

Using Bioinformatics to Analyze DNA Methylation in *Fundulus heteroclitus*

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Abstract

DNA methylation is an epigenetic mark that can alter an organism's genome and how they adapt to their environment. *Fundulus heteroclitus* is a small teleost fish that ranges a wide temperature gradient and is a model organism for understanding evolutionary processes. We used bioinformatics to investigate the role of DNA methylation within *F. heteroclitus* in regulating processes that contribute to temperature adaptations. Methylation causes CpG sites to mutate, so heavily methylated genes will have a low observed vs. expected CpG ratio (CpG O/E ratio). We used these ratios to identify regions of CpG islands, which are unmethylated regions of high GC content. We found that regions relating to metabolic processes were significantly overrepresented within CpG islands and identified 105 metabolic genes that have been evolutionarily conserved over time, including transcription factors, forkhead box proteins, and GTPase activators. Future directions include confirming our bioinformatic analysis using methylation-sensitive high-resolution melting.