

Genetic variation in the genomes of the threespine stickleback *Gasterosteus aculeatus*

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G. aculeatus is a good model for studying population genomics. It exists in two morphs, freshwater and marine, that differ in their morphological, physiological and behavioral traits, and these traits have evolved repeatedly in freshwater populations from marine ancestors all over the world. We use next-generation sequencing to study the genetic variation of the natural marine and freshwater stickleback populations, and of experimental freshwater populations formed ~30 years ago from crosses of marine and freshwater ancestors. We confirm the previously identified QTLs responsible for stickleback phenotypic variation, and find new QTLs. Furthermore, our results show that in the experimental freshwater populations, strong selection favoring the freshwater alleles in these QTLs acted over the time of the experiment. Over these 30 years, selection increased the mean frequency of the freshwater alleles in multiple loci from 50% to 70-80%. It was prominent when the founder population was relatively large, and consisted of 20 individuals; by contrast, drift prevailed in the experimental population founded by a cross of only two individuals.