



GENOME STERLET STURGEON

Skype March 31, 2020 Genetics 21 Views

Scientists Decode Genome of Sterlet Sturgeon

An international team of researchers from the United States and Europe has produced the first high-quality genomic sequence for the sterlet (*Acipenser ruthenus*), a small species of sturgeon from Eurasia.



The sterlet (*Acipenser ruthenus*). Image credit: Andreas Hartl.

Sturgeons are among the oldest species on Earth in terms of evolutionary history. They are the ancestors of more than 30,000 species of bony fish that occur today and thus of more than 96% of all living fish species and about half of all known vertebrate species.

Sturgeons are distributed from subtropical to subarctic rivers, lakes and coastlines of Eurasia and North America.

They are long-lived and reproduce late, usually not before reaching an age of ten years. In many sturgeon species, adults migrate repeatedly from the sea into freshwater to spawn.

Sturgeons are celebrities among fishes because of their pre-ovulation female gametes, known as caviar.

Despite their ancient lineage, peculiar biological features and economic value, sturgeon genomes have

remained largely unexplored.

“Sturgeon genomes are an important piece of the puzzle that helps us understand the ancestry of vertebrates. And this has been missing until now,” said co-lead author Professor Manfred Schartl, a researcher at the University of Wuerzburg, Texas State University and Texas AM University.

“Their external appearance has changed very little since that time and this is also evident in their genetic material, the DNA,” added first author Dr. Du Kang, from the University of Würzburg.

The team successfully assembled a high-quality chromosome-level reference genome for the sterlet sturgeon.

The analysis revealed that the genome comprises 1.8 billion base pairs, 120 chromosomes and about 47,500 protein-coding genes.

It also revealed a very low protein evolution rate that is at least as slow as in other deep branches of the vertebrate tree, such as that of the coelacanth.

“The rate of protein evolution of the sterlet is similar to that of the coelacanth or of sharks — two fish species that have been roaming the oceans almost unchanged for more than 300 million years as well,” said co-lead author Dr. Matthias Stöck, an evolutionary biologist in the Leibniz-Institute of Freshwater Ecology and Inland Fisheries.

The scientists found that sturgeons branched off onto their own evolutionary path at some point during the Upper Devonian or Carboniferous period about 345 million years ago.

They also found that the sterlet duplicated its genome some 180 million years ago, leaving the species instead of the regular two with four sets of chromosomes, which is called tetraploidy.

“Such processes have repeatedly had a major impact on the evolution of the vertebrate genome,” Professor Schartl said.

“Already their ancestors underwent ‘whole genome duplication’ twice in their evolutionary history. Some species went through this process as many as three or four times.”

The fact that surprised the researchers was that the duplication happened so far back in the long history of the sturgeon.

“Over this long time span, we would have expected the genome to change more profoundly because in

tetraploid organisms gene segments are often lost, silenced or acquire a new function over time,” said Professor Axel Meyer, an evolutionary biologist at the University of Konstanz.

The exact genomic state of sturgeons was long controversial among scientists.

While considered polyploid by some, which means that the genome was duplicated multiple times, others interpreted the sturgeon as a functional diploid, which refers to a species that first duplicated its genome to become tetraploid but then reduces the gene content again as it evolves. Although the chromosomes are still present in two pairs, they divide their tasks among themselves.

“We have found out that the sterlet has not returned to a diploid state. Instead, it has retained an unexpectedly high degree of structural and functional polyploidy,” Professor Schartl said.

“This retention can be ascribed to the slow pace of molecular evolution of most fractions of the sterlet genome.”

The results were published in the journal *Nature Ecology and Evolution*.

K. Du *et al.* The sterlet sturgeon genome sequence and the mechanisms of segmental rediploidization. *Nat Ecol Evol*, published online March 30, 2020; doi: 10.1038/s41559-020-1166-x

