Great Lakes Fishery Commission

For Immediate Release
August 24, 2021

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International team assembles the Lake Trout genome

First-ever genome could unlock mysteries of this key native species

Ann Arbor, MI—An international team of U.S. and Canadian researchers have recently completed assembling, for the first time, a reference genome for lake trout – one of the most well-known and well-studied native fish species in the Great Lakes region. A reference genome is a standardized digital sequence or map of nucleic acids, which code the building blocks of life, assembled into a set of genes. The genome assembly was presented in a paper recently published in the journal Molecular Ecology Resources titled "A chromosome-anchored genome assembly for Lake Trout (*Salvelinus namaycush*)." With this completed genome assembly, scientists will now have the tools to reveal the genetic foundation for traits that have allowed lake trout to take advantage of the myriad habitats and conditions across the species' North American range. Moreover, the assembly will help scientists understand why different types of lake trout (called "morphotypes") survive and reproduce in the various ways they do. With this knowledge, fishery managers will be better equipped to take steps that will support lake trout conservation and restoration, in the wild and through the help of hatcheries.

The paper is available at http://doi.org/10.1111/1755-0998.13483.

Lead Investigator, Dr. Louis Bernatchez, Universite Laval said "This was a huge and synergistic international team effort that led to the production of one of the best fish genomes being assembled thus far. Beyond representing a unique set of genomic resources for a broad array of applications, such as marker development for studies of genetic population structure, mixed-stock analysis, and monitoring the success of hatchery programs, the lake trout genome will also contribute to an international effort toward understanding the evolution of the entire salmonid family by means of comparative genomics."

Salmonid (i.e., the family to which the lake trout belongs) genomes are notoriously difficult to assemble due to their highly repetitive nature and an abundance of duplicated genomic regions with highly similar sequences—meaning, larger proportions of sequences are repeated multiple times in the genomes of salmonids relative to many other animals. These regions are a byproduct of an ancient whole-genome duplication event that occurred between 80 and 100 million years ago within the ancestor of all Salmonids. The genomes of all vertebrates are also believed to have undergone multiple rounds of whole genome duplication, and the lake trout genome (in addition to genomes that have been produced for other Salmonids) will be valuable for exploring the evolutionary processes at play following these extreme events.

To overcome challenges associated with assembling a complex Salmonid genome, the researchers produced gynogenetic doubled haploid individuals, which are specially bred to lack diversity and only possess maternal DNA. The authors then used a combination of DNA sequencing technologies to assign 84.7% of the genome to 42 chromosomes that ranged in size from 22 to 98 million base pairs (building blocks of proteins) in length. The authors also produced a mitochondrial genome assembly that describes the locations of 37 genes that allow cells to produce energy, a map describing patterns of recombination across the genome, meaning, a description of how the genome is reorganized during reproduction, and a gene expression dataset that was used to determine the locations of genes within the larger genome. They also identified pairs of chromosomes resulting from the ancient Salmonid genome duplication event and delineated genomic regions with patterns of delayed sequence divergence between duplicated chromosomes.

The newly available reference genome will be a valuable tool for population geneticists and fisheries biologists collaborating on conservation-oriented research in addition to comparative genomics researchers interested in exploring the evolutionary consequences of whole-genome duplication. Lake trout express striking levels of biodiversity in Lake Superior and historically dominated nearshore and deep-water habitats across the Great Lakes; however, much of this diversity was lost over the last century.

“This work is a vital missing link in our efforts to restore lake trout, a key native species throughout the Great Lakes and North America,” said Professor William Taylor of Michigan State University, chair of the Great Lakes Fishery Commission. “The newly released genome assembly will allow researchers to better understand the genetic basis for traits that allowed lake trout to exploit a diversity of niches and habitats across their range. Additionally, the genome will allow researchers to identify genes and biological processes associated with variation in survival and reproductive success between hatchery populations that were used to reintroduce lake trout to the Great Lakes following significant declines in abundance and distribution that occurred during the mid-20th century due to over-fishing, pollution, and the introduction of invasive species, such as sea lampreys.”

"I'm extremely excited to see how people might draw from this resource over the next few years,” said Seth Smith of Michigan State University, the study’s lead author. “Lake trout are central to the culture of the Great Lakes region and have faced so many conservation challenges over the last decades. Having a publicly available map of the lake trout genome removes most of the initial hurdles associated with doing conservation-oriented genomic research, makes it significantly easier to compare results across studies, and will hopefully quicken the pace of scientific discovery."

The lead author on the paper is Seth Smith, who is currently a doctoral student in the Department of Integrative Biology and the Ecology, Evolution, and Behavior (EEB) program at Michigan State University. Co-authors include Eric Normandeau, Haig Djambazian, Pubudu N. Mudiyanselage, Andrew Muir, Joannis Ragoussis, Chantelle Penney, Kim T. Scribner, Gordon Luikart, Chris C. Wilson, and Louis Bernatchez from Michigan State University, Université Laval, the University of Montana, McGill University, Trent University, the Ontario Ministry of Northern Development, Mines, Natural Resources and Forestry, and the Great Lakes Fisheries Commission. This research was funded by the Great Lakes Fishery Commission (L. Bernatchez and Andrew Muir) and CanSeq150 (L. Bernatchez and J. Ragoussis; McGill University).

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