

THE GENETIC IMPACTS OF ESCAPED FARMED ATLANTIC SALMON ON THE WILD SALMON POPULATIONS IN NORWAY

Introduction:

The aquaculture industry's exponential growth in the past decades has contributed to environmental challenges the industry now have to face. One of the most persistent and significant issues of them all is farmed escapees and subsequent genetic interaction with wild populations.

Escaped farmed salmon enter the rivers to spawn and interbreed with the wild stocks. This creates a hybrid with lower viability and may have consequences for the stock's future. The aim of the study is to examine whether there is a connection between the number of escaped farmed salmon and genetic changes in the Norwegian wild Atlantic salmon population, in the 13 different production areas in Norway.

We hypothesize that increased farmed salmon escapees, will lead to a higher genetic change in the wild Atlantic salmon population.





Ingen genetiske endringer observert
Svake genetiske endringer indikert
Moderate genetiske endringer er påvist
Store genetiske endringer er påvist

Results:

The data is obtained from a monitoring program performed by the Norwegian Institute of Marine Research. The number of escapees is a result of the average number in each production zone 1-13 in Norway in the time period 2014-2018.

Methods:

Data collection:

The fishing methods used were sports-, autumn- and breeder fishing, as well as drift counting and shell analysis. In some waterways salmon were caught by traps and video recordings. Each escaped farmed salmon caught is euthanized to ensure no further genetic crossing and the possibility of re-catch.

Genetic changes in wild salmon in rivers in Norway, because of escaped farmed salmon, are surveyed and mapped by Institute of Marine Research. Number of salmon escapes between 2014 - 2018 in Norway, is taken from the Norwegian Directorate of Fisheries website.

Data analysis:

The data from each river considers the number of salmon examined, the size of

Figure 1 presents the correlation and relationship between escapees and amount of genetic crossing by linear regression. The x-axis shows the number of escaped fish while the y-axis shows the genetic crossing.

The linear regression line shows a slight increase in genetic crossing in relation to increasing escapees. The results indicate that the genetic crossing is higher when the number of escapees is high. However, the graph also shows a large spread in the observations. The linear model returns the formula 5.188 + 8.989e-05x = y, with an R-squared of 0.06467 and p value of 0.4018.



Relationship between genetic crossing and escapees in year 2014-2018

the wild population, fishing effort, fishing area, methods used and time of survey. The survey will give an overview about the relative genetic changes from escaped farmed salmon in the rivers. The monitoring program divides the rivers into 13 different production areas, to ensure a representative collection of data and a comparison between them.

Linear regression:

Linear regression was used to generate a plot that shows the relationship between the number of escaped salmon and the amount of genetic crossing in wild salmon. Figure 1: The relationship between the number of escaped salmon and percentage genetic crossing for 13 different production zones. The relationship is presented with linear regression $(5.188x + 8.989e-05 = y, R^2 = 0.06467, p = 0.4018)$. The regression line shows a weak positive correlation between the parameters.

Conclusion:

The results indicate that the genetic crossing is higher when the number of escapees is high. The genetic changes increases with higher genetic crossing. The results therefore supports the hypothesis. However, due to the large spread in the observations and a large p-value, the credibility of the data and our conclusion is weakened.

