

New genomic mechanisms of fish survival in the extreme cold revealed

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An international team based at the University of Cambridge and the Wellcome Sanger Institute in the U.K., the University of Oslo in Norway as well as institutes in the Netherlands, Switzerland and the U.S. has sequenced the genomes of 24 Antarctic fish species. Their work, published in *Nature Communications*, enables the study of how these fish

survive in the subzero Southern ocean, and sheds light on the evolutionary history of these iconic animals.

Notothenioids are a unique group of fish species. They live in the [cold waters](#) below the Antarctic ice, largely isolated from the rest of the marine world by a circular current around the continent. The Notothenioids have evolved [antifreeze proteins](#) which allow them to survive the [water temperatures](#), which can reach -2°C —an environment hostile for most species. One subgroup of notothenioids—called "icefish" have lost their oxygen-binding hemoglobin proteins and that makes them the only vertebrates known to not have red blood cells.

The researchers sequenced the genomes of 24 species of notothenioid fish. These new genome data were generated using the latest long-read technologies, which enabled the team to determine the sequence of complex, repetitive regions of DNA in the genome that it has not previously been possible to decipher. Using these new data they explore the evolutionary history of the notothenioids and the mechanisms that support adaptation to extreme cold. They show that the cold-resistant notothenioids split off from other species about 10.7 million years ago, which is more recent than was previously thought, and many new species started evolving rapidly at approximately 5 million years ago.

Several genomic characteristics have aided the survival and establishment of this group. The researchers found that the size of the genome has doubled in the species that specialize in [extreme cold](#), such as the family of Channichthyidae or "icefish." This expansion of the genome size was due to a large increase in the number of genomic elements known as transposons which have the ability to copy themselves into new positions within the [genome](#) and can potentially introduce new functions.

At the same time, functions that are normally considered essential for

survival such as the production of hemoglobin, have been lost in the "icefish."

"Survival in such a [harsh environment](#) requires additional compensations of the organism, and these fish have developed special proteins that act as antifreeze to stop them from freezing," says Dr. Iliana Bista.

"These fish are the only vertebrates known to have completely lost their hemoglobins, and their blood looks white. This is remarkable because hemoglobins are needed to transport oxygen through the body; their loss in icefish is only possible because oxygen dissolves better in water at very low temperatures, and because of additional genomic and physiological adaptations."

"Notothenioid fish live at the edge of viability. Sequencing a broad collection of their genomes gives insights into how they have evolved to survive there, and supports our understanding of a critical ecosystem. This study is a great example of how advances in genomics are revolutionizing our ability to understand biodiversity across the world," says Professor Richard Durbin.

More information: Iliana Bista et al, Genomics of cold adaptations in the Antarctic notothenioid fish radiation, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-38567-6](https://doi.org/10.1038/s41467-023-38567-6)

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