

Patterns of genomic divergence during adaptation to fresh water in the threespine stickleback *Gasterosteus aculeatus*

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 compared the gene pools of two marine samples of *G. aculeatus* from the White Sea with the gene pools of samples from two old freshwater lakes near sea shores. We confirmed the previously identified short genomic regions responsible for adaptation of stickleback to fresh water, and found new regions. Furthermore, we studied two artificial freshwater stickleback populations originated in 1978 from equal numbers of marine and freshwater individuals and found strong selection favoring the freshwater alleles in these regions acted over the time of the experiment. Over these 33 years, selection increased the mean frequency of the freshwater alleles in regions found in our study from 0.5 to 0.57 and 0.78 in two artificial populations and from ~0.1 to 0.37 and 0.63 in two natural populations.