

Breakthrough for DNA investigations of escaped salmon

The debate over the potential genetic effects of escaped farmed salmon on wild salmon goes back for more than 20 years. As early as the 1980s, large numbers of escaped salmon were being registered in the sea and in a number of wild salmon stocks. With the aid of new DNA methods, we can now study salmon stocks and how these change as a result of escapes; studies that would have been impossible only a few years ago.

BY ØYSTEIN SKAALA

The new methods also make it possible to draw up genetic profiles of a salmon stock in a given river on the basis of the DNA in old salmon scales. This means that we can now compare old profiles with the profiles of the stock in the same river today.

Large numbers of escaped salmon have found their way to such rivers as the Etnelvv, Oselv, Vestre Jakobselv, Namsen and many others. Are these and other important stocks now so mixed up with

farmed salmon that they have lost their own particular characteristics, or do we still have wild salmon stocks that have not been affected by escaped farmed salmon? With the new DNA profiling methods we will finally be able to answer this question.

EVIDENCE OF GENETIC CHANGES

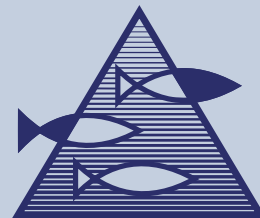
In 2004, the Institute of Marine Research (IMR) published the DNA profiles of the five



The new DNA method was used in autumn 2006 to trace escaped salmon back to a specific sea-cage.

Photo: Tore Wiers





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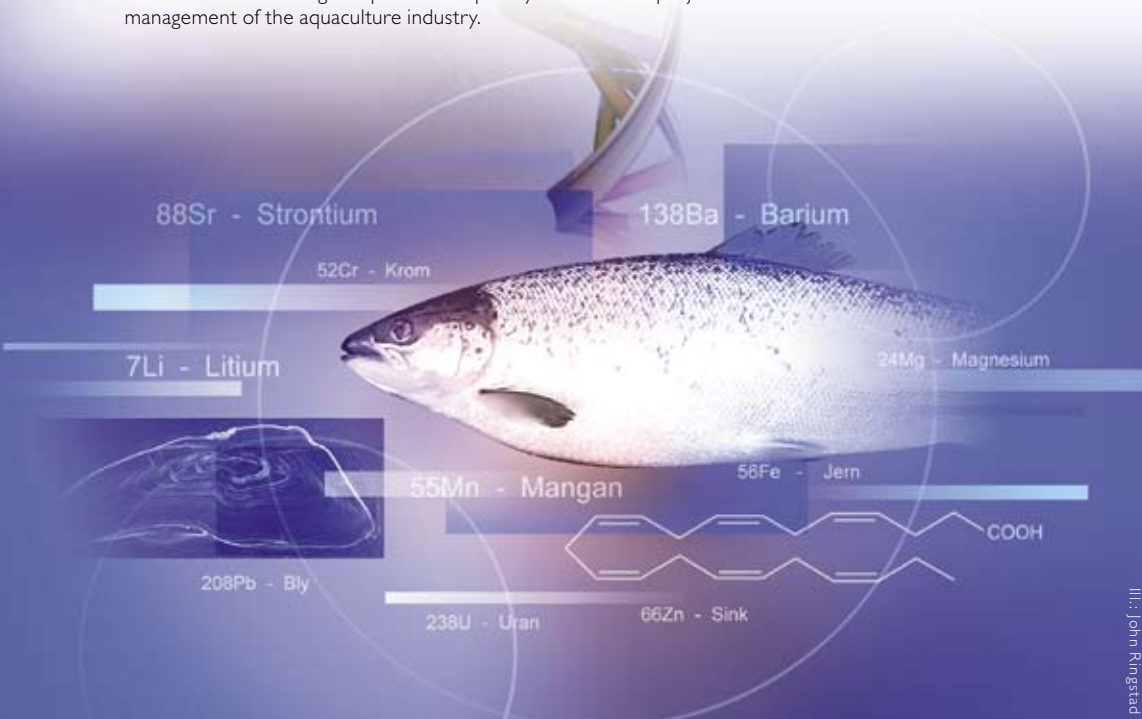
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Population genetics

The method for tracing escapees developed by the TRACES project will be a useful tool for management of the aquaculture industry.



Ill.: John Ringstad

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most important farmed salmon lines, and of a selection of wild salmon stocks. This is the largest DNA study ever published on Norwegian salmon. With the aid of these profiles, we were able to distinguish the five farmed lines to an accuracy of about 97%, while farmed salmon could be distinguished from wild salmon to an accuracy of 96%.

DNA profiles drawn up on the basis of DNA in old salmon scales suggest that the salmon stock in the Rivers Håelv, Namsen, Etne and Granvin have remained stable. However, genetic changes were found in salmon in the Rivers Vosso, Opo and Eio, that is, three out of seven studied populations, all of which have a high immigration rate of escaped salmon.

SUCCESSFUL PRACTICAL APPLICATION

In autumn 2006, local fishermen in the Romsdalsfjord in western Norway reported a sudden increase in catches of escaped salmon, although no escapes in that area had been reported to the Directorate of Fisheries. When asked, none of the fish farmers in the area said that they had lost fish. In collaboration with IMR, the Directorate of Fisheries collected samples from all the sea-

cages in the region. Samples were taken from a total of 16 sea-cages in seven farms. DNA was also extracted from 29 of the escapees and was typed for 15 genetic markers.

The results showed that none of the 29 escapees could be matched to 12 of the 16 sea-cages, but that 20 of the 29 escapees (69%) matched the genotypes of the salmon in one specific sea-cage; i.e. a very clear signal. The police authorities concluded that the results were sufficiently strong to warrant a full investigation of the owner of that particular sea cage.

DOES NOT REQUIRE TAGGING

The method for tracing escapees developed by the TRACES project is a “stand-by” method for rapid intervention that uses only naturally occurring characteristics of the fish, such as DNA profiles, so that artificial tagging is unnecessary. Moreover, there is no need to store material or data, as each escapee is treated as a separate case. The method has proved to be successful under certain conditions and can therefore be utilised in the management of the aquaculture industry, but will be developed further to increase the accuracy of the results.

