

Stickleback genomes shining bright light on evolution (w/ Video)

February 26 2010



This is William Cresko, a biologist at the University of Oregon, in his office in January 2010. His lab teamed with a second UO lab on a comprehensive genetic comparison of populations of saltwater and freshwater threespine stickleback, finding regions of genes involved in their evolution. Credit: Photo by Jim Barlow

Twenty billion pieces of DNA in 100 small fish have opened the eyes of biologists studying evolution. After combining new technologies, researchers now know many of the genomic regions that allowed an ocean-dwelling fish to adapt to fresh water in several independently evolved populations.

The discovery -- made possible in a project funded by the National Science Foundation and National Institutes of Health -- involved threespine stickleback fish taken from three land-locked freshwater Alaskan lakes and two ocean populations. The work appears in the Feb.

26 issue of [PLoS Genetics](#), an open-access online publication of the Public Library of Science.

A six-member UO team across two separate labs combined Illumina massively parallel sequencing with a specialized technology that they developed. They then compared the genomes of 20 fish each from Alaska's Bear Paw, Boot and Mud lakes, and 20 each from saltwater populations in Rabbit Slough and Resurrection Bay.

All sites are located along Alaska's south-central coast. Researchers found that all of the fish were closely related in most of their genomes, but with differences in very specific regions. Each fish contains 500 million base pairs of DNA. Researchers were surprised to find that across the independently derived populations very similar regions were identified, indicating that the same genes may be evolving when stickleback adaptation is repeated in different lakes. Researchers now are focusing efforts to understand which specific genes are involved in such adaptation.

The approach taken in the study, said William A. Cresko, professor of biology and member of the UO's Center for Ecology and [Evolutionary Biology](#), could be applied to other organisms. "It would be fascinating to determine whether similar results would be found in studies of ocean-dwelling sockeye salmon and their freshwater counterparts the Kokanee, for example," he said. The findings, presented at professional conferences, he added, already are fueling research efforts in a variety of other organisms around the world.

Sticklebacks are a small silver-colored fish, barely two inches in length; they are found throughout the Northern Hemisphere in both oceans and freshwater.

"Populations of freshwater stickleback arise when new habitats open up

and are colonized," Cresko said. "Alaska has a lot of lakes that have been around only about 10,000 years, formed after glaciers receded. Instead of dying out when they were cut off from saltwater, they evolved very rapidly and in a lot of ways, such as in their bones and armor, the shapes of their jaws, as well as coloration and behavior. When one population no longer recognizes and won't mate with another population, they effectively become a new species, so some of the regions we are identifying may be important for speciation, too."

Sticklebacks have long been a focus for behavioral biologists because of their complex courtship rituals. Only recently have they come under genetic and genomic scrutiny, and the UO has been at the forefront of such studies. Until recently, efforts focused on small numbers of traits, tracking just a few genes at a time. In a 2006 talk on campus, Cresko outlined the challenges of the research, saying that faster, cheaper DNA-analyzing tools were needed to scan entire genomes. In the audience was Eric Johnson of the UO's Institute of Molecular Biology.

For the next three years, Cresko and Johnson worked to develop a technique they called Restriction-site Associated DNA -- the development of which helped spawned Floragenex, a UO technology spinoff company -- and subsequently combined it with a genomic revolution called Next Generation Sequencing using a genome-analyzer tool known as Illumina's GA2 sequencer.

"We combined two technologies to develop sequence RAD (restricted-site associated DNA) tags," Cresko said. "With this, we can quickly look across entire genomes and ask new questions: Can we find genomic regions that were altered due to natural selection? And then compare this with a completely evolved population? How many regions are the same, how many are different?"

Previous research using RAD markers had focused on finding

differences between samples grown in labs, Johnson said, "but many interesting biological questions can't be assayed in a lab, and many species of animals cannot be reared in a lab."

"Bill's lab showed that RAD markers can detect differences between natural populations, and his lab developed new analytical tools to understand the data," Johnson said. "It is a great fit for RAD markers, because they sample a [genome](#) at a higher density than other marker systems and provide DNA sequence data at a low error rate -- two crucial aspects for this kind of study."

Once the technology was ready, it took Cresko's team about six months to run the [DNA](#) analyses. Now that the technique is operating smoothly, the same experiments might be done in several weeks, he said.

Under a new NSF-funded project under the American Recovery and Reinvestment Act, Cresko and Frank von Hippel, a University of Alaska biologist, are looking closely at another set of stickleback populations. They are working on lakes formed when the 1964 Alaska earthquake lifted several offshore islands 10 meters (32.8 feet) in four minutes. "We hope to learn something about these fish while they are still evolving, literally, from an ocean population to a freshwater one," Cresko said.

More information: [www.plosgenetics.org/article/i ... journal.pgen.1000862](http://www.plosgenetics.org/article/i...journal.pgen.1000862)

Provided by University of Oregon

Citation: Stickleback genomes shining bright light on evolution (w/ Video) (2010, February 26) retrieved 26 April 2024 from <https://phys.org/news/2010-02-stickleback-genomes-bright-evolution-video.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.