

Researchers sequence the first genome of myxini, the only vertebrate lineage that had no reference genome

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Credit: University of Malaga

An international scientific team including more than 40 authors from seven different countries, led by a researcher at the University of Malaga

Juan Pascual Anaya, has managed to sequence the first genome of the myxini, also known as hagfish, the only large group of vertebrates for which there has been no reference genome of any of its species yet.

This finding, published in the journal *Nature Ecology & Evolution*, has allowed for deciphering the evolutionary history of [genome](#) duplications that occurred in the ancestors of vertebrates, a group that includes humans.

"This study has important implications in the evolutionary and molecular field, as it helps us understand the changes in the genome that accompanied the origin of vertebrates and their most unique structures, such as the complex brain, the jaw and the limbs," explains the scientist of the Department of Animal Biology of the UMA Pascual Anaya, who has coordinated the research.

Thus, this study, which took almost a decade, was carried out by an [international consortium](#) that includes more than 30 institutions from Spain, United Kingdom, Japan, China, Italy, Norway and the United States, including the University of Tokyo, the Japan research institute RIKEN, the Chinese Academy of Science, and the Centre for Genomic Regulation in Barcelona, among others.

Ecological link

The myxini are a group of animals that inhabit deep ocean areas. Known for the amount of mucosa they release when they feel threatened, a focus of research of cosmetic companies, and also for their role as an ecological link in the seabed (since they are scavengers and are responsible for eliminating, among other things, the corpses of whales that end up at the bottom of the sea after dying), until now their genome had not been sequenced due to its complexity.

They are composed of a large number of microchromosomes, which in turn are composed of repetitive sequences. This is in addition to the difficulty of accessing biological material.

"Besides, these microchromosomes are lost during the development of the animal, so that only the genital organs maintain a whole genome," says Juan Pascual Anaya.



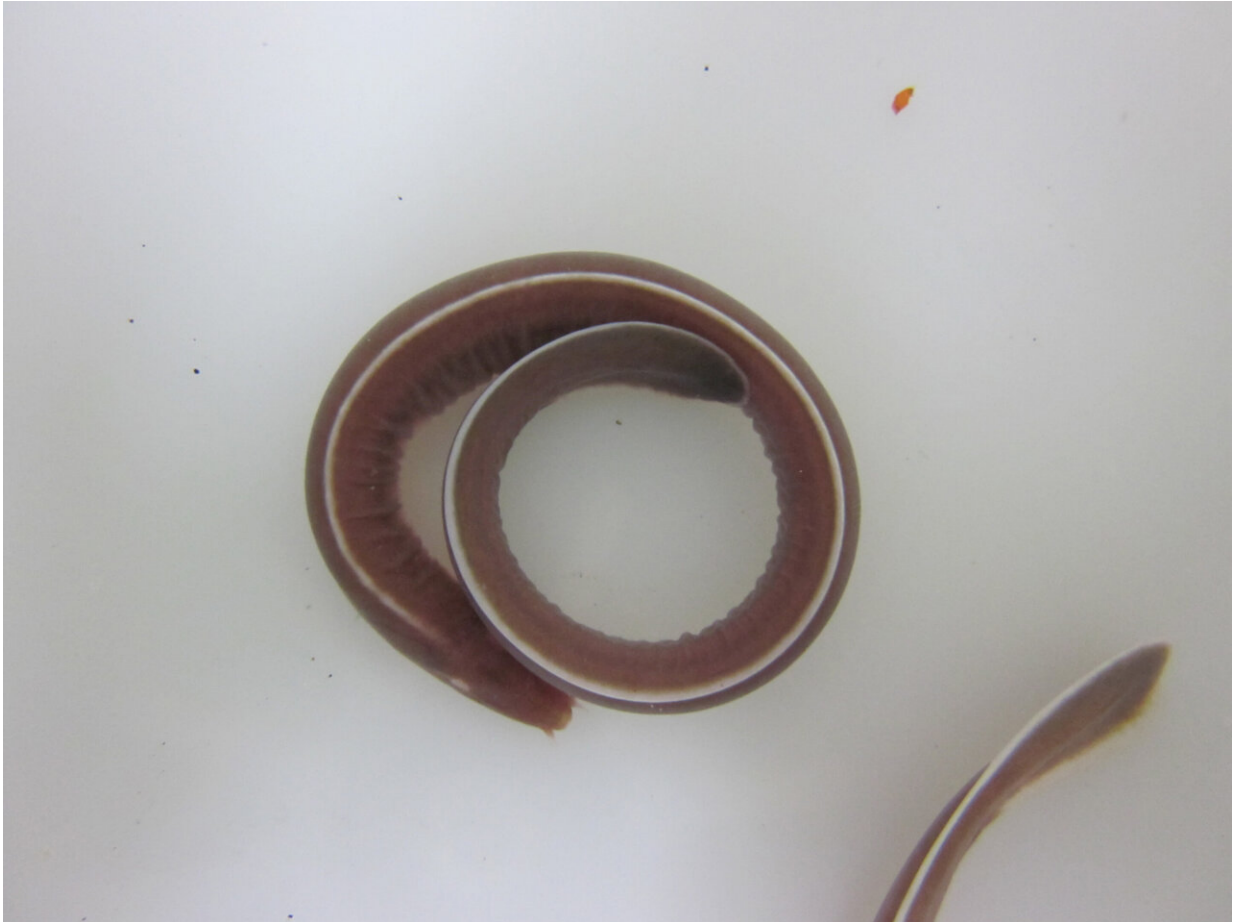
Credit: Universtiy of Malaga

Genome duplications

For this study, the sequenced genome was that of the *Eptatretus burgeri*, which lives in the Pacific, on the coasts of East Asia. To achieve this, the researchers generated data up to 400 times the size of its genome, using advanced techniques of chromosomal proximity (Hi-C) and managing to assemble it at chromosome level.

"This is important because it allowed us to compare, for example, the order of genes between this and the rest of vertebrates, including sharks and humans, and thus solve one of the most important open debates in genomic evolution: the number of genome duplications, and when these occurred during the origin of the different [vertebrate](#) lineages," says the UMA scientist, who adds that thanks to this we now know that the common ancestor of all vertebrates derived from a species which genome was completely duplicated once.

Later, according to Pascual Anaya, the lineages that gave rise to modern mandibular and non-mandibular vertebrates separated, and each of these re-multiplied its genome independently: while the former, which includes humans, duplicated it, the latter tripled it.



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Evolutionary impact

An analysis of the functionality of genomes, based on extremely rare samples of myxini embryos, carried out in the laboratory of Professor Shigeru Kuratani of RIKEN; and a study on the possible impact of genome duplications on each vertebrate, developed together with the Professor at the University of Bristol and member of the Royal Society Phil Donoghue, complete this multidisciplinary research that is key to understanding the evolutionary history of vertebrates.

The study provides perspectives on the genomic events that likely drove the appearance of important characteristics of vertebrates, such as [brain structure](#), sensory organs or [neural crest cells](#), and among them, an increase in regulatory complexity (a greater number of switches that turn genes on/off).

More information: Hagfish genome elucidates vertebrate whole-genome duplication events and their evolutionary consequences', *Nature Ecology & Evolution* (2024). [DOI: 10.1038/s41559-023-02299-z](https://doi.org/10.1038/s41559-023-02299-z)

Provided by University of Malaga

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