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A TRANSCRIPTOMIC COMPARISON SUGGESTS AN INFLUENCE OF THE DOMESTICATION PROCESS ON EGG QUALITY IN EURASIAN PERCH (*Perca fluviatilis*)

Rocha de Almeida, T.⁽¹⁾, Alix, M.⁽¹⁾, Schaerlinger, B.⁽¹⁾, Le Cam, A.⁽²⁾, Montfort, J.⁽²⁾, Toomey, L.⁽¹⁾, Bobe, J.⁽²⁾, Chardard, D.⁽¹⁾, Fontaine, P.⁽¹⁾

⁽¹⁾University of Lorraine, Unit of Research Animal and Functionality of Animal Products, USC 340 INRA, Vandoeuvre-les-Nancy, France. ⁽²⁾INRA, UR1037 Fish Physiology and Genomics, Campus de Beaulieu, Rennes, France. Email: berenice.schaerlinger@univ-lorraine.fr

Introduction

Fish populations, both domesticated and wild, are dependent upon the production of good quality eggs. Beside the morphological aspect, the egg quality is determined by its molecular content. In this context, the analysis of the maternal mRNA is a practical approach once they are essential for numerous cellular processes occurring during embryogenesis. The domestication of the Eurasian perch is currently under process and some reproductive issues have been reported, among which variable egg quality. The present study aims at analyzing a potential impact of the domestication process on the egg transcriptomic content and hence on their quality.

Methods

Two broodstock populations were used. The first one, considered as domesticated (D), is originated from breeders reproduced in captivity for several generations in a fish farm. The second one is F1 generation from broodstock caught in the Geneva Lake. Both populations were reared under similar conditions in our facilities from the juvenile stage (3 months) and their reproduction cycle was induced in the same RAS conditions using a photo-thermal program of 10 months. In total, 31 spawn were sampled (13 D and 19 F1). One portion was artificially fertilized with a pool of sperm from 3 males and monitored (survival rates at various stages) to assess egg quality. Another portion was frozen to study the eggs gene expression pattern using microarray analyses.

Results and Discussion

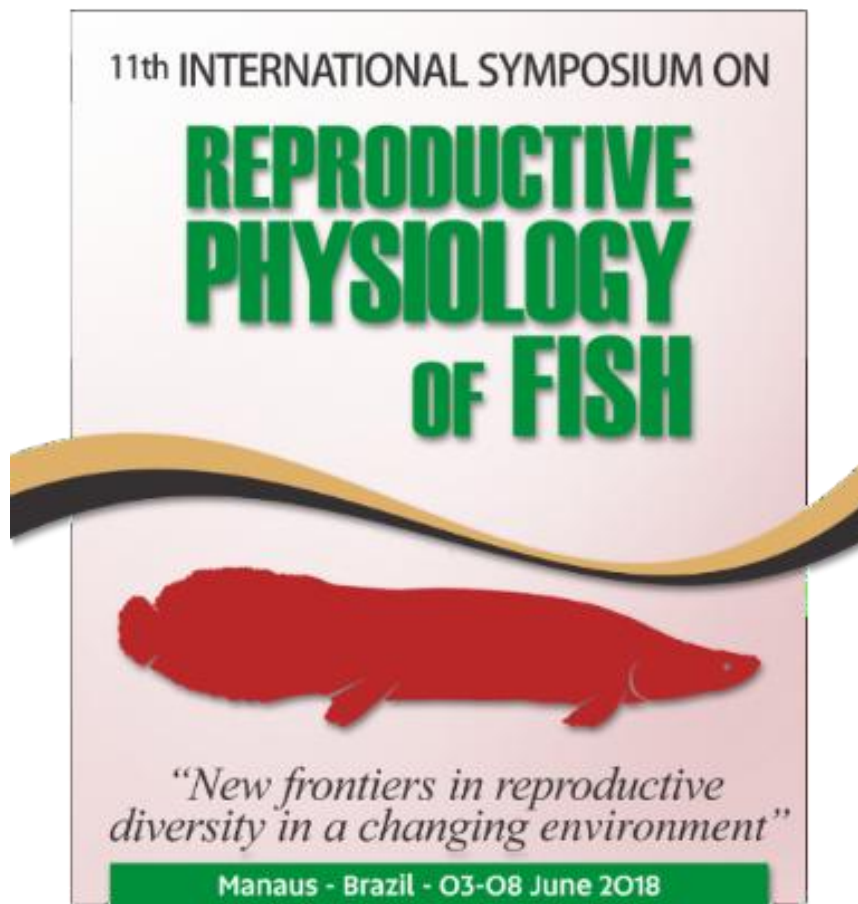
Higher survival rates at 48, 72 and 120hpf ($p < 0.05$) was observed in embryos from the F1 population, showing this population produced eggs of better quality. The analysis of mRNA content of the eggs revealed more than 300 genes differently expressed between both populations ($p < 0.05$). Interestingly, an unsupervised average linkage clustering analysis of these genes split apart the two populations showing a clear different pattern of gene expression between them. The main differently expressed genes (\log_2 fold-change > 4) are involved in functions as the anterior-posterior patterning and mRNA degradation potentially contributing for the differences in early lethality in both populations.

Conclusion

The domestication process may cause genetic and epigenetic changes both leading to transcriptomic modifications. As consequence the fish biology is affected in several ways, including egg quality variation. The identification of molecular pathways affected in a domesticated population opens new research areas to better understand the modifications occurring during the domestication process related to gametes quality.

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PROGRAM AND ABSTRACTS



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