

# 581. Optimizing genotyping effort in aquaculture breeding programs by pre-selection of candidates

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## Abstract

Highly fecund aquaculture species provide more opportunities to optimize genotyping effort in genomic selection programs through selective genotyping and pre-selection than other livestock species. The aim of this study is to optimize pre-selection in a simulated fish breeding program to achieve the highest genetic gain per genotyped fish under restricted inbreeding. We simulated breeding programs in R with pre-selection among all selection candidates, between full sib families and within full sib families and several pre-selection intensities within each of the strategies. Pre-selection always reduces genetic gain. However, when genotyping costs are taken into account, genetic gain per genotyped fish can be increased with pre-selection. Pre-selecting 40% of the candidates from all available selection candidates produced the highest additional genetic gain per genotyped fish.

## Introduction

Aquaculture species are highly fecund and can produce large numbers of candidate offspring, and most fish breeding programs can produce sufficient numbers of sibs for sib testing if desired. Depending on the size of the candidate population, genotyping all available candidates can be prohibitively costly. However, genotyping costs can be reduced, for example by selectively genotyping the reference population (Gowane *et al.*, 2019), genotyping using cheaper, lower density SNP panels (Kriaridou *et al.*, 2020) or pre-selection of candidates. Pre-selection based on phenotypes measured at an early age can increase genetic gain (Martinez *et al.*, 2006), but Sae-Lim *et al.* (2013) showed that postponing pre-selection can be more effective because the genetic correlations between phenotypes measured closer to harvest and breeding goal traits are higher than for early phenotypes.

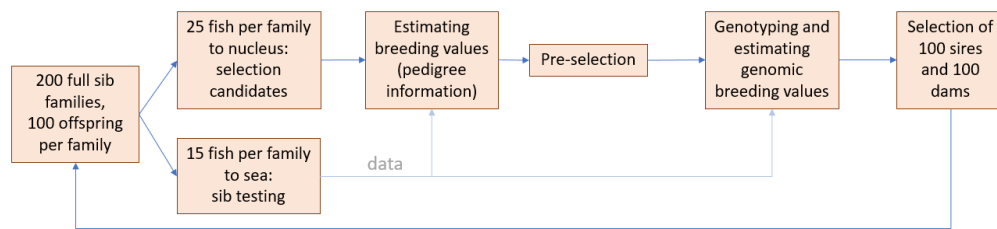
In this study, we focus on reducing genotyping costs by adding a pedigree-based pre-selection step immediately before genotyping and genomic selection. We aim to optimize this pre-selection to achieve the highest genetic gain per genotyped fish under restricted inbreeding, by simulating and comparing the predicted outcomes from a range of scenarios.

## Materials & methods

To perform pedigree based preselection we simulated a family-based rainbow trout breeding program with controlled spawning, using stochastic simulations in R (Figure 1). We simulated the traits tagging weight, weight in nucleus measured on selection candidates, and weight at sea measured on sibs of the candidates in the production environment. Heritabilities and genetic correlations used (Table 1) are estimates from a real breeding program.

**Table 1.** Heritabilities (diagonal) and genetic correlations.

	Tagging weight	Weight nucleus	Weight sea
Tagging weight	0.26	0.38	0.29
Weight nucleus		0.33	0.64
Weight sea			0.32



**Figure 1.** Design of the breeding program.

We simulated pre-selection based on a multi-trait selection index of traditional, pedigree-based estimated breeding values (EBVs) to identify fish for genotyping and final selection based on an index of genomically estimated EBVs (GEBVs) and optimal contribution selection to identify 100 replacement sires and 100 replacement dams each generation.

We simulated three pre-selection strategies: (1) the top 10, 20, 40, 60 or 80% of all selection candidates regardless of family membership (ALL); (2) the top 10, 20, 40, 60 or 80% selection candidates within each full sib family (WITHIN); or (3) the top 10, 20, 40, 60 or 80% of the full sib families (BETWEEN). The pre-selected and genotyped proportion varied between 400 and 3,200 selection candidates. The accuracy of the GEBV of weight at sea was simulated as a constant based on a reference population of 2,000 fish per generation. The accuracy of the GEBV for weight in the nucleus depended on the number of pre-selected and genotyped fish.

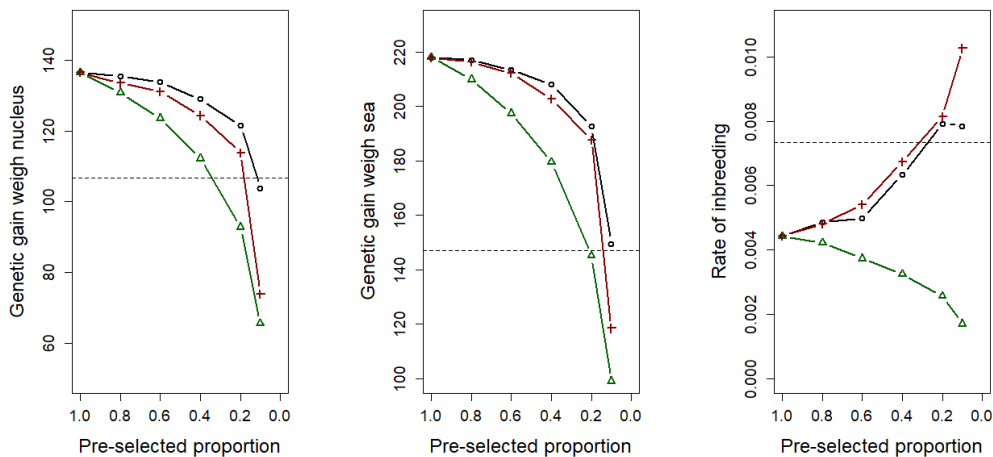
We simulated ten generations of selection for each scenario and calculated the average genetic gain and rate of inbreeding from 20 replicates. The additional genetic gain per genotyped fish was calculated as the difference in genetic gain with and without pre-selection divided by the number of genotyped fish.

## Results

Without pre-selection, the genetic gain was 136.4 and 217.9 grams per generation for weight in the nucleus and weight at sea with genomic selection, and 106.7 and 147.2 grams per generation with pedigree selection. The rate of inbreeding was 0.73 and 0.44% without pre-selection with final selection based on EBV and GEBV, respectively.

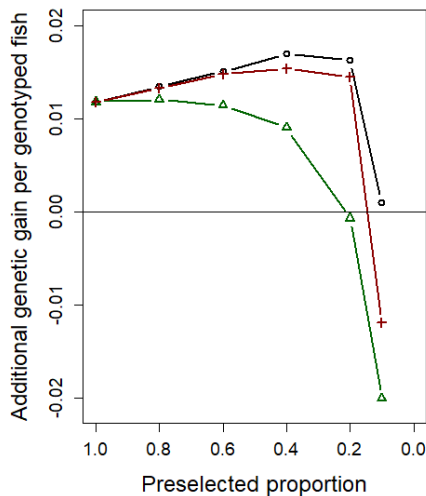
Pre-selection always reduced genetic gain compared to genotyping all candidates (Figure 2). Genetic gain for both weight in the nucleus and weight at sea declines more rapidly with decreasing pre-selected proportion for the WITHIN strategy than for the ALL and BETWEEN strategies, except at the lowest pre-selected proportion. Regardless of the pre-selected proportion, the highest genetic gains were obtained for the ALL strategy. Pre-selected proportions smaller than 0.20 always resulted in genetic gains that were comparable or lower than gains from selection based on pedigree-based EBVs.

In the ALL and BETWEEN strategies, the rate of inbreeding increased when the pre-selected proportion decreased, but for the WITHIN strategy, the rate of inbreeding decreased. The rate of inbreeding increased most for the BETWEEN strategy to a value slightly exceeding the acceptable threshold of 1% with a 10% pre-selected proportion.



**Figure 2.** Genetic gain and rate of inbreeding. Genetic gain and rate of inbreeding by pre-selected proportion for the ALL ( - O - ), BETWEEN ( - + - ) and WITHIN ( - Δ - ) strategies. The --- reference line is the genetic gain and rate of inbreeding without genotyping.

The ALL and BETWEEN pre-selection strategies increased additional genetic gain per genotyped fish (Figure 3). For these two strategies, additional genetic gain per genotyped fish was highest at a pre-selected proportion of approximately 40%. Additional genetic gain per genotyped fish for the WITHIN strategy was maximized when nearly all candidates were genotyped (Figure 3). Additional genetic gain per genotyped fish for weight in nucleus followed a similar pattern to weight at sea (results not shown).



**Figure 3** Additional genetic gain per genotyped fish for weight at sea. Lines are for the strategies ALL ( - O - ), BETWEEN ( - + - ) and WITHIN ( - Δ - ).

## Discussion

Our simulations predict that pre-selection always reduces genetic gain compared to genotyping all candidates, but the relationship is highly non-linear. This non-linearity leads to an intermediate optimum in terms of genetic gain per genotyped fish. If a fixed budget is available for the breeding program, then pre-selection intensity can be adjusted to efficiently use the available budget. Applying the optimal pre-selection strategy and intensity can reduce genotyping cost while limiting the effects on genetic gain. Pre-selection at an earlier age can also limit cost for the breeding program (Sea-Lim *et al.*, 2013, Martinez *et al.*, 2006). However, this reduction is cost is due to lower rearing cost. The pre-selection in this study will not reduce rearing cost, only genotyping cost.

The choice of pre-selection strategy is important because it influences both the genetic gain and rate of inbreeding. To limit the effect of pre-selection on rate of inbreeding, optimal contributions in the pre-selection could be implemented in the ALL strategy. The rate of inbreeding was reduced when pre-selection took place within a full sib family. However, the WITHIN strategy is not recommended for pre-selection, given that the rate of genetic gain reduces more rapidly with this strategy. This rapid reduction may be because the number of families was much larger than the number of candidates per family.

Pre-selection among all selection candidates resulted in the highest genetic gain, because more fish from the best families could be selected compared to the scenarios in which pre-selection took place within a family. In the BETWEEN strategy, the number of selected families was lower than in the ALL strategy. Therefore, it prevents selecting good fish from families with lower average breeding values, especially at lower selected proportion.

Postponing pre-selection can result in higher genetic gains due to higher genetic correlations between the traits (Sae-Lim *et al.*, 2013). In this study, the pre-selection was immediately before genomic selection. However, pre-selection decreased the genetic gain, because the pre-selection was based on EBVs instead of GEBVs, which resulted in lower accuracies in the pre-selection step compared to genotyping all candidates and therefore lower genetic gains.

For a low genotyping budget, the BETWEEN strategy could be further optimized because the pre-selected proportion will be small, and final selection takes place mostly within the small number of pre-selected full sib families. This provides an opportunity to reduce the genotyping costs by using low density SNP panels and genotyping only the phenotypically most extreme fish from the training population, because within-family haplotype blocks can be accurately traced using low-density SNP panels and most of the within-family variance can be captured by genotyping only the phenotypically most extreme sibs for the training population (Ødegård and Meuwissen, 2014).

## Conclusions

Our simulation results indicate that the reduction in genetic gain due to pre-selection is smallest when pre-selection takes place among all selection candidates. When genotyping cost are taken into account, higher genetic gains per genotyped fish are achieved with pre-selection. Pre-selecting approximately 40% from all selection candidates resulted in the highest additional genetic gain per genotyped fish.

## Acknowledgements

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