

The herring genome provides new insight on how species adapt to their environment

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How species genetically adapt to their environment is a central question related to the evolution of biodiversity. In a new study scientists at Uppsala University and their colleagues report that whole genome sequencing of Atlantic and Baltic herring revealed hundreds of loci underlying adaptation to the brackish Baltic Sea or timing of reproduction. The study is published today in eLife.

The Atlantic herring is one of the most abundant fish in the world and has been a crucial food resource in northern Europe. One school of herring may comprise billions of fish, and it has been estimated that just the weight of the eggs that herring spawn along the coast of Norway is three times higher than the weight of the Norwegian population! Previous studies based on very few genes had hardly revealed any genetic differences among herring from different geographic regions. This was unexpected since Atlantic herring is one of the few marine species that can reproduce throughout the brackish Baltic Sea, which can be about a tenth as salty as the Atlantic Ocean. This unexpected finding could be explained in at least two different ways. Firstly, perhaps Atlantic herring are flexible enough to adapt to very different environments (i.e. high or low salinity) without much genetic change. Secondly, the previous studies only looked at a handful of sites in the Atlantic herring's genome and so it is possible that [genetic differences](#) at other genes control this fish's adaptation instead.

"I was involved in one of these early studies as an undergraduate student at Stockholm University in the late 1970s and during the last 35 years I

have wondered which of these explanations are the correct one," explains Leif Andersson professor at Uppsala University, Swedish University of Agricultural Sciences and Texas A&M University, who led the study. I was convinced that by applying the new sequencing technologies that have revolutionized biology we would eventually get the final answer.

"The new study reveals that the Atlantic herring is a near ideal model to study genes underlying ecological adaptation," says Leif Andersson. Firstly, it is highly adaptable and it shows a considerable diversity in spawning time. Secondly, the population size is enormous which makes random fluctuations in the frequency of gene variants of minor importance. Thus, the signal-to-noise ratio for detecting natural selection is exceptionally good in this species.

Now the scientists have sequenced entire genomes from groups of Atlantic and Baltic herring and revealed hundreds of sites that are associated with adaptation to the Baltic Sea. The study also identified a number of genes that control when these fish reproduce by comparing herring that spawn in the autumn with those that spawn in spring. This is important because natural populations must carefully time when they reproduce to maximize the survival of their young. These new findings provide compelling evidence that changes in protein-coding genes and stretches of DNA that regulate gene expression both contribute to adaptation. The study also showed that variants of genes that contribute to adaptation were likely to evolve over time by accumulating multiple sequence changes affecting the same gene.

"The Atlantic herring has a rich toolbox composed of gene variants that underlies its ability to adapt to its environment," explains Sangeet Lamichhaney PhD student and shared first author. Different subpopulations of herring have their own optimal sets of adaptive gene variants. For instance, autumn-spawning herring and spring-spawning

herring from the Baltic Sea both have gene variants that favour adaptation to low salinity. However, autumn-spawning Baltic herring also share gene variants that control timing of reproduction with autumn-spawning herring from the North Sea.

The study has many important implications.

"The herring fishery is the fifth largest fishery in the world and the wealth of information on herring population biology that we now reveal can be used to develop more accurate stock assessments and thereby more sustainable fishery," says Alvaro Martinez Barrio, scientist at Science for Life Laboratory and shared first author. Furthermore, our identification of genes controlling the timing of reproduction have implications for how species can cope with climate changes as the optimal time for reproduction may change as a consequence of global warming.

A characteristic feature of good science is that it answers old questions but raises new questions for future research. The scientists have now revealed more than 500 loci in the herring genome that is underlying ecological adaptation and this provides a gold mine for future research. Some of these genes have previously been associated with disease in humans and are therefore often well studied whereas the functions of others are completely unknown.

"I am convinced that further research on this rich collection of genes associated with ecological adaptation will lead to new basic knowledge about gene functions that will be relevant also for human medicine since the majority of [genes](#) in herring are also found in humans and are expected to have similar functions," says Leif Andersson.

More information: Alvaro Martinez Barrio et al. The genetic basis for ecological adaptation of the Atlantic herring revealed by genome

sequencing, *eLife* (2016). [DOI: 10.7554/eLife.12081](https://doi.org/10.7554/eLife.12081)

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