

Researchers explore the hagfish genome, reconstruct the early genomic history of vertebrates

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Hagfish are a type of jawless fish that typically live in deep ocean waters far from the light of the sun. Credit: Masakazu Suzuki, Ph.D., Department of Science, Graduate School of Integrated Science and Technology, Shizuoka

University, Japan

A study by a group of researchers at the University of Kentucky in collaboration with scientists in four other countries has been published in *Nature*. Their study is titled "[The hagfish genome and the evolution of vertebrates.](#)"

Jeramiah Smith, Ph.D., a professor in the Department of Biology in the College of Arts and Sciences, collaborated with an international research group to piece together the hagfish genome and better understand the early evolution of vertebrates.

Hagfish are a type of jawless fish that typically live in deep ocean waters far from the light of the sun. They are scavengers that play an important role in marine ecosystems. These weird creatures are perhaps best known for their ability to produce huge amounts of slime to protect themselves from predators. Hagfish and lampreys are the only surviving jawless fish.

What do these unusual fish contribute to science? Their [genetic material](#) helped researchers like Smith, along with postdoctoral scholars Nataliya Timoshevskaya, Ph.D., and Vladimir Timoshevskiy, Ph.D., piece together a comprehensive picture of vertebrate genome evolution and improve our understanding of how the large collection of genes with our own genomes came to be.

This work expands upon Smith's previous research on the genome of lampreys.

"In this project, we analyzed the genome of the brown hagfish to help resolve some difficult questions about early vertebrate evolution," said Smith. "We know it was accompanied by a series of ancient polyploidization events—a genetic change where more than the usual two sets of chromosomes end up in cells."

In looking at the brown hagfish, researchers were able to resolve new details of genome duplication events, predating the origin of modern vertebrates (animals with a backbone or spinal column) around 500 million years ago, in jawed and jawless vertebrates.

The team of researchers also compared hagfish and lamprey genomes to point out the genetic changes separating the two jawless fish and the unique biology of hagfish.

"Over time, hagfish lost the genes related to developing organs like eyes and cartilage," said Smith. "However, we saw hagfish have also expanded a few gene families, including slime-producing genes."

Because hagfish evolved millions of years ago, Smith said conventional methods to study [evolutionary history](#), or phylogenetics, didn't give researchers the answers they sought.

"We used the hagfish [genome](#) and a new approach focused on chromosome-scale phylogenetics to fully resolve this history of ancient vertebrate polyploidies," said Smith. "In doing so, we were also able to identify, for the first time, a collection of genes that are also regulated by a natural form of genetic engineering in [hagfish](#) 'programmed DNA elimination' where some genes are deleted during development.

"Reconstruction of the early genomic history of vertebrates provides a valuable foundation for understanding where most of the genes in humans and other animals came from, and how genomes work in

general," said Smith. "This research also further explores the evolution of vertebrates and gives us an opportunity to learn more details about our deep ancestry."

More information: Ferdinand Marlétaz et al, The hagfish genome and the evolution of vertebrates, *Nature* (2024). [DOI: 10.1038/s41586-024-07070-3](https://doi.org/10.1038/s41586-024-07070-3)

Provided by University of Kentucky

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