

STUDY OF GENE EXPRESSION DURING HIGH TEMPERATURE SEX REVERSAL IN OREOCHROMIS NILOTICUS





aquaculture

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Abstract

We study the expression of some genes during thermal treatment in Nile tilapia. This preliminary experiment is part of a global project with the aim of identifying all the targets genes of which (1) the expression and (2) the state of methylation, is modified during a high temperature masculinizing treatment. Our results show an up-regulation of the cerebral aromatase (cyp19a1b) at the level of the trunks during the treatment. We also observed an increase in the expression of DNA methyltransferase involved in the generation of new methylations at the heads (dnmt3a). Finally, the treatment generally induces an increase in expression of 3 genes (hsp90, hsp70, dnajb1) involved in the stress response.

Introduction and Objective

Nile tilapia (Oreochromis niloticus) displays a sex determination process dependent on several genetic and environmental factors. High temperature (36.5°C) applied during the critical period of phenotypic sex differentiation (between 10 and 30 days post fertilization (dpf)) have a masculinizing effect. Recently, involvement of epigenetic mechanisms (DNA methylation) in the regulation of genes involved in the sex determination process during thermal inversion was highlighted. In this study we compared the expression of genes involved in (1) de novo (dnmt3a) and maintenance (dnmt1) of the methylation pattern ; (2) response to stress (hsp90, hsp70 and dnajb1) ; (3) sex determinism (brain aromatase, cyp19a1b) ; in heads and trunks of undifferentiated tilapias juvenile during high temperature treatment and untreated controls.





Discussion and Conclusions

We observe an unexpected up-regulation of brain aromatase (cyp19a1b) in trunk of developing Nile tilapia. Moreover, we could show that cyp19a1b expression is increased during high temperature treatment (14dpf, 4 days treatment) in trunk, and at the end of the treatment (23dpf, 13 days treatment) in head. High temperature treatment also affects the expression of DNA methyltransferases. The increased expression of dnmt3a, which is involved in de novo methylation of the DNA, could lead to the introduction of a new methylation pattern in the genome following treatment. These methylations could be involved in the regulation of expression of those genes that are involved in the sexual determination process, such as aromatase. In contrast, the maintenance methylase gene dnmt1 is down regulated in trunk.

Finally, the treatment modified the expression of Heat Shock Proteins genes. In general, hsp70 and hsp90 are up-regulated. The dnajb1 gene doesn't seem to be directly impacted by the treatment at 14 dpf, but at 23 dpf we observed a strong up-regulation in heads and trunks.

The aim of our work is to identify a correlation between the expression of certain genes critical in sex determinism and their methylation state. These preliminary



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