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PROGRAM AND ABSTRACTS

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Testis mRNA expression in wild and hatchery-produced greater amberjack (*Seriola dumerili*)

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INTRODUCTION

The greater amberjack (*Seriola dumerili*) is a promising emergent aquaculture species. Males caught from the wild and reared in captivity exhibited small seminiferous tubules, a precocious arrest of spermatogenesis and high levels of apoptosis. In the present study, we report a comparative analysis of testis transcriptome of wild *versus* hatchery-produced fish, as part of a research aiming at describing the effects of rearing in captivity on gene expression throughout the reproductive axis.

METHODS

Three wild and 6 hatchery-produced greater amberjack males were sampled on 31 May - 01 June 2021. Wild fish were caught around Lampedusa (Sicily, Italy) and sampled immediately. Hatchery-produced fish belonged to a broodstock produced from fertilized eggs obtained through hormonal induction of spawning and reared in a sea cage at Argosaronikos Fishfarming S.A. (Salamina, Greece). Fish reproductive state was evaluated by gonado-somatic index (GSI) and gonad histological analysis. Total RNA was extracted from testis samples, checked for quantity and quality and then used to prepare the mRNA libraries. A pooled sample was then submitted to sequencing through the Illumina NextSeq platform (Illumina Inc., U.S.A.) using paired-end 2x75 strategy. Sequencing raw data were qualitychecked, cleaned and aligned onto the greater amberjack reference genome using state of the art bioinformatics tools as well as in house scripts. Read counts per gene and differential gene expression analysis was carried out and pathways involving differentially expressed genes (DEGs) were investigated using KEGG (http://www.genome.jp/kegg/pathway.html).

RESULTS & DISCUSSION

Testes from wild greater amberjack (WIDL) showed normal spermatogenic activity. Among the six hatchery-produced fish, four showed normal spermatogenesis (non-dysfunctional farmed fish, NF) and two showed evident reproductive dysfunction (dysfunctional farmed fish, DF), characterized by low GSI, smaller seminiferous tubules and reduced spermatogenic activity. The three groups underwent a comparative transcriptome analysis using the RNA-seq technology. Nine libraries were produced, each of them resulting in the production of 25 million paired-end reads. About 90% of reads were uniquely mapped to the reference genome. A high number (2157) of DEGs was found between WILD and DF groups and between DF and NF groups (1986). The analysis of KEGG pathways evidenced that the observed reproductive dysfunction was associated to cell death, cell cycle and proliferation pathways. The present study improved our understanding of the molecular mechanisms underlying spermatogenesis impairment of greater amberjack reared in captivity. Ongoing analyses of pituitary and hypothalamus transcriptome will provide a comprehensive view of the effects of confinement in captivity on the reproductive axis of this species.

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