

Population genomics of parallel phenotypic evolution in stickleback across stream–lake ecological transitions

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Understanding the genetics of adaptation is a central focus in evolutionary biology. Here, we use a population genomics approach to examine striking parallel morphological divergences of parapatric stream–lake ecotypes of threespine stickleback fish in three watersheds on the Haida Gwaii archipelago, western Canada. Genome-wide variation at greater than 1000 single nucleotide polymorphism loci indicate separate origin of giant lake and small-bodied stream fish within each watershed (mean F_{ST} between watersheds = 0.244 and within = 0.114). Genome scans within watersheds identified a total of 21 genomic regions that are highly differentiated between ecotypes and are probably subject to directional selection. Most outliers were watershed-specific, but genomic regions undergoing parallel genetic changes in multiple watersheds were also identified. Interestingly, several of the stream–lake outlier regions match those previously identified in marine–freshwater and benthic–limnetic genome scans, indicating reuse of the same genetic loci in different adaptive scenarios. We also identified multiple new outlier loci, which may contribute to unique aspects of differentiation in stream–lake environments. Overall, our data emphasize the important role of ecological boundaries in driving both local and broadly occurring parallel genetic changes during adaptation.

Keywords: genome scan; F_{ST} outlier; ecological speciation; *Gasterosteus*; single nucleotide polymorphism