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ANALYSIS OF GENETIC VARIABILITY OF DNA METHYLATION IN RESPONSE TO AN EARLY TEMPERATURE STRESS IN RAINBOW TROUT

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We aim to investigate the potential role of epigenetic marks in the expression of phenotypes and their variability in fish, in particular genetic variability of epigenetic marks in response to an environmental stress. In this context, rainbow trout isogenic lines are the material of choice. Within each line, all fish have the same genome i.e. there is no genetic variability. This allows the comparison of epigenetic marks among several individuals with the same genotype. The environmental stress chosen here is temperature because several studies have reported genetic determinism of thermotolerance. Moreover, rainbow trout isogenic lines have recently been characterized for their response to temperature and the existence of a high between-line variability was shown. The aim of this study is to contribute to the understanding of why certain lines are more tolerant to temperature stress than others, by investigating the implication of epigenetic mechanisms in the variability of the response to temperature. More specifically, the objective of this study was to test whether temperature regime experienced during early development leads to epigenetic modifications within and between lines. Nine rainbow trout isogenic lines were chosen. For each line, half of the eggs were incubated at standard temperature (12°C) and the other half at high temperature (16°C), from eyed-stage to hatching. At eyed-stage just before hatching, analysis of global DNA methylation was performed with LUMA (LUminometric Methylation Assay) on 3 pools of 5 eggs per line and per incubation temperature. LUMA analysis revealed significant differences between lines but little or no effect of incubation temperature. Also, for 6 out of the 9 isogenic lines, genomewide patterns of methylation were analysed by EpiRADseq on the same biological material. EpiRADseq is a reduced-representation library-based approach which has been recently developed and tested on a single clone of water fleas. The protocol was here modified to account for genetic variability and allow both within and between-lines comparisons. Globally, very few loci were differentially methylated between the two incubation temperatures. Thus, in the future, the impact of a longer exposure to high temperatures during early development will be tested.

Keywords: epigenetics, DNA methylation, temperature, early stress, rainbow trout

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