

# Research on stickleback fish shows how adaptation to new environments involves many genes

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Gasterosteus aculeatus. Image: Wikipedia.

A current controversy raging in evolutionary biology is whether adaptation to new environments is the result of many genes, each of relatively small effect, or just a few genes of large effect. A new study published in *Molecular Ecology* strongly supports the first "many-small" hypothesis.

McGill University professor Andrew Hendry, from the Department of Biology and the Redpath Museum, and evolutionary geneticists at Basel University in Switzerland, studied how threespine stickleback fish adapted to lake and stream environments in British Columbia, Canada. The authors used cutting-edge genomic methods to test for genetic differences at thousands of positions ("loci") scattered across the stickleback genome. Very large genetic differences between lake and stream stickleback were discovered at more than a dozen of these loci, which is considerably more than expected under the alternative "few-large" hypothesis.

By examining four independently evolved lake-stream population pairs, the researchers were further able to show that increasing divergence between the populations involved [genetic](#)

[differences](#) that were larger and present at more and more loci.

As these results were obtained using new high-resolution [genetic methods](#), it is conceivable that previous perceptions of adaptation as being a genetically simple process are simply the result of a bias resulting from previous lower-resolution genomic methods.

"I suspect that as more and more studies use these methods, the tide of opinion will swerve strongly to the view that adaptation is a complex process that involves many genes spread across diverse places in the genome," says Prof. Hendry.

**More information:** [onlinelibrary.wiley.com/doi/10.1111/j.1365-3113.2012.04550.x/abstract](http://onlinelibrary.wiley.com/doi/10.1111/j.1365-3113.2012.04550.x/abstract)

Provided by McGill University

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