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## Optimal utilization of genetic resources in aquaculture

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### ABSTRACT

This paper uses a vertically integrated salmon farming company as a case study to describe how quantitative genetics and decision support optimisation tools have been used in an aquaculture breeding programme. The complex tasks of maximising genetic progress while managing genetic diversity and avoiding inbreeding are considered at two levels. The first level relates to the management of a nucleus breeding structure for which long term genetic progress and management of genetic diversity are the primary objectives. The second level relates to the tactical selection among available broodstock candidates and their mating to avoid inbreeding. The importance of both effective data management systems and practical implementation of theoretical genetic principles is emphasised.

**Keywords:** aquaculture; inbreeding; nucleus; co-ancestry; salmon.

### INTRODUCTION

On a global scale, aquaculture is a rapidly growing industry, driven largely by expansion in low income food deficit countries. However, a number of developed countries have a significant interest in high value aquaculture species including finfish and shellfish. It is in these areas that applications of advanced production and genetic selection technologies have been focused. For example in New Zealand Pacific salmon and Greenshell<sup>TM</sup> Mussels each earn significant export revenue. A number of other aquaculture industries with considerable economic potential are also developing.

Aquaculture species are typically characterized by very high reproductive rates. This creates considerable opportunity for large-scale production of commercial offspring from elite individuals. However, along with the resulting potential for high rates of genetic progress comes the risk of a rapid narrowing of the genetic base of the farmed population. This could lead to reduced opportunities for future genetic progress, and increased risks that a considerable proportion of the farmed population would be inbred. There have also been difficulties with the control of the reproductive cycle of some of the species (e.g. controlled timing of sexual maturity), resulting in practical limitations to what can be achieved in a breeding programme. With improved understanding of hatchery techniques of the various species, many of these impediments are being overcome.

This paper briefly describes the application of several selection tools to a large, vertically integrated salmon company, The New Zealand King Salmon Company Ltd. Opportunities to integrate these tools in other New Zealand aquaculture industries are discussed, as are some opportunities for parallel developments in other New Zealand livestock industries.

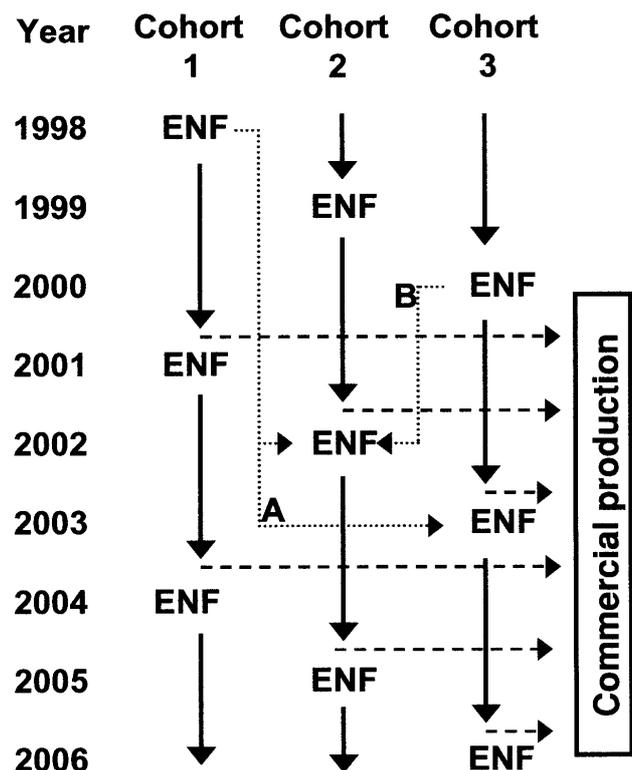
### SELECTION TOOLS IN SALMON

#### Overview of breeding program structure

Figure 1 shows the structure of the salmon example used as a case study in this paper. There are three cohorts of families running simultaneously, as the most common age for reproductive maturation is 3 years of age. Thus nucleus families consisting of approximately 80 large full sib groups

are established (denoted ENF in Figure 1) annually. All fish die shortly after reproductive maturation and breeding, so that transfer of genes among the cohorts must take place through two deliberate mechanisms. The first (marked as A in Figure 1) involves storage of frozen milt with subsequent insemination of eggs within another cohort one or more years later. The second (marked as B in Figure 1) involves using fresh milt from a maturing two year old male to fertilize the eggs of a three year old female in another cohort.

**FIGURE 1:** Structure of the salmon breeding population. The letters ENF denote the establishment of nucleus families for evaluation, with solid lines indicating the primary sourcing of new families within cohorts based on a three year maturation and breeding cycle. Horizontal lines indicate the use of mature salmon from the breeding programme to produce an annual brood for commercial production. Dotted lines indicate connections among cohorts established using frozen milt (A), and by using males achieving reproductive maturity at two years of age (B).



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Thus, after either two or three years, maturing fish within the nucleus families become candidates for two separate selection decisions. The first decision is whether or not to use the individual as a parent for the next generation of nucleus families. Because only a few fish are required for this purpose, fish selected to become nucleus parents are high performing individuals within elite families. The second selection decision involves whether or not to use the fish to produce the commercial brood, and if so, which type of commercial production system the offspring should be most suited to.

### **Selection criteria**

The breeding merit of each individual fish is assessed by statistical Best Linear Unbiased Prediction (BLUP) analysis based on its own records and the records of its close relatives (predominantly large groups of full sibs and cousins). Individual fish are tracked using electronic tags inserted into their body cavity when they reach approximately 10 grams at 5 months of age. Several traits are recorded for the brood-stock candidates themselves. However, a subset from each full sib family is maintained in a close to commercial production system and harvested to provide detailed information on post slaughter quality traits. Total genetic merit selection indexes are computed using breeding values for each trait, and sets of economic values specific to several different production systems, and also for the nucleus. The traits recorded include weight and whether or not sexual maturation has occurred at both two and three years of age in brood-stock selection candidates, and harvest traits indicating flesh production and quality in the subset tested under close to commercial production conditions. Further details on the traits recorded and their genetic properties are beyond the scope of this paper.

### **Selecting nucleus parents**

The selection of parents in each generation to set up new nucleus families is divided into two steps due to practical constraints. The first step involves calculation of the number of individuals each full sib family should contribute to the set of new parents. This is done in the context of maximizing the expected genetic progress while maintaining co-ancestry among the parents, and hence maintaining acceptable levels of genetic variation. Meuwissen (1997) developed a method that achieves this when selecting individual parents using an optimisation algorithm. An adaptation of this algorithm to consider optimal selection of full sib family contributions (Amer & Symonds, 2000) is used in the salmon breeding program.

The second step in the selection of new parents involves identifying elite individuals within families. Because all fish within a full sib family have equal relationship to each other, and to all other fish, co-ancestry can be ignored in this step. Thus, selection is based on an index of BLUP breeding values for merit as a nucleus parent. However, it is not always the top ranked fish within a family that is ultimately used as a nucleus parent, as there is no guarantee that the best fish will mature sexually at the appropriate time. This is also the reason for the adaptation to the optimum selection algorithm to select families, rather than individuals, and the two-step selection process.

### **Mating nucleus parents**

Each parent selected for the nucleus is mated only once. Because a large number of families contribute more than one parent to the next generation nucleus, full sib and cousin relationships are predominant among the new nucleus fish. A pseudo-factorial mating structure is generated by crossing the selected parents from a single family with parents from as many different other families as possible. Nucleus parents are matched so that any inbreeding in the resulting progeny is maintained below a pre-specified threshold. This is achieved by manually checking a matrix of unacceptable family crosses, with the construction of the matrix being based on co-ancestry coefficients among the families.

### **Selecting parents for the commercial brood**

New Zealand King Salmon operate three commercial production systems in which both the absolute and the relative economic importance of the primary selection traits differs substantially. Thus, each candidate parent has to be sorted for use among the three production systems, or alternatively, rejected and not used at all. The decision is not clear cut, as single fish might be quite suitable to produce offspring in more than one production system, and it is not necessarily optimal, or feasible, to assign every fish to the production system that they are most suited to. A sorting algorithm is therefore used to optimise the allocation of parents to each production system. The sorting algorithm optimises the sum of indexes of assigned fish, where the index for each fish used in the sum corresponds to the production system to which it has been assigned to be a parent. The algorithm is constrained such that the appropriate numbers of each sex of fish are assigned to production strategies based on planned future production levels. Mating pairs are established such that the co-ancestry between parents is below a pre specified threshold.

## **DISCUSSION**

While not all aquaculture species are limited to a single breeding opportunity per lifetime, the characteristics of having a high reproductive potential and a difficult to manage breeding time window are common to many aquaculture species. Thus, the genetic decision support tools described here will be relevant to many other breeding programmes as they overcome problems associated with hatchery management. These decision support tools are underpinned by standard quantitative genetics technologies such as database management, genetic parameter estimation and BLUP prediction of breeding values which are more familiar to people working in the terrestrial livestock industries. Thus, we expect that there will be an important role for quantitative geneticists in the development of practical, cost effective, breeding schemes for expanding aquaculture industries.

Similarly, there may be opportunities to accelerate rates of genetic progress in New Zealand's terrestrial livestock species using decision support tools such as those described here. For example, inbreeding and a narrowing of the genetic base are of concern to a number of sheep breeders. In many cases, these are avoided through the application of rough rules of thumb, which while effective for controlling inbreeding, can be inefficient in terms of lost opportunities

to breed from elite individuals. The method used to sort breeding candidates for use in alternative commercial production systems should also be of value in large vertically integrated animal farming companies.

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