

ABSTRACTS

SESSION 9: EPIGENETICS

GROWTH-ASSOCIATED DNA METHYLATION AND HYDROXYMETHYLATION MARKS IN NILE TILAPIA MUSCLE

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Abstract

Fish domestication is a rather complex process that results from a combination of random genetic drift, artificial selection for specific traits and adaptive selection to captivity conditions. The number of domesticated fish species of commercial importance is still limited but several breeding programmes have been established to selectively improve relevant traits, such as growth. In Nile tilapia (*Oreochromis niloticus*), growth performance has been dramatically increased through selective breeding to achieve an increase in weight of 10-15% per generation over more than 6 generations. The aquaculture industry has recently acknowledged the potential of epigenomic programming as a means of improving growth but little is known about the mechanisms underlying epigenetic regulation of muscle growth in fish. Cytosine methylation (5mC) and hydroxymethylation (5hmC) are the two main DNA modifications that play a key role in epigenetic regulation of gene expression in animals. The aim of this study was to compare the muscle methylomes and hydroxymethylomes between fast- and slow-growing full-sib Nile tilapia. Associations between 5mC/ 5hmC and growth performance revealed that epigenetic regulation of growth affects several genes and biological processes in a sex-specific manner. In female Nile tilapia, hyperhydroxymethylation of one gene of the ERM family was associated with improved growth. Moreover, methylation levels at 63 CpG positions were significantly different between small and large fish regardless of their gender. These CpGs were mostly intergenic but some were linked to genes involved in biological processes related to histone methylation and binding. If validated, such growth epimarkers could be used in future breeding programmes integrating epigenomic selection.

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Keywords: Epigenetics; Domestication; Selective Breeding; Nile tilapia; Growth

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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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Abstract

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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IS TEMPERATURE DRIVING SEX CHANGE IN BARRAMUNDI (*LATES CALCARIFER*)?

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Abstract

The ability to control sex is one of the most important factors for the commercialisation and efficient propagation of fish species, due to influences on reproduction, growth and product quality. Recent evidence suggests that epigenetic modifications and subsequent changes in gene expression may control adult sex change in sequential hermaphrodite; however, how different environments can influence sex change through epigenetic changes is unknown. Using Australian barramundi (*Lates calcarifer*) as an experimental model, this research investigated the role of temperature on DNA methylation and expression of key sex-related genes in a protandrous (male-to-female) sequential hermaphrodite. Although previous evidence suggests temperature is a direct regulator of sex change in barramundi, our results indicate a more complex system of regulation and sexual development than previously thought. Our goal is to better understand how environmental manipulations can influence sex change in this important tropical farmed fish and lead to the development of sex control strategies for aquaculture.

Keywords: Lates calcarifer, temperature, sex change, DNA methylation, gene expression

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