

The contribution of alternative splicing to adaptation in threespine stickleback

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Alternative splicing regulates which parts of a gene are kept in the messenger RNA and has long been appreciated as a mechanism to increase the diversity of the proteome within a species. Recently, it has also been suggested as a mechanism underlying adaptation and phenotypic evolution. Consistent with this prediction, there are a few cases in which alternative splicing has been shown to mediate specific phenotypic differences within species or to differ more broadly between populations adapted to different environments. However, the overall contribution of alternative splicing to phenotypic evolution and adaptation is unknown. In this study we asked whether alternative splicing played a role in adaptation to divergent marine and freshwater habitats in threespine stickleback (*Gasterosteus aculeatus*). We examined both differentially expressed and differentially spliced genes (DEGs and DSGs) between pairs of marine-freshwater stickleback across the northern hemisphere and compared the overlap of these genes with genomic regions of high differentiation between marine and freshwater populations. Thus far, we find that both DEGs and DSGs are enriched in these regions, but differentially spliced genes are more enriched than differentially expressed genes. Although further work is needed, these data suggest that differential splicing may play an important role in adaptation to divergent marine and freshwater habitats in threespine stickleback.