

# Evolution in action: Genetic study may answer why we have plenty of fish in the sea

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A model for evolutionary change. Sticklebacks are small migratory fish that have colonized many lakes and streams of the Northern Hemisphere (California stream male shown here). Scientists have recently decoded the genome of 21 populations around the world, making it possible to identify how genes change when organisms adapt over and over again to new environments.

(PhysOrg.com) -- Three-spine sticklebacks aren't as pretty as many aquarium fish, and anglers don't fantasize about hooking one. But biologists treasure these small fish for what they are revealing about the genetic changes that drive evolution. Now, researchers have sequenced the stickleback genome for the first time, and they have discovered that as fish in different parts of the world adapted to live in fresh water, the same sites in the genome were changed time and again.

Their findings, published April 5, 2012, in the journal *Nature*, indicate

that changes to both genes and, more commonly, stretches of DNA that control gene activity, have driven sticklebacks' adaptation to fresh water environments.

"The cool thing about these fish is that they've colonized a whole series of new environments in the last 10,000 to 20,000 years," says Howard Hughes Medical Institute (HHMI) investigator David Kingsley of Stanford University School of Medicine. As the glaciers melted at the end of the last ice age, marine sticklebacks ventured into fresh water, settling in rivers, lakes, and streams. The fish adapted to their new homes. Compared with their marine relatives, freshwater sticklebacks tend to be smaller and sleeker, with less bony body armor. The challenges of surviving in new habitats also prompted modifications to their teeth, jaws, kidneys, coloration, and numerous other traits. Moreover, this pattern of colonization and adaptation has repeated itself in several areas where sticklebacks live, including the east and west coasts of North America, western Europe, and eastern Asia. "A world-wide collection of lakes and streams became countless natural evolutionary experiments," says Kingsley.

These evolutionary experiments afford researchers the opportunity to uncover the genetic changes responsible for particular adaptations. In previous studies, Kingsley and colleagues have teased out three examples. In 2005, for instance, the researchers reported in *Science* that freshwater sticklebacks typically carry certain versions of the gene *Ectodysplasin*, which helps set the number of bony plates along a fish's side. Rare in marine sticklebacks, the reduced armor variants presumably became prevalent in most streams and lakes because less body armor was advantageous in fresh water, where speed was a better defense against local predators. However, Kingsley notes, this kind of detective work, which focuses on a particular morphological trait, relies on laborious techniques to map and pinpoint evolving genes, and took about five years to complete. In addition, he says, individual case studies

can't provide a general picture of the types of DNA changes most often used when fish adapt to new surroundings. To get that overview, the researchers needed the complete stickleback genome sequence.

For their latest study, Kingsley, scientists from the Broad Institute of MIT and Harvard, and an international team of collaborators started by sequencing the genome of an Alaskan freshwater stickleback to serve as a standard for comparison. That was an achievement in itself, yielding the first complete stickleback genome sequence. Next, the team followed suit with the genomes of twenty additional sticklebacks from around the world, including ten ocean stickleback varieties found around North America, Europe, and Japan, as well as the genomes of ten freshwater relatives from nearby freshwater locations. They then analyzed the sequences to identify DNA regions that changed whenever the fish made the move from salt water to fresh.

The researchers found 147 "reused" regions in the fish's genome. That suggests that each time the fish left the sea, variants in this same group of genes helped remodel the fish into forms that were better suited to fresh water, Kingsley says.

So what are these genes? The reused regions include the key armor genes that Kingsley and colleagues previously identified, and many others involved in metabolism, developmental signaling, and behavioral interactions between animals. The study highlights some genes in which alterations likely aid fish adapting to life in a less salty environment. These genes, which are in the WNT family that helps orchestrate embryonic development, adjust the size of small tubes in the kidney that are involved in conserving salt. Freshwater fishes tend to lose salt to their environment, so they need longer tubes to recapture it from the fluid filtered by the kidneys instead of excreting it in their urine.

The stickleback sequences also allowed the researchers to tackle one of

the most contentious issues in evolutionary biology. Researchers have battled over what type of genetic changes spur evolution. Some scientists argue for changes to the coding sections of the genome, the portions that cells read to make proteins. More influential, other researchers contend, are alterations to regulatory DNA, which controls the activity of genes. "Here, it isn't either-or," says Kingsley. The team's analysis suggests that both kinds of changes occurred during stickleback evolution, but regulatory changes were about four times as common. "We finally get an idea of the relative contributions of both mechanisms, to a whole range of traits that have evolved in the wild," says Kingsley.

Using genome sequences to analyze the sticklebacks' natural evolutionary experiments "is showing us the genetic mechanism through which animals adapt to different environments," says Kingsley. With this approach, "we can find the key genes that control evolutionary change, helping to bridge the gap between alterations in DNA base pairs and the appearance of new traits in natural populations."

**More information:** The paper "The genomic basis of adaptive evolution in threespine sticklebacks" will be published in the 4 April 2012 issue of the journal *Nature* and available at [www.nature.com/nature/journal/...ull/nature10944.html](http://www.nature.com/nature/journal/...ull/nature10944.html)

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