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The dissemination of genetic improvement in salmon production

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ABSTRACT

A simulation study was conducted to investigate the potential advantage of two-step selection for dissemination of genetic gains in salmon production through a system with a nucleus breeding population, a multiplier tier and a grow-out tier. Results demonstrated that *profit* (measured in the grow-out tier in generation 8) can be substantially increased through production and dissemination of specialised stocks suited for e.g. specific production environments or markets. Truncation selection alternatives in two steps with varying selection proportions were compared to random sampling of parents in both dissemination steps: from the nucleus to the multiplier and from the multiplier to the grow-out tier. Strategies where truncation selection was used in one step and random sampling of parents in the other step were also tested. The selection alternatives with truncation selection in both steps gave on average between 31% and 26% higher *profit* than random selection. The selection alternative with an extremely low truncation selection proportion in two steps would on average give 2% higher *profit* than the selection alternative with extremely low truncation selection proportion from the nucleus to the multiplier (1st step), and a normally low truncation selection proportion from the multiplier to the grow-out (2nd step). However, the former alternative yielded five times fewer eggs. The study also showed that one step of truncation selection and one of random sampling of parents, irrespective of the order, would give on average about 19% higher *profit* compared to random selection in two steps. The effect of the correlation between the nucleus/multiplier breeding goal and the breeding objective of the grow-out was that profit was highest when the correlation was high. With a negative genetic correlation between the traits, *profit* was still high if the trait with the highest heritability (i.e. the trait measured on candidate itself) had the highest economic value. It was concluded that selection of specialised stocks for specific breeding objectives in two steps from the nucleus via the multiplier and to the grow-out could increase *profit* by 24%. Specific breeding objectives would also give more flexibility for a final product when the grow-out producers could ask for unique trait-combinations for their fish.

1. Introduction

The primary aim of applied breeding programmes in aquaculture is to improve the productivity and thus the profitability. For salmonid species, a family based breeding program typically consists of three tiers; i) a breeding nucleus that produces candidates for the next generation of nucleus families and for the multipliers, ii) the multiplier tier that produces fingerlings for the grow-out tiers and iii) the grow-out tier that produces slaughter fish (Gjedrem, 1985). In most cases, the material provided by the multipliers merely reflects the average genetic level of the material the multiplier receives from the nucleus, as no selection pressure is applied at this stage, but Toro (1998) suggested development of specialised parent lines and Gjerde and Gjedrem (Gjedrem, 2005; Gjerde, 2005) raised a more detailed idea of producing more customised genetic material suited for specific farm environments and market segments.

Skagemo et al. (2010) demonstrated that the profits can be significantly increased by production and dissemination of fish especially suited for specific production environment or markets. By optimising the selection of parents producing the animals disseminated from the nucleus to the grow-out tier an additional selection response corresponding to approximately 1.5 generations of selection in the nucleus was achieved. This is possible due to higher selection intensity and lower restrictions on rate of inbreeding when selecting for dissemination than when selection of parents for the nest nucleus generation. The simulation done by Skagemo et al. (2010) was designed to reflect the situation for a marine species with extremely high fecundity, and theoretically without need for a multiplier tier in the dissemination scheme. Hence, it was assumed that improved genetic material was distributed directly from the nucleus to the grow-out tiers, facilitating only one step of selection in the dissemination. However, for salmonids like Atlantic salmon (*Salmo salar*) with a widespread commercial production, but dramatically lower fecundity, ranging between 1200 and 1800 eggs per kg dam (Lysenko, 1997; Randall, 1989) multiplier tiers are needed. Hence an optimised two-step dissemination strategy involving non-random sampling of parents from nucleus tier to the multiplier tier

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and from the multiplier tier to the grow-out tier can potentially increase the profits for these species.

The aim of this paper is to compare the profit in the grow-out tier using computer simulation of alternative genetic dissemination strategies for Atlantic salmon/salmonids populations. The effects of the following variables were investigated: i) selection proportion from the nucleus tier and the multiplier tier, ii) the genetic correlation between the traits in the breeding goal, and iii) the economic weights assigned to the traits in the nucleus, multiplier and grow-out tiers.

2. Materials and methods

Selection methods were compared through stochastic simulations and the parameters of the simulated schemes are summarized in Table 1. The simulation scheme applied reflects the structure of the Norwegian salmon industry, which consists of a closed nucleus tier and one multiplier tier required for scaling the production of commercial roe to the sector's need, but was for computational reasons rescaled to about 10% of realistic population size. Selection proportions were kept at the realistic level.

2.1. Simulated nucleus population

In the simulated nucleus population, 4000 candidates and equally many test-sibs were born every generation. Among the selection candidates, the parents needed to produce 100 full sib families were selected by optimum contribution selection (Meuwissen, 1997) to create the next nucleus generation. Rate of inbreeding was restricted to 1% per generation. Selection was based on the number of families (matings), rather than the number of offspring, as done by Sonesson et al. (2005), to reflect a fish breeding strategy. Optimal contribution selection maximizes the genetic response given a constraint in rate of inbreeding and facilitates comparing selection schemes at the same rate of inbreeding. The selection candidates as for the nucleus were also selection candidates for the multiplier tier. Two traits were simulated: one typical production trait (CAND), which was measured on the selection candidates, and one typical disease or slaughter trait (SIB), which was measured on the test-sibs.

Table 1
Parameters of the schemes.

Parameters of traits	
Traits	2 (CAND, SIB)
Heritability (CAND, SIB), h^2	0.4, 0.1
Genetic correlation between the traits, r_g	−0.5, 0 or 0.5
Recordings	
- CAND	Candidates
- SIB	Sibs of candidate
Selection of parents in the nucleus	
Number of male selection candidates	2000
Number of female selection candidates	2000
Number of families	100
Number of test animals per family	40
Recordings in the nucleus	
- CAND	4000 candidates
- SIB	4000 sibs of candidates
Economic weights (w_{CAND}/w_{SIB})	50/50
Selection	Optimum contribution on TMI
Inbreeding constraint using optimum contribution	1% per generation
Selection of parents for the multiplier	
Number of parents Sires: Dams	50:200 or 5:25
Economic weights (w_{CAND}/w_{SIB}) to multiplier	50/50 as in nucleus
Selection	Optimum contribution on TMI
Selection of parents for the grow-out	
Number of male selection candidates	2000 from the nucleus
Number of female selection candidates	6000 from the multiplier
Number of parents Sires:Dams	10:600 or 5:120
Recordings in the multiplier	
- CAND	6000 female candidates
Economic weights (v_{CAND_T}/v_{SIB_T})	
- Sires	20/80, 50/50, 80/20
- Dams	100/0
Selection	
- Sires	random and truncation selection on TMI
- Dams	random and truncation phenotype selection on CAND
Number of generations	8
Number of replicated simulations	50

2.2. Simulation of multiplier tier and grow-out tier

Fish to be used as parents for the multiplier tier were selected among the selection candidates produced in the nucleus tier and mated hierarchically to produce 6000 female offspring. Nucleus selection candidates could hence be selected as parents for both the nucleus and the multiplier tiers. The offspring born in the multiplier got single phenotypic records for CAND and were selection candidates for the grow-out tier. Grow-out fish were created by mating sires produced in the nucleus with dams produced in the multiplier tier hierarchically. Different combinations of selection methods and selection fractions were compared, and these are summarized in Table 2. In short, truncated selection in one or both of the dissemination steps was compared to random sampling of parents and different selection fractions were compared when truncated selection was used. When truncation selection was used for the multiplier tier, economic weights of the two traits were equal, like when selecting for the nucleus tier, but inbreeding was not restricted. When truncation was applied for the grow-out tier, the sires were selected based on total merit index for grow-out (TMI_g), which was estimated as $TMI_g = v_{CAND} * EBV_{CAND} + v_{SIB} * EBV_{SIB}$, where EBV_{CAND} and EBV_{SIB} were estimated breeding values for CAND and SIB, respectively and v_{CAND} and v_{SIB} were the relative weights for the traits CAND and SIB, respectively in the grow-out tier. The relative weight of CAND was 20, 50 or 80% of the total economic weight. The dams of the grow-out tier were selected from the multiplier tier based on truncated phenotypic selection for the trait CAND only, since no own or sib information was available for the trait SIB in the multiplier tier. Correlations between total merit index in the nucleus (TMI_n) and TMI_g (r_g) were estimated as

$$r_g = \frac{w_{CAND} \times v_{CAND} + w_{SIB} \times v_{SIB} + w_{CAND} \times v_{SIB} \times cov + w_{SIB} \times v_{CAND} \times cov}{\sqrt{\sigma^2_{BVn} \times \sigma^2_{BVg}}}$$

(Skagemo et al., 2010), where cov was the genetic covariance between CAND and SIB, w_{CAND} and w_{SIB} were the economic weights for CAND and SIB, respectively, σ^2_{BVn} and σ^2_{BVg} were the variances of the breeding goal in the nucleus and grow-out tiers, respectively. These were estimated by the formulas: $\sigma^2_{BVn} = w^2_{CAND} + w^2_{SIB} + 2 \times w_{CAND} \times w_{SIB} \times cov$ and $\sigma^2_{BVg} = v^2_{CAND} + v^2_{SIB} + 2 \times v_{CAND} \times v_{SIB} \times cov$. The differences in economic weights between the nucleus/multiplier tiers and the grow-out tier, together with the variations in genetic correlation between the two traits, resulted in r_g to vary between 0.6 and 0.93 (Table 3).

Table 2
Selection strategies from the nucleus tier to the multiplier tier, and from the multiplier tier to the grow-out tier.

Strategy	Selection for multiplier tier			Selection for grow-out tier		
	Method	Nr sires	Nr dams	Method	Nr sires	Nr dams
Rand	random	50	200	random	10	600
Rand_Trunc	random	50	200	truncation	50	600
Trunc_Rand	truncation	50	200	random	50	600
Trunc_basic	truncation	50	200	truncation	10	600
Trunc_intense	truncation	5	25	truncation	10	600
Trunc_extreme	truncation	5	25	truncation	5	120