Epiclonality alterations may contribute to adaptation of sticklebacks to different osmotic conditions.

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The expansion of the methodological capabilities of modern molecular biology is the foundation for the birth of new hypotheses regarding seemingly well-studied cellular processes. For example, during tissue differentiation, the epigenetic profiles of some cells may be more effective for the processes of adaptation to new conditions, which will constitute the epigenetic clonality of the population. Three-spined stickleback is a convinient model organism for studying adaptation processes at epigenetic level due to its possibility to inhabit environments with different osmotic conditions. In this work, we investigate the epigenetic clonality of the freshwater and marine stickleback populations. For this purpose, bisulfite sequencing of 48 fishes was performed. 24 fishes were taken from a freshwater environment and 24 from a marine environment. On average, 65 million pairs of 100-b reads were sequences per sample. Paired reads were mapped to the gasAcu1 genomic assembly using the Bismark program with standard parameters. For each sample, the methylation (Shannon's) entropy was calculated with a window of 4, 5 and 6 CpG. The obtained values of entropy were compared between freshwater and marine conditions using the F-test (with Benjamini-Hochberg adjustment procedure). Thus, we obtained 6526 intervals, which shifted their level of epigenetic heterogeneity in the freshwater environment as compared to the marine one. Using the intervals, we obtained a list of genes whose promoters changed epiclonality. GO Enrichment analysis of these genes revealed set of terms mostly associated with positive and negative epigenetic regulation of gene expression. Overall, these data allows to make a hypothesis that the genes that carry out epigenetic regulation may themselves be under the pressure of the epigenetic component of selection. And this alteration in epiclonality may contibute to adaptive changes. This work was supported by Russian Science Foundation (RSF) grant 19-14-00347.