

## **Quantitative aspects of salmonid breeding**

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### **Abstract**

Effective salmonid breeding programs require good definition of traits of economic importance, and knowledge of the genetics underlying them. Optimal selection and mating schemes to improve performance can be proposed based on accurate estimation of heritabilities and genetic correlations among these traits. In this paper, some basic quantitative principles of salmonid breeding programs are defined and illustrated with an example from the Atlantic Broodstock Development Program.

### **Introduction**

Breeding programs are used around the world to improve performance of many livestock species, including salmonids (e.g. <sup>2,3,4</sup>). They essentially consist of 2 steps: selection of parents, and mating. This paper describes some of the basic quantitative principles of breeding programs and illustrates with a simple example from the Atlantic Broodstock Development Program (ASBDP).

### **Selection**

Selection is the process that determines which fish become parents. There are different levels of selection: selecting individual fish out of the entire population (mass selection), selecting particular families out of the population (between-family selection), or selecting individual fish out of each family (within-family selection). Combinations of these can also be done. The number of parents selected (selection intensity) must attempt to balance the rate of genetic improvement needed with maintenance of suitable genetic variation.

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To improve a population, only the fish with the best genes should be selected as parents. A breeding value is a quantitative calculation of the value of a fish as a genetic parent, and is a measure of the potential performance of its offspring. Therefore the 'best' fish are those with the best breeding values. The definition of 'best' depends on the economic importance of traits and their underlying genetics.

### ***Traits***

A trait can be defined as any observable or measurable characteristic <sup>(5)</sup>. In salmonid culture, there are usually several economically important traits, such as growth, grilse percentage, meat colour and fat content, and disease resistance. The importance of a trait to a producer depends on the product, consumer demands, market prices, and production environment. Calculating the correct economic value of a trait requires thorough knowledge of the production situation, including geography, available resources (feed, labour, and equipment), and management practices. Economic values can be very specific to the production situation, and need to be re-evaluated regularly as the market and management practices evolve.

### ***Genetic parameters of traits***

The genetics underlying a trait are described by the genetic parameters of heritability and correlation. Genetic parameters are specific to each trait and to each production situation. Calculation of these parameters requires some knowledge of the environmental factors mentioned above, as well as information on the genetic history of the fish (e.g. current family structures in the population, or pedigrees). The more accurately these factors are described, the more accurately genetic parameters can be estimated, and the faster improvement can be made.

Heritability describes how a fish's performance for a trait is passed from generation to generation. An animal's measurement performance (phenotype) for a trait is due to a combination

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of factors, both environmental and genetic. The genetic factors can be further divided into additive, dominance and interaction effects. Selection programs work on the additive genetic effects, which are the only effects that are transmitted from parent to offspring. At a population level, heritability ( $h^2$ ) is defined as the proportion of the total phenotypic variance that is due to additive genetic variance. Generally, livestock product (or carcass) traits such as body weight or meat cut size have high heritability ( $>0.40$ ), while production traits such as growth rate and feed efficiency have moderate heritability, and reproductive and survival traits have low heritability ( $<0.15$ ). Traits with low heritability are not likely to respond well to selection, because very little of the fish's final performance is actually due to the genes that are carried over generations.

Heritability is estimated in a many different ways, all of which look at the resemblance of relatives' phenotypes. Animals can be compared with their parents, siblings, or entire pedigrees over multiple generations. Estimation methods range from fairly simple analyses of family covariances, to more complex models that account for several environmental factors and complex family relationships. The appropriate method for a given situation depends on the data available.

Correlations describe the strength of relationships between traits and how a change in phenotype for one trait might affect phenotypes in another trait. In a positive correlation, performances for both traits increase together. In a negative correlation, as performance for one trait increases, the performance for the other trait decreases. A correlation of zero means there is no relationship between the traits. Like heritability, correlations between trait phenotypes can be due to environmental or genetic factors, so in selection programs the genetic correlation is of particular interest. Often, the phenotypic correlation between traits is a fairly good estimate of

genetic correlation, but this is not always the case. More accurate estimates of genetic correlations require that measurements for both traits be made on the same individuals.

### ***Ranking and Multiple-trait selection***

To select parents, individuals and families are ranked according to their breeding values for traits of importance. If no other information is available, then phenotype can be used for selection, because it is directly proportional to the breeding value. The phenotype, however, includes non-additive factors, so genetic change in the offspring cannot be predicted. If genetic parameters have been calculated, more accurate estimated breeding values (EBVs) may be calculated. Ranking of potential parents is straightforward when selection is done for a single trait. When two or more traits need to be improved (usually the case for any livestock production) there are a few different options. The two most common approaches to multiple-trait selection are independent culling and index selection.

In independent culling, a breeding value threshold is set for each trait below which individuals or families are culled. To be selected, animals must reach the thresholds for all traits. Independent culling is easy to set up, but valuable genes may be lost with this method. If animals have good breeding values for most, but not all traits, then they will still be culled. This is especially likely to occur if traits are negatively correlated.

In index selection, potential parents are ranked by an index value ( $I$ ). An estimated breeding value for each trait is multiplied by an economic value ( $v$ ) and the animal's total  $I$  is the sum of these weighted breeding values:

$$I = v_1 * EBV_1 + v_2 * EBV_2 + v_3 * EBV_3 + \dots$$

Economic values may be simply numbers describing the proportional importance of each trait or actual currency values for the profit made by increasing performance for a trait. The advantage

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of index selection over independent culling is that individuals that have good breeding values for some traits, but not all, may still be selected as parents if those traits are important enough. In some cases this may allow more intense selection while maintaining a suitable population size.

## **Mating**

The second step in a breeding program is deciding how the selected animals will be mated. Since salmonids are fertilised externally and artificially, there is a variety of mating choices that are not so easily produced in other livestock species. In aquaculture, mating designs usually aim to retain as much genetic variation as possible in a population (thus reducing the accumulation of inbreeding effects). The simplest mating strategy is random one-to-one matings where each male is only mated to one female to produce full-sib families. When some family information is available, some restrictions on the matings should be imposed; matings of siblings should be especially avoided. Hierarchical (or nested) mating can be done where an animal is mated to a number of other animals, but this strategy reduces the effective population size and is not necessary in high-fecundity salmonids in production situations. Traits with low heritabilities may be improved with cross-breeding strategies which capitalise on non-additive genetic effects (dominance and epistasis). These include factorial (diallel) matings, crossing of distinct sire and dam lines, or rotational crossing schemes. Non-additive improvements obtained from crossing lines are only seen in the progeny of those crosses, and are not carried to subsequent generations.

## **An example of breeding at the ASBDP**

### ***Data and Traits***

Seventy-one full-sib families were fertilised at the ASBDP hatchery in the fall of 1997. Families were raised in separate tanks until smolting, when families were marked and combined. Smolts were raised to harvest in production sea cages while individuals from each family were

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held for broodstock. In the fall of 2000, harvest weight and grilse data were collected at the processing plant. Tissue samples were collected near-infrared analysis done for carcass quality traits. The final data set consisted of individual weight and grilse status for individual fish in each family, and individual colour fan, astaxanthin, canthaxanthin, fat and moisture measurements within each family.

### ***Genetic parameters***

Heritability of each trait was calculated by full-sib analysis using restricted maximum likelihood (REML). Body weight, canthaxanthin, fat, and moisture contents were moderately heritable (Table 1), therefore these traits are predicted to respond to selection.

Estimates of phenotypic correlations were partial correlation coefficients from multivariate analysis of variance in SAS©. Weight had a low but significant positive phenotypic correlation with astaxanthin level (Table 1). Therefore selection for increased weight should cause astaxanthin levels to rise, which is favourable, but no related changes are expected in any other trait.

### ***Selection and Mating***

Some breeding objectives for the ASBDP are to reduce the amount of grilse, increase growth rate, and increase flesh colour. Therefore, the traits chosen for selection were grilising rate, harvest weight, and canthaxanthin level. Independent culling was done to remove families with high percentages of grilse. Index selection on harvest weight and canthaxanthin level was done on the remaining families. For each trait, family phenotypic values were calculated by dividing SAS© General Linear Model procedure least squares means by the population mean. Weight was considered to be five times as important as canthaxanthin, and an index value was calculated for each family accordingly. Families were ranked according to their index values and

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the top 25 families were selected. The index selection calculations are demonstrated in Table 2, and Tave <sup>(6)</sup> has described a similar method.

Two males and two females were randomly chosen from each selected family and one-to-one random matings were done, avoiding full-sib matings. The resulting 50 full-sib families were raised in separate freshwater tanks. Samples from each family were also taken and combined over two replicate tanks. A control population was also formed by mating individuals from random families. The control population was combined over another two replicate tanks. Later comparison of selected and control groups will allow evaluation of selection response.

## **Conclusion**

The success of any breeding program depends on understanding the production situation and the genetics underlying important traits. A breeding objective needs to be well defined in terms of which traits are of importance to the industry and what their economic values are. The ASBDP selection and mating schemes described in this paper are very simple compared to some other livestock breeding programs. Future studies will investigate more accurate methods of estimating genetic parameters and breeding values. Of particular interest is the use of passive integrated transponder (PIT) tags to track individuals over freshwater and seawater production stages. Availability of individual data and pedigrees will allow the use of more accurate methods for prediction of breeding values and will result in better selection and faster genetic progress.

## **Notes and References**

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**Table 1. Heritability estimates (diagonals) and phenotypic correlations (partial correlation coefficients\* on off-diagonals) among harvest weight and carcass traits.**

	Weight	Asta.	Cantha.	Colour Fan	Fat	Moisture
Weight	0.15	0.306	0	0	0	0
Astaxanthin		0.073	0.527	0.414	0.325	-0.278
Canthaxanthin			0.153	0.481	-0.127	0.077
Colour Fan				0.06	0	-0.151
Fat					0.179	-0.986
Moisture						0.204

\* non-zero correlations are significant at  $\alpha=0.05$ .

**Table 2. Calculation of family phenotypic and index values for body weight and canthaxanthin level.**

Rank	Family #	Weight		Canthaxanthin		Index Value $I = 5P_W + P_C$
		Mean	$P_W$	Mean	$P_C$	
1	11	19.15	1.29	7.014	1.08	7.549
2	16	18.61	1.26	7.182	1.10	7.391
3	70	19.06	1.29	6.168	0.95	7.388
4	63	18.85	1.27	6.317	0.97	7.340
5	46	18.31	1.24	7.148	1.10	7.286
6	57	18.02	1.22	6.513	1.00	7.088
7	23	18.20	1.23	5.865	0.90	7.053
8	49	17.51	1.18	7.379	1.14	7.050
9	36	17.78	1.20	6.499	1.00	7.008
10	17	17.85	1.21	6.339	0.98	7.005
∴	∴	∴	∴	∴	∴	∴
Population		14.8	1	6.500	1	6