FT system received mechanically filtered and UV sterilized seawater from Bream Bay NZ. The RAS used mechanical drum filtration, moving bed biofiltration, a protein skimmer and UV treatment. RAS tanks had a 24h light photoperiod and FT an ambient photoperiod. We automatically fed the RAS tanks 10 times over 24 hours and FT tanks hourly during daylight hours. We split the RAS fish into two tanks approximately halfway through growout to maintain commercially relevant densities, but not the FT fish. We fed both systems a ration based on NIWA's size and temperature-dependent growth model (unpublished). Figure 1 shows the between systems and temporal variation in temperature and dissolved oxygen.

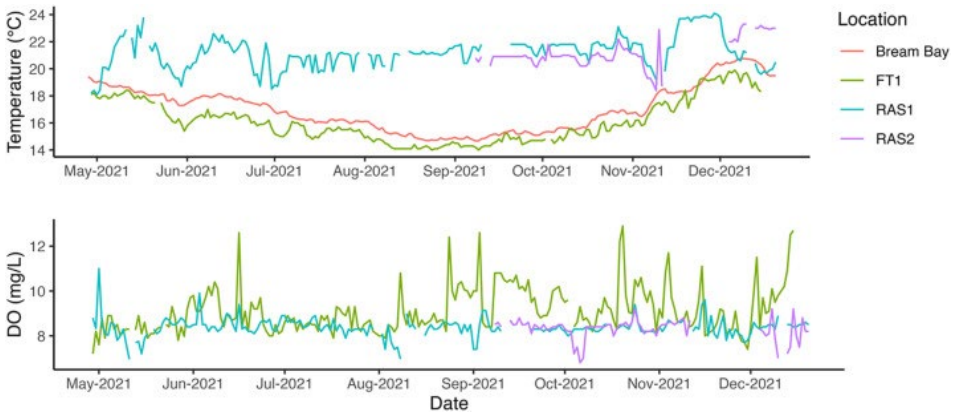

Figure 1. Temperature and DO (dissolved oxygen) variation in Bream Bay and the experimental systems

We measured harvest weight (HW) and harvest length (HL) on all experimental fish after 378 days (RAS, n=1820, mean HW ~1.9kg) and 412 days (FT, n = 306, mean HW ~1.4kg), and collected a 3mm fin clip stored in 100% ethanol. We sent these and parental fin clip samples to AgResearch (Lincoln, New Zealand) for genotyping using genotyping-by-sequencing (GBS, Elshire *et al*. 2011), parentage assignment, and genomic relationship estimation using R scripts developed by AgResearch (Dodds *et al*. 2015, Dodds *et al*. 2019). Based on the parentage assignments, individuals were also assigned to their spawning/hatching events (HatchGroup). Downstream data processing and analyses used R software (R Core Team 2024).

Statistical analysis. We fitted a four-trait animal model treating the same trait measured in different environments treated as separate traits using ASReml-R (Butler 2023) in the following model:

$$y_{i,j,k,l} = u_i + \text{HatchGroup}_j + \text{Tanks(Env)}_{i,k} + r_l + e_{i,j,k,l}$$

where:$y_{i,j,k,l}$ is a vector of phenotypic values of the four traits (HW-RAS, HL-RAS, HW-FT, and HL-FT); u_i is a vector containing the mean for the four traits (i=1-4); HatchGroup is a fixed effect to account for differences between the five batches of experimental fish produced on different dates (j = 1-5); $\text{Tanks(Env)}_{i,k}$ is the fixed effect for the combination of tanks a fish passed through, nested within each environment (k = 1-2 for FT, 3-6 for RAS); r_l is random additive genetic effect of the l-th individual; $e_{i,j,k,l}$ is a vector of random residuals for each individual l. The between-environment

residual covariances are assumed to be zero because individual fish only have data from one of the two environments.

The heritability for each trait was estimated as the additive genetic variance ($\sigma^2{}_a$) divided by the phenotypic variance ($\sigma^2{}_p$), $h^2 = \frac{\sigma^2 a}{\sigma^2{}_p}$ and the between-environment genetic correlations as the genetic correlation $r_{a,RjFj}$ of the same trait j in different systems as $r_{a,RjFj} = \frac{COV(\sigma^2{}_{a,Rj}, \sigma^2{}_{a,Fj})}{\sigma_{a,Rj}\sigma_{a,Fj}}$.

RESULTS AND DISCUSSION

Table 1 presents the estimated (co)variance components. Table 2 presents the heritabilities, genetic, and phenotypic correlations between the four traits. These estimates indicate that all four traits are sufficiently genetically variable and heritable for improvement. As well, the between-environment genetic correlations that represent the magnitude of GxE are all moderate (0.46 to 0.61), indicating that there is substantial re-ranking of the parents between the two environments.

Table 1. Additive genetic variance (σ_a^2), residual variance (σ_E^2), and phenotypic variance (σ_P^2 for both traits in both environments estimated with the G from the full GBS dataset. Standard errors are shown in parenthesis, HL = Harvest Length, HW = Harvest Weight, RAS = Recirculating Aquaculture System, FT = Flow Through System

TRAIT	ENVIRONMENT	σ_a^2	σ_E^2	σ_P^2
HL	RAS	3.96 (0.40)	3.63 (0.20)	7.59 (0.33)
HW	RAS	0.066 (0.006)	0.047 (0.003)	0.11 (0.005)
HL	FT	2.54 (0.62)	1.60 (0.39)	4.14 (0.39)
HW	FT	0.034 (0.007)	0.015 (0.004)	0.05 (0.005

As the two production systems were smaller-scale analogues of commercial farms, more research is required to rigorously extend these analyses to real-world production systems and to identify the specific environmental factors that drive them using more complex models (Sae-Lim *et al*. 2014). However, the differences between the two environments in the current study were most likely smaller than those between commercial RAS and alternative production systems such as sea cages. As a "rule of thumb" breeders consider between-environment genetic correlations < 0.8 as potentially problematic as they indicate substantial re-ranking of selection candidates (Robertson 1959) and therefore different selection decisions.

Table 2. Genetic correlations (se), below shaded diagonal; phenotypic correlations (se), above shaded diagonal; and heritabilities (se, shaded diagonal for both traits in both environments. n.e. = non- estimable phenotypic correlations due to fish being in different environments. HL = Harvest Length, HW = Harvest Weight, RAS = Recirculating Aquaculture System, FT = flow through system

	HL-RAS	HL-FT	HW-RAS	HW-FT
HL-RAS	0.52 (0.03)	n.e.	0.90 (0.01)	n.e.
HL-FT	0.57 (0.10)	0.61 (0.11)	n.e.	0.88 (0.01)
HW-RAS	0.92 (0.01)	0.46 (0.10)	0.59 (0.03)	n.e.
HW-FT	0.54 (0.10)	0.88 (0.04)	0.54 (0.10)	0.70 (0.10)

More quantitatively these estimated genetic correlations imply that if selection was undertaken exclusively in one of these production systems, approximately half to 60% of the genetic gain

generated would transfer to the other system. Consequently, these patterns may have important implications for the design of the genetic improvement programme.

The most obvious option to address this complication is to establish largely separate breeding programmes to maximise the rate of genetic gain in specific production systems. However, that approach dramatically increases the costs of the programme(s) and/or constrain the utility of the genetic gains produced. An alternative is to select for stable performance across production systems (i.e. generalists) that perform well in a range of conditions. This "norm of reaction" approach (Sae-Lim *et al*. 2014) would likely result in slower genetic gain in all systems but is simpler and less costly than setting up separate breeding programmes for each production system and would produce "across-the-board" benefits for all producers. A third option is to estimate breeding values in multiple environments in a single programme and offer producers custom spawns between parents with high breeding values in their systems. This would likely require maintaining a larger population of candidates to provide a wider range of options.

CONCLUSION

GxE interactions between research-scale RAS and alternative production systems represented by FT are strong enough to complicate the design and implementation of genetic improvement programmes producing genetic gain to a range of Haku production systems. More research is required to extend these conclusions to real world systems and identify the causal environmental parameters driving these interactions.

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