



SalmoBreed

BREEDING FOR INCREASED SEA LICE RESISTANCE IN ATLANTIC SALMON



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This poster describes how genomic selection increases the advantages of breeding, and how the result of systematic breeding for sea lice resistance over a 10 years' period has resulted in a more robust farmed salmon.

Introduction

Breeding for fish with natural high sea lice resistance is a non-medical, sustainable tool. SalmoBreed AS has selected for fish with high resistance toward sea lice since 2006 using family selection. From 2016, ova bred with use of genomic selection has been commercially available to farmers.

Materials

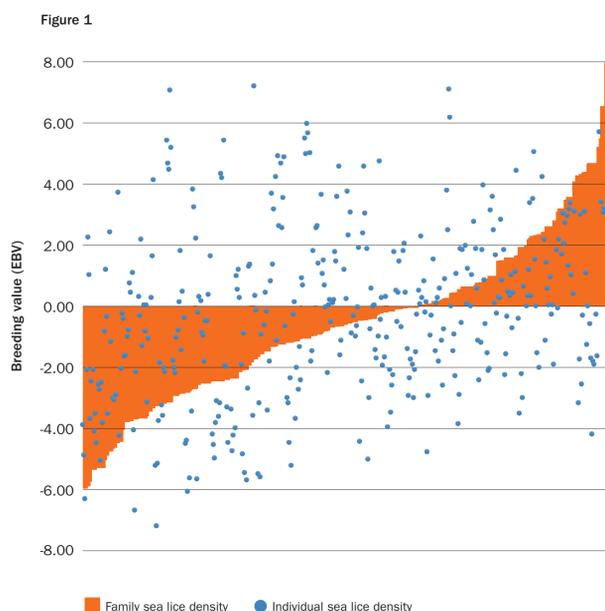
Breeding candidates were evaluated on sea lice robustness by breeding values across family (EBV) and breeding values within families (GEBV). Family EBVs were created based on the phenotype of the full sibs and an A-matrix (pedigree) by traditional BLUP. The SalmoBreed population was originally built on four subpopulations, over time merged to one. Merge of subpopulations and usage of frozen semen across yearclasses, give genetic links between the subpopulations; a trend analysis is achievable to compare families of all yearclasses independent of subpopulation (Table 1).

Table 1: Dataset for trend analysis of Sea Lice density.

Year classes	8
Generations	3
Individuals	21.119

Within family variation using genomic selection.

Within family variation of YC 2013 was estimated with genomic selection (GS). GS comprises a state of the art set of methods that utilize genomic information to improve the accuracy of genetic evaluations (Meuwissen *et al.*, 2001). Genome wide breeding values (GEBVs) are estimated from genomic selection, and evaluates breeding candidates based on the genome and phenotype (Figure 1). YC2013 created



the families of YC2016. The training data used for the genomic evaluations consisted of 1421 genotyped fish; 1367 offspring with phenotypic sea lice counts and 54 parents without lice counts. In addition, phenotypic sea lice count from 7293 fish of 517 families from year classes 2013 and 2014 were provided and used for the genomic evaluations. Genotypes from the training data were obtained using a customized Affymetrix 27K SNP arrays, while candidates were genotyped using a customized Affymetrix 57K SNP array. Imputation was done to fill up the gaps in the individuals genotyped with the 27K SNP array.

Results and conclusion

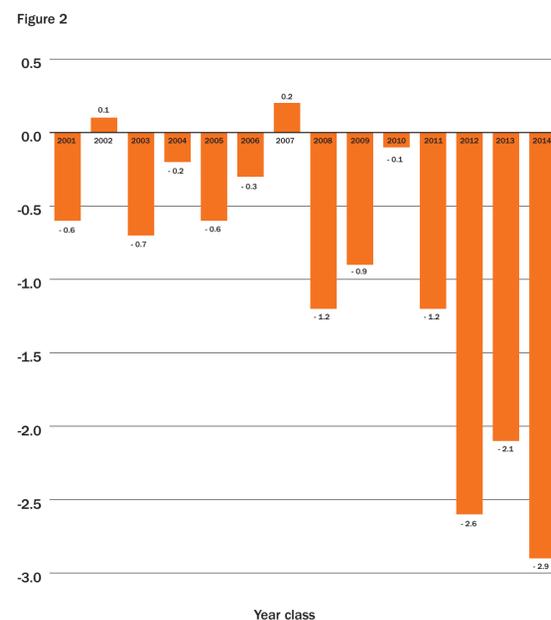
The main upside from genomic selection is to capture the within family variation with sufficient accuracy.

Trend analysis using family EBV show that our breeding nucleus' robustness toward sealice has increased with 9% over 2 generation (Figure 2).

The use of genomic selection provides sufficient accuracy for selection of candidates, and will triple genetic response compared to family EBV (Table 2). Compared to traditional methods, the use of genomic selection increases the accuracy of estimated breeding values, providing more certainty in selection of candidates.

Table 2: Estimated genetic response for lice density, comparing selection according to EBV with GEBV as selection criteria.

Selection of the 500 best breeding candidates	Genetic response in GEBV (%)	
	No. of top selected candidates	500
Family EBV	-0.77	-1.19
Individual GEBV	-3.09	-4.19



References

Meuwissen, T. H. E., Hayes, B. J., & Goddard, M. E. (2001). Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, 157(4), 1819–1829. <http://doi.org/11290733>