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GROWING AOTEAROA NEW ZEALAND'S AQUACULTURE INDUSTRY THROUGH BREEDING AND GENOMICS: PROGRESS, CHALLENGES AND FUTURE OPPORTUNITIES

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SUMMARY

The aquaculture industry in Aotearoa New Zealand recognises that the application of selective breeding is an essential part of its business and is an important way to generate cumulative production and product quality gains. Many of the larger finfish and shellfish companies have established in-house breeding programmes and selected juveniles can also be accessed from breeding programmes established by research organisations. Three salmon farming companies are applying genomic selection, including a smaller company where genomic selection based on genotyping-by-sequencing is cost-effective. Within these programmes, significant genetic gains have been demonstrated across multiple generations. New traits such as thermotolerance and summer survival, needed to combat climate change, have been identified as new priorities for selection in finfish and shellfish. Families have been phenotyped and estimated breeding values generated to accelerate selection for climate change resilience. Two new finfish species, kingfish and snapper, are also being developed for aquaculture with multi-generation breeding programmes already in place. Selective breeding enhanced by genomic selection provides the industry with an essential climate change adaptation tool to ensure future survival and growth.

INTRODUCTION

Selective breeding (i.e. artificial selection), has made a significant contribution to the growth of Aotearoa New Zealand's aquaculture industry (Camara and Symonds 2014; Symonds *et al*. 2019). The first family-based breeding programmes were established in the 1990s and have been the foundation for improved stock management and significant production gains in all three key farmed species (Pacific oysters (*Crassostrea gigas)*, Greenshell™ mussels (*Perna canaliculus)* and King (Chinook) salmon (*Oncorhynchus tshawytscha*)). A genomic-based selective breeding programme for recently commercialised yellowtail kingfish (haku in te reo Māori) (*Seriola lalandi*) has also been established, and pre-commercialisation selective breeding of Australasian snapper (tāmure in te reo Māori) (*Chrysophrys auratus*) is underway. In contrast to terrestrial livestock, fish and shellfish have very high fecundity, shorter generation intervals (2-3 years), and relatively high heritabilities for economically important traits. These are key factors which define the design of breeding programmes in aquaculture. Breeding objectives have become more complex over the years with harvest quality traits and survival, as well as growth, all now being part of the selection process. Marine heatwaves are occurring more frequently around coastal Aotearoa New Zealand (Montie *et al*. 2024) and are often considered to be an important causal factor for summer mortality (Copedo *et al*. 2023; Ericson *et al*. 2023). These warming waters have generated new challenges for the aquaculture industry (Cummings *et al*. 2021; Greenhough *et al*. 2025) and for some companies heat tolerance is now a key trait in their breeding objectives. To enhance selection and provide more accurate gains for critical climate resilience traits, genomics resources are now available for all dominant farmed species and are applied by multiple salmon farming companies. This paper summarises the history of aquaculture selective breeding in Aotearoa New Zealand, discusses the successes and future challenges, and shows how selective breeding and genomics can help overcome these to enable future growth.

MATERIALS AND METHODS

Programme design, breeding objectives and selection strategies. For salmon, the first breeding programme was established in 1994 and was based on the production of full and half-sib families. Since then, two additional commercial salmon breeding programmes have been established, based on family or individual evaluation and genomic selection. A typical family-based breeding programme design for salmon is shown in Figure 1.

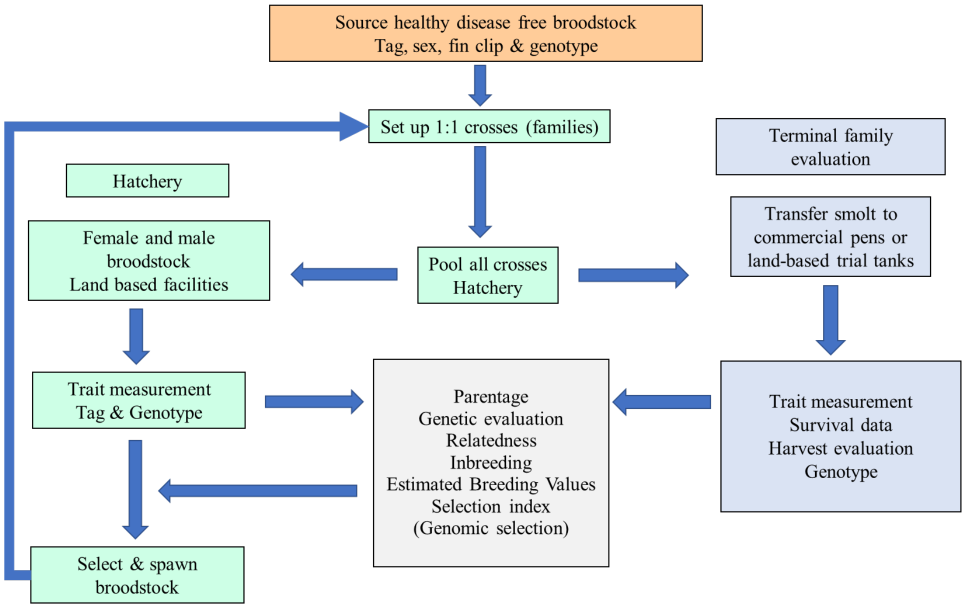

Figure 1. Example outline of a salmon breeding programme

Growth, usually based on weight at harvest or weight prior to spawning, is a priority trait for all three salmon programmes. In the family-based programmes quality traits are also included such as fillet colour and fat. More recently survival traits and thermotolerance have been introduced as priority breeding objectives. Thermotolerance (specifically, the ability to endure elevated water temperatures) is assessed in tank-based temperature challenges using families, and/or by evaluation of the survival of the same families over summer in a farm-based sea pen (Symonds *et al*. 2025).

Greenshell™ mussels (GSM), have been selectively bred since 2002 using family-based selection. The initial traits focussed on yields: shell length, meat weight and meat condition score, and were associated with significant heritabilities and substantial genetic gain. Traits were often evaluated at multiple farm sites to account for genetic x environment interactions. More recently, resilience traits, including thermotolerance to improve survival and growth during periods of elevated temperature, have been investigated and found to be significantly influenced by genetics (Delorme *et al.* 2024, Ericson *et al.* 2024; Scholtens *et al.* 2025). Phenotypic selection for GSM thermotolerance is possible utilising tank-based challenges and/or field assessments of summer survival.

The Cawthron Institute initiated a family-based Pacific oyster breeding programme in 1999 with the initial objectives of breeding for fast-growing oysters with good shell shape and a high meat-to-shell ratio using a combination of between- and within-family selection (Camara and Symonds 2014). In 2010, sudden mass mortalities of both cultured and wild oyster populations on the North Island and in Cawthron's oyster hatchery on the South Island, were caused by a highly pathogenic variant of the oyster herpes virus (OsHV-1 µ-var). This led to a shift in the programme's objectives and strategies, with surviving broodstock selected from field trials at OsHV-1infected sites. While OsHV-1 has become naturalised in most New Zealand oyster populations, commercial survival rates have rebounded thanks, substantially, to selective breeding. The current breeding strategy now combines survival, growth and quality traits, such as shell shape. Families are typically evaluated on multiple sites to account for genetic x environment interactions.

Genetic parameter estimation. Methods for evaluating key traits for the three major species have previously been published (Camara and Symonds 2014; Camara *et al.* 2017; Symonds *et al.* 2018, 2019, 2025; Gutierrez *et al.* 2020; Ericson *et al.* 2023; Scholtens *et al.* 2022, 2023, 2025). The number of families evaluated typically ranges from 20 to 135 depending on the species. Genetic models are usually fitted using Restricted Maximum Likelihood as implemented in standard software such as ASReml (Gilmour *et al.* 2009). More details of the statistics and animal models can be found in the publications above.

Genotyping-by-sequencing (GBS) for commercial and research evaluations is routinely conducted by GenomNZ (AgResearch) for salmon (Symonds *et al.* 2019; Scholtens *et al.* 2022). These evaluations include families and/or broodstock in two commercial salmon breeding programmes (Scholtens *et al.* 2023). The application of GBS includes parentage assignment, estimating genomic relatedness matrices, inbreeding, and measures of genetic diversity. GBS methods have also been developed for selective breeding programmes in kingfish (Jacob *et al.* 2025), for GSM (Ashby *et al.* 2018; Hess *et al.* 2018) and Pacific oysters (Vignier *et al.* 2025) but are not yet routinely applied in commercial shellfish breeding programmes. All these applications make use of the cost-effective GBS methods developed by AgResearch, implemented in the open-source software KGD (Dodds *et al.* 2015).

Genomic selection (GS) is employed by all salmon commercial breeding programmes, the snapper and the kingfish programmes. This allows for within family selection for traits which cannot be measured on selection candidates (e.g. slaughter traits). Because kingfish can only be group-spawned, selection is based on individual genomic breeding values (GEBVs). Optimal contribution methods are used to manage long-term inbreeding and genetic diversity in genomic and pedigree-based selection programmes. The benefits of genomic selection have also been assessed in Pacific oysters using a medium-density SNP array for oysters for improvement of resistance to OsHV-1 (Gutierrez *et al.* 2020).

Selection indices. Estimated breeding values (EBVs) are calculated for all candidate broodstock using either pedigree-based Best Linear Unbiased Prediction (BLUP) or Genomic-BLUP methodologies. The analysis is based on individual data recorded on previously selected parents and selection candidates (e.g. harvest weight, deformities), family-level survival based on mortality during field or tank challenges, and family-level quality traits based on measurements taken from sacrificed animals. Trait prioritisation and economic weightings are used to develop selection indices determined by the commercial companies and their genetics providers.

Kingfish. After over a decade of R&D to develop reliable hatchery and production systems, the National Institute of Water and Atmospheric Research (NIWA) recently initiated demonstration-scale commercial production and a genomics-based genetic improvement programme to improve production in yellowtail kingfish. The programme initially used a selection index that included growth rate and skeletal deformities and aims to supply genetically elite larvae, fry, and broodstock to both the fledgling NZ industry and the rapidly growing, global industry. Currently the focus is on performance in land-based recirculating aquaculture systems (RAS). RAS provides increased environmental control in the face of climate change, enhanced biosecurity, and absolute escape prevention that eliminates genetic interactions between selectively bred and wild stocks. The programme has also assessed the potential for genotype-by-environment interactions (Jacob *et al.* 2025). The mating design is based on a rotational breeding scheme using four-year cycles in which four-year-old males are mated with five-year old females to minimise the generation interval and conserve genetic diversity.

Snapper. Due to its commercial, recreational, and cultural importance, a breeding programme was initiated by Plant & Food Research using broodstock collected between 1994–2006. F1 populations were produced from 2004–2009, followed by F2 in 2013, which underwent domestication selection for survival and reproduction in captivity. A major shift came in 2016 with genomics-informed breeding, enabling full pedigree reconstruction and genomic breeding values for moderately heritable traits like length and weight (Ashton *et al.* 2019a). To support breeding, genomic resources were developed including a genome (Catanach *et al.* 2019, Blommaert, *et al.* 2024), linkage map (Ashton *et al.* 2019b), transcriptome (Wellenreuther *et al.* 2019), SNP chip (Montanari *et al.* 2023) and QTL identification (Ashton *et al.* 2019b; Ruigrok, *et al.* 2022, Sandoval *et al.* 2022). The F3 (2018) and F4 (2021) generations were selected using genomic data, marking the onset of precision breeding focused on growth and production traits.

RESULTS AND DISCUSSION

Salmon. Most of the key production traits for salmon are moderately to highly heritable (Symonds *et al.* 2000, 2019; Scholtens *et al.* 2022, 2023) and have shown improvement after generations of selection since the mid-1990s. For example, growth is no longer production limiting for The New Zealand King Salmon Co. Ltd. (NZKS) (Zac Waddington, *unpublished data*). Some unfavourable genetic correlations have been uncovered, for example between harvest weight and body fat, requiring incorporation of fat into the selection index to avoid increased fat content (Symonds *et al.* 2019). Higher body condition has also been found to be a risk factor for spinal curvature (Scholtens *et al.* 2022). Recent evaluation of thermotolerance (Symonds *et al.* 2025) has shown that survival and time to death during a temperature challenge are both moderately heritable, demonstrating the potential to improve thermotolerance through selection. The aim is to apply between and within family genomic selection to increase selection accuracy and improve gains for these thermotolerance traits, now a priority for NZKS due to increasing ocean temperatures.

Greenshell mussel family evaluation also demonstrated the potential for genetic gain in multiple production traits (Camara and Symonds 2014). Selective breeding combined with the development of improved hatchery technologies for juvenile production has dramatically improved production for one of the largest GSM farming companies (SPATnz, 2020). There is now significant interest by the wider industry in investing in new GSM hatcheries enabling the development of new breeding programmes and improving industry growth and resilience, and reducing reliance on wild caught spat.

With the challenge of increasing summer mortality in GSM, the recently determined estimated high heritability (0.48±0.10) for survival under simulated severe heatwave conditions was very encouraging, suggesting that if heat tolerance is included in a selection index, there is adequate genetic variation to allow genetic improvement in this trait (Scholtens *et al*. 2025).

Pacific oysters. Selective breeding to improve resistance to OsHV-1 has been successful (Camara *et al*. 2017) and survival is no longer the major threat that it was in 2010. Increasing emphasis is being placed on selecting traits such as tolerance to low salinity and applying genomic selection. The oyster family programme has developed from small scale research to a commercial programme utilised by New Zealand's largest oyster farming company to produce superior farmed product. There is increasing interest and investment in building new land-based oyster hatcheries that is also enabling further establishment of family-based breeding programmes.

Kingfish. The heritabilities of weight, length, and morphological development in juvenile yellowtail kingfish exposed to current and projected water conditions representing future global warming and ocean acidification is low but significant (Munday *et al*. 2019). Table 1 (Camara, *unpublished data*) presents estimates of genetic parameters for three production traits. All traits are sufficiently genetically variable to support a response to selection, but there is an unfavourable genetic correlation between growth (weight) and the probability of deformities that must be taken into account in the selection index to prevent an undesirable correlated response to selection on growth.

Table 1. Genetic parameter estimates (se) for kingfish traits grown in RAS. Heritability (bold) on the diagonal, genetic correlations below the diagonal, and phenotypic correlations above the diagonal.

Trait	Tagging weight	Harvest weight	Deformities at harvest
Tagging weight	**0.433** ± 0.039	0.302 ± 0.028	-0.048 ± 0.023
Harvest weight	0.325 ± 0.069	**0.560** ± 0.033	0.021 ± 0.023
Deformities at harvest	-0.020 ± 0.115	0.165 ± 0.103	**0.102** ± 0.020

Snapper. In 2024, the F5 generation of snapper was created, which shows faster growth, higher survivorship, and improved FCRs (Moran *et al*. 2023; Samuels *et al*. 2024). Heritabilities for the three growth-related traits, fork length, peduncle length, and weight, were similar, averaging 0.27 in the first year and declining to 0.10 by the third year (Ashton *et al*. 2019a). Snapper exhibit rapid growth at optimal temperatures between 18–21 °C, while growth slows significantly and nearly ceases at temperatures below 14 °C. The overarching aim is to develop a fast-growing, robust snapper strain, mirroring gains achieved in red sea bream (*Pagrus/Chrysophrus* major) and gilthead sea bream (*Sparus auratus*), to support a sustainable and commercially viable warm water resilient aquaculture industry in New Zealand.

Challenges and future opportunities. The three main aquaculture species encountered significant challenges during the first 20 to 30 years as the industry developed. The emerging RAS-based kingfish industry and anticipated snapper industries will likely follow this pattern. Selective breeding helped overcome these challenges, from improving OsHV-1 resistance to enhanced growth and product quality despite some unfavourable genetic correlations. More recently new challenges have emerged as climate change has exacerbated the frequency of marine heat waves, reduced salinity due to freshwater run off during floods and increased pathogen risks, accelerating the need to breed for climate change resilience, including thermotolerance and disease resistance. Researchers and industry are developing relevant tank and farm-based challenges to define and measure the accurate resilience phenotypes required for successful selection. The increasing application of genomic selection over the next few years will improve genetic gains across the industry.

CONCLUSIONS

Successful selective breeding programmes have demonstrated genetic gains for all three main commercial aquaculture species either through centralised programmes or in-house programmes operated by individual companies. The priority traits that are selected continue to evolve, especially as new challenges emerge such as increasing temperatures and new diseases. Breeding programmes are seen as key to the future adaptation of the industry to climate change. Genomic selection will become more widespread over the next few years as the additional gains and accuracy it provides become evident. However, breeders must stay ahead of the game, by selecting for the uncertain future and not just for business as usual.

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