

Genome sequencing paves the way for more sustainable herring fishery

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An international team of Swedish, Norwegian, Danish and Irish scientists has used whole genome sequencing to characterize 53 herring populations from the Atlantic Ocean and the Baltic Sea. They have

developed genetic markers that make it possible to better monitor herring populations and avoid overfishing. The study is published in the journal *eLife*.

"This project provides a 'toolbox' in the form of genetic markers for cost-effective screenings that can be applied to monitor [herring](#) stocks throughout their [life history](#) from the [larval stage](#) to the adult stage," concludes Professor Arild Folkvord of Bergen University, who led the GENSINC project, which this study is part of. "It will now be possible to distinguish different stocks when they are mixed on the feeding grounds, for instance, which will help set fishing quotas that harness sustainable exploitation of genetically defined stocks."

The Atlantic herring is one of the most abundant vertebrates on Earth. It has been estimated that the total breeding [stock](#) of herring in the Atlantic Ocean and adjacent waters amounts to about one trillion fish.

Herring constitute this enormous biomass because they feed on plankton. They in turn are an important food resource for other fish, seabirds and sea mammals like the fin whale. Herring fishery has been an important food resource since humans colonized Northern Europe. Herring are schooling fish and therefore susceptible to overfishing because many tons of herring can be caught in a single haul during fishing, and in the past several stocks of herring have collapsed due to overfishing.

A grand challenge for the future is to avoid overfishing and maintain viable stocks of marine fish exploited in marine fishery. Stocks of herring are defined by where and when they spawn, but until now no efficient genetic markers have been available for distinguishing different stocks.

When Professor Leif Andersson of Uppsala University, who has led the [genetic analysis](#), first started to study the Atlantic herring in the late

1970s, only a handful of [genetic markers](#) could be used. To their surprise, scientists found that all the markers they analyzed occurred at the same frequency across all populations of herring. The reason for this lack of genetic differences for most [genes](#) is that the [population](#) size is huge and there is [gene flow](#) between populations, making the frequencies of gene variants stable over time and space.

"In the present study we have sequenced the entire genome and studied millions of genetic variants," explains Dr. Fan Han, a former Ph.D. student at Uppsala University and first author on the article. "Now our resolution is completely different, we find very clear genetic differences for a limited number of genes that appear to distinguish all major stocks of Atlantic herring."

The researchers found gene variants for a few hundred genes that are particularly important for the genetic adaptation to factors such as differences in spawning season, salinity and water temperature at spawning. These are the gene variants that are most useful to distinguish different stocks.

"The results of this study make Atlantic herring particularly well suited for studies on the impact of global warming on fish populations," explains Leif Andersson. "Some of the detected gene variants are strongly associated with water temperature at spawning. The gene variants that occur at a very high frequency in the waters surrounding Ireland and Great Britain, which are the warmest waters where herring reproduce, are expected to become more common further north as the seawater gets warmer."

More information: Fan Han et al. Ecological adaptation in Atlantic herring is associated with large shifts in allele frequencies at hundreds of loci, *eLife* (2020). [DOI: 10.7554/eLife.61076](https://doi.org/10.7554/eLife.61076)

Provided by Uppsala University

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