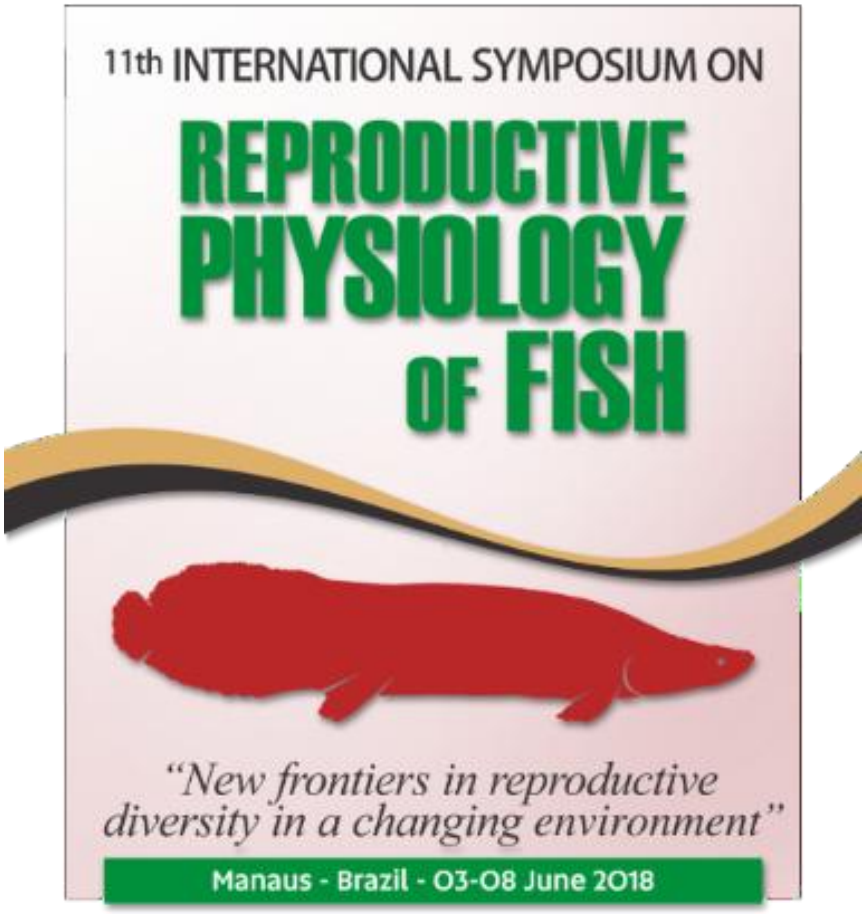
PROGRAM
AND
ABSTRACTS



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THE TAMBAQUI (*Colossoma macropomum*) TRANSCRIPTOME AT SEX DIFFERENTIATION STAGE

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Introduction

As females of tambaqui (*Colossoma macropomum*) are heavier than males at harvest, farming all-female populations would be more profitable. Unraveling the genetic and physiological mechanisms involved in sex determination and sex differentiation is then a fundamental objective in order to achieve sex control in this species. Therefore, we produced and assembled individual transcriptome libraries of juveniles sampled just prior to the gonadal sex differentiation in order to identify genes putatively related to testicular or ovarian differentiation in tambaqui.

Methods

Ten juveniles (20 to 33 mm - total length) were decapitated and the remaining trunk was used to extract total RNA (Trizol). Genomic DNA was removed (RQ1 RNase-free kit; Promega). Total RNA was sequenced (Illumina – HiSeq 2000) and a *de novo* transcriptome was assembled using the Trinity pipeline. Based on the transcription of classical genes involved in sex differentiation as well as genes exhibiting similar transcription profiles, the fish were grouped into two different clusters (putative males, n = 3; and putative females, n = 7). For differential expression analysis between the groups (by Trinity pipeline), data of only three females were used. Finally, the sex differentially expressed genes were manually checked out in the four remaining females' data.

Results and Discussion: The juveniles were grouped into male-like group (MLG) and female-like group (FLG), according to the expression of classical (sex differentiation) genes. The main functional categories of genes (according to Gene Ontology) significantly enriched in the MLG were cellular process, metabolic process and catalytic activity. More specific terms within these categories are the metabolic process of fatty acid, steroids and biosynthesis of steroids. Among these genes, their encoded proteins include the enzymes HSD3β e HSD17β3, which are important enzymes involved in testosterone synthesis. The main functional categories significantly enriched in the FLG were developmental process, metabolic process and biological regulation. Some terms involve organ development, biosynthetic process and transcriptional factors, such as the *fox* family (*foxl2* exclusively expressed in the FLG and *foxo3* upregulated in the FLG) and the WNT/βcatenin/FST signaling pathway. The data indicates that androgen synthesis is involved in testicular differentiation while *fox* family and *wnt* seem to be the main path for ovarian development.

Conclusion: Based on gene transcription, the testicular differentiation in tambaqui seems to be androgen dependent. On the other hand, the formation of ovary is trigged by transcription factors classically involved in structural development of organs, as already identified in female-developing of other teleost's species. Moreover, the transcriptome libraries assemblies will now serve as basis for further investigation to unravel the mechanisms that drive these processes in tambaqui, our main native species.