

# Genetic buzzer-beater genes may save fish

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Two distinct populations of rainbow trout -- one in Alaska, the other in Idaho -- share a genetic trait that could have huge implications for fisheries conservation and management, an eight-member research team reports.

The common trait is a similar rapid rate of development that has allowed these different salmomid subspecies to adapt to their native rivers in Alaska and Idaho. The researchers, in a paper put online ahead of publication in the journal *Molecular Ecology*, say the similarity, a gene variant, resides in a specific portion of their genomes from where this local adaptation is triggered.

Understanding and applying that knowledge could help guide current and future efforts to save species on the brink of extinction and help rejuvenate dwindling populations, especially as changing conditions alter fish environments, says lead author Michael R. Miller, a National Science Foundation-funded doctoral student in the University of Oregon lab of co-author Chris Doe, a UO biologist and Howard Hughes Medical Institute investigator.

The research employed two technologies developed at the UO: the cloning technology pioneered on [zebra fish](#) 35 years ago by [molecular biologist](#) George Streisinger and a speedy genome-analysis tool known as RAD (restriction-site associated DNA markers). Miller and UO biologist Eric Johnson, with input from William Cresko, also a UO biologist, published their initial RAD-tagging technique in 2005.

The clone lines of rainbow trout used in the study were provided by co-author Gary H. Thorgaard, a fish geneticist at Washington State University. He had worked briefly as a postdoctoral researcher with Streisinger in 1978 to learn about a then-developing zebra-fish cloning technique later detailed in a 1981 Nature paper.

Rainbow trout (*Oncorhynchus mykiss*) are members of the salmon family. They have a natal homing instinct in which they return to their native streams or rivers to spawn. Occasionally, some end up in other locations and have to adapt, or evolve, to survive in a new habitat. In studying the genetics of populations in the North Fork Clearwater River in north-central Idaho and in the Swanson River of south-central Alaska, researchers noted similar, speedy rates of development -- a conserved trait that generally is not the case in rainbow trout, Thorgaard noted.

"We found that these two very distinct populations are using the same conserved variant of the same gene sequence to achieve this adaptation," Miller said. "We have not identified the exact gene or gene mutations, but we have identified a region of the genome that is very similar."

RAD gene-sequencing technology allowed the researchers to sort through the fish genomes -- [rainbow trout](#) populations have between 58 and 64 chromosomes -- until they isolated the gene variants, also known as mutations or alleles. "RAD gives us much better details with a much higher resolution on genetic markers than what we could ever see before," Thorgaard said.

"RAD is being applied widely in the field of fisheries genetics," Miller said. "This technology is having a huge impact on salmon genetics, for conservation, management and restoration."

The findings suggest that the same genetic method of adaptation may be used by other salmonids, which includes salmon, steelhead trout, char,

freshwater whitefish and graylings. The gene variant found in the study may have arrived just in time for struggling fish populations, researchers said.

"The study suggests that the same genetic types that are associated with adaptation in one [population](#) may also be used by another experiencing similar conditions in another area," Thorgaard said. "This increases our understanding of how adaptation occurs and could help in characterizing populations for conservation purposes."

Potentially, Miller said, matching fish with the same genetic variants could prove beneficial in increasing populations in distressed areas. "Many southern populations, in California, for instance, are already extinct or depressed, and these populations likely contain gene variants that may become important for the future adaptation of more northern populations as the environment changes," he said. "If these populations go extinct, we are potentially hindering the future adaptability of other populations."

Provided by University of Oregon

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