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New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine



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The dramatic radiation of sticklebacks in different post-glacial environments provides a unique opportunity to study the genetic and developmental mechanisms that underlie rapid evolutionary change in vertebrates. We have developed a number of genomic and genetic tools to study a wide range of morphological, physiological and behavioral traits in sticklebacks. A large collection of microsatellite markers has been developed for use in genome-wide linkage mapping of interesting traits in crosses between different stickleback populations.

generated and EST sequencing projects have begun to isolate stickleback homologs of developmental control genes. Genomic libraries have been built to compare chromosome regions of interest from both anadromous and freshwater stickleback populations. One of these libraries has been used to assemble overlapping contigs of BAC clones for chromosome walking and mapping. The recent development of methods to make transgenic sticklebacks, these tools should make it possible to identify the genetic basis of different evolutionary traits in stickleback, and to begin to answer longstanding questions about the numbers and timing of the appearance of new morphological, physiological, and behavioral traits during vertebrate evolution.



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