# Combating sea lice through salmon genes

Breeding as a preventive, non-medicinal measure for reducing sea lice attachment in Atlantic Salmon

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SalmoBreed started a systematic breeding strategy in order to reduce the amount of sea lice attached to the fish already in 2007. We define the most resistant brood fish and select them to breed for the next generation in preference to weaker brood fish candidates – both for our own breeding nucleus and for the fish that are picked to produce ova that are sold to fish farmers. Breeding is a long-term project, but the effect is long lasting and it can mean big cost savings for the industry and better animal welfare as a result of healthier fish.

We hear it every day, and the signals from the Norwegian Minister of Fisheries, Per Sandberg, could not be clearer: The industry will not be permitted to grow significantly unless the sea lice problem is brought under control. The industry is taking the sea lice problem very seriously! As it has done for a long time. Us geneticists are also involved. Work is continuously being done to systematically promote resistance against sea lice attachment in salmon.

## Distribution over the number of sea lice attached per fish
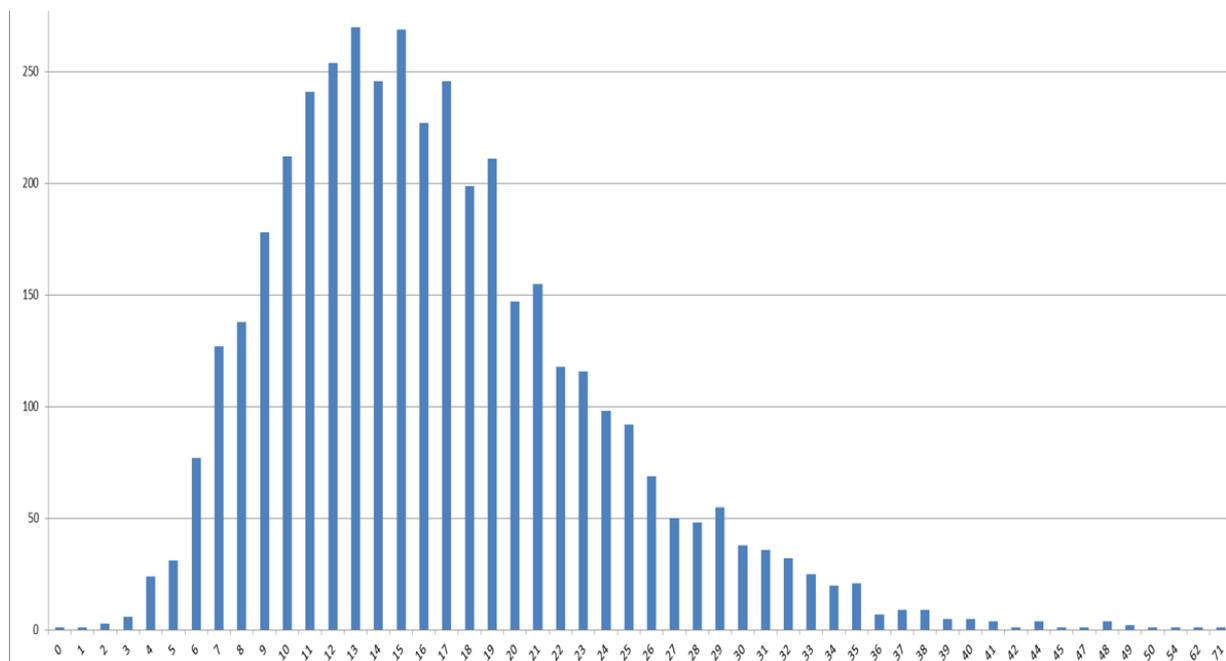
Figure 1. *There is a massive variation between individuals when it comes to the number of sea lice counted per fish during a challenge test. This count was carried out in 2014 and showed an average of 14 lice per fish. The numbers varied from 0 to 71 sea lice per fish.*

Breeding is a long-term, complex project

Sea lice density has a hereditability between 15 and 25% (Gjerde et al., 2011). This means that we can alter the sea lice robustness highly through systematic breeding. We collect information through challenge and field tests. Every year we send full siblings of our brood fish candidates from each of our 300 families in the nucleus to an annual sea lice challenge test. Here, the fish are exposed to sea lice for a given period in land-based tanks under controlled conditions. Each individual fish is traced back to its family using a PIT tag. The sea lice attached to the fish are counted, and DNA samples are taken by cutting off the fish's adipose fin. Some years, we also collect information from fish in commercial production before they are treated for sea lice. **Figure 1** shows the variation between individuals in the challenge test that was carried out in 2014.

The adipose fins are sent to a laboratory in Ireland. Laboratory technicians and molecular geneticists extract the DNA from the adipose fin, and make it visible to the robots to detect the genotypes of the fish. Such a detection is performed at another laboratory in Denmark.

The Atlantic Salmon DNA consists of approx. 3 billion base pairs distributed over 29 chromosome pairs. Through research, we have selected almost 58,000 markers (SNPs, pronounced 'snips') that show great variation from one individual to the next. These markers are used to rank the brood fish candidates. The technicians at the Danish laboratory define them and save them in large data files. **Figure 2** shows how sea lice resistance is genetically related. We now have three important components we can use in the breeding work: the number of sea lice we found on each fish (also referred to as a value of the phenotype), its kinship and its genotype. Then the extensive and complex task of estimation begins to rank the brood fish candidates from the best to the worst brood fish based on its performance.
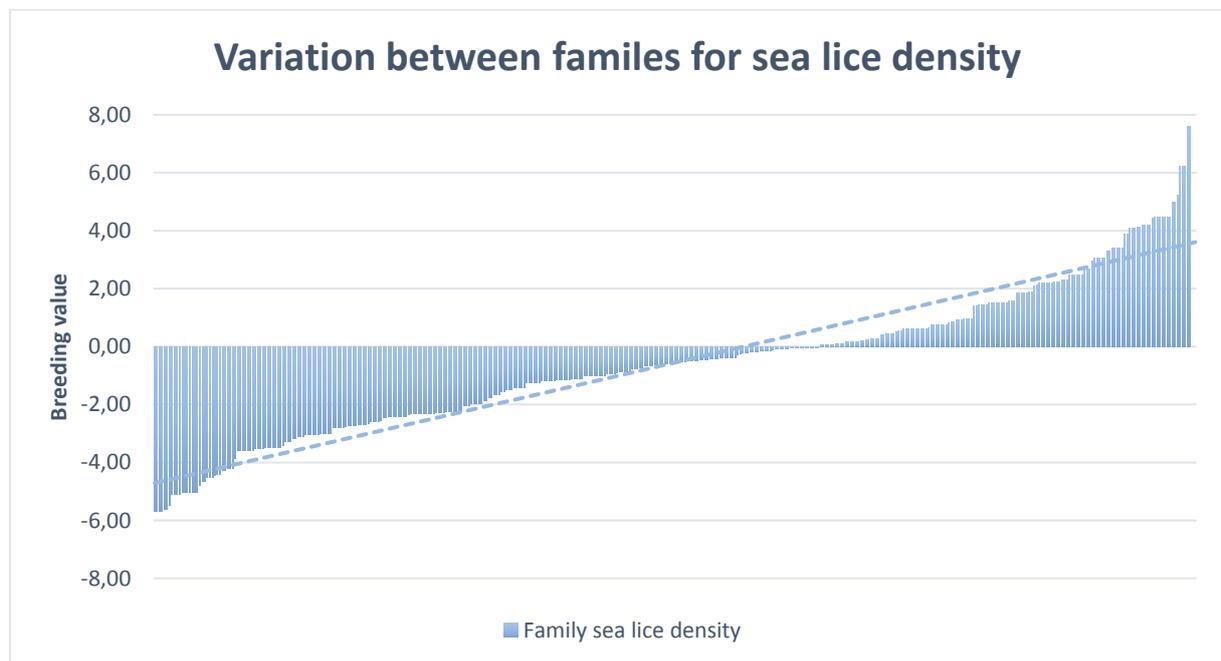
Figure 2. *Each family shows that they are genetically predisposed to contract sea lice to a varying degree. Here is the ranking of our families that were ready for breeding in autumn 2015, showing that sea lice attachment is definitely a heritable property.*

The number crunchers

At the foot of the mountains innermost in the fjord in Sunndalsøra sits a team of highly qualified and dedicated geneticists from Akvaforsk Genetics, studying, analysing and computing. These geneticists

have both quantitative and molecular genetics expertise, and they have access to super computers that can process enormous amounts of data.

First, the raw data from the genotypes are quality controlled. The SNPs that show little variation between individuals are removed. So are DNA tests that are damaged or contaminated for various reasons. Only good SNPs and DNA tests make it through to the analyses. The dataset with the genotypes is now cleansed and ready.

The current situation in Norway means that we will not be able to fully exploit the potential of salmon farming until the industry has brought the sea lice problem under control. One of the solutions lies in the DNA.
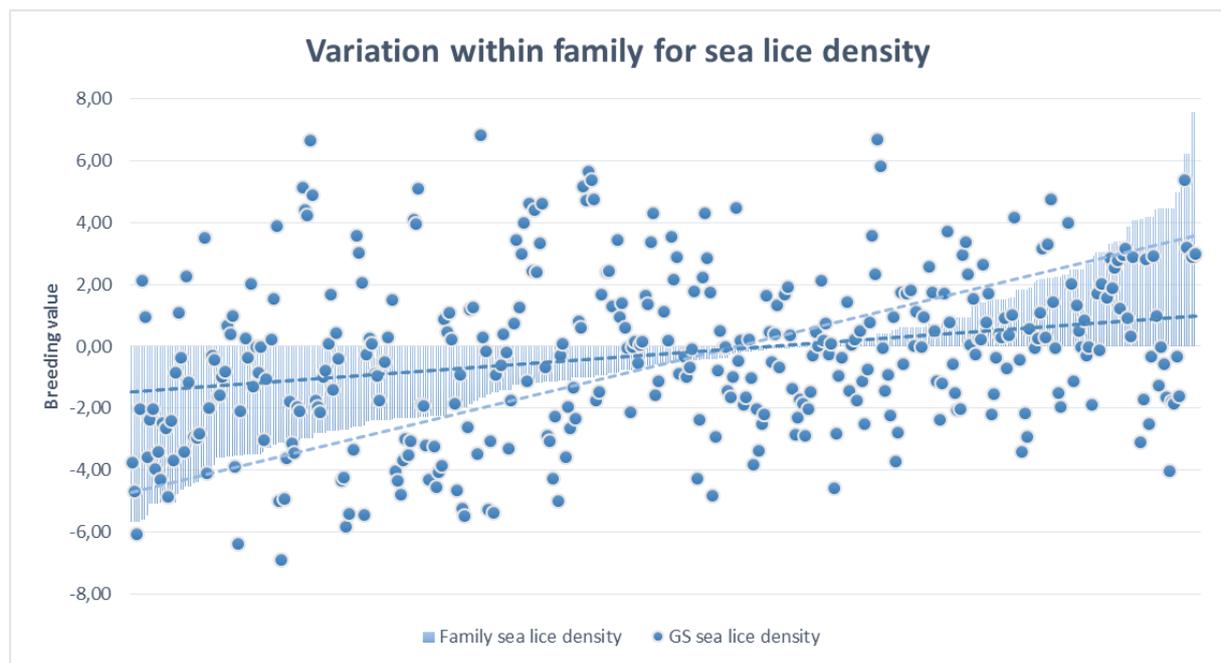
Figure 3. *There is great variation within families. The figure shows how SalmoBreed's breeding candidates perform based on genomic selection in relation to what family they belong to. This makes it possible to select candidates at an individual level instead of at the family level, thereby increasing the precision and genetic progress, while at the same time reducing the rate of inbreeding.*

Linking sea lice density to DNA codes through genomic selection

The number of sea lice attached to each fish is standardised, so that we have a measure of sea lice density per kilo of fish. All genetic expressions from the 58,000 SNPs in each individual fish are then linked to phenotype of sea lice density. An catalogue is thereby developed of all the combinations of genetic expressions that can arise in a fish given the amount of sea lice attachment it has. New tests are added to the catalogue and the data basis becomes more and more complete. This means that we get estimates with higher accuracy.

We can now link the phenotypes and the genotypes of the fish from the challenge test to the fish we are considering using for breeding purposes. Through big pedigree matrices developed on the basis of DNA and genealogical data, we use information from the relatives that have undergone challenge tests. We compare the genotypes and estimate what kind of seal lice density we could expect for the breeding candidate if it were to undergo the same challenge test as its relatives. This is what we call genomic selection (Meuwissen et al., 2001).

From family to individual

A fish is born into a family of 10,000 to 20,000 full siblings. Breeding work on fish has therefore worked very well at a family level. Through challenge tests, we have ranked the families by how well they do in terms of sea lice resistance, and have done a selection for breeding based on family values.

Using genomic selection and genotype information directly for each breeding candidate, enables us to hand pick the best breeding candidates right down to the individual level. It has namely emerged that there is great variation within families. Even in the best families, there may be individuals who will perform poorly despite the family being the best on average, while we can also find outstanding candidates in the poorest families. We can thus include all the best candidates from across families, while excluding poor candidates that would otherwise have been assumed to be exceptional brood fish. Through genomic selection, we manage to refine our estimates even more, which will enable us to achieve the goal of increased sea lice resistance twice as quickly as before. **Figure 3** shows an example of individual variation within families.

Speeding up the genetic gain

The current situation in Norway means that we will not be able to fully exploit the potential of salmon farming until the industry has brought the sea lice problem under control. One of the solutions lies in the DNA. Breeding and genetics are fantastic tools that can make future generations stronger. SalmoBreed has now speeded up the genetic gain by using genomic selection to create the most sea lice resistant fish. In this way, we are contributing to ensure fewer rounds of delousing, cutting costs for the industry and improving animal welfare for the fish.

References

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