DIFFERENTIAL EXPRESSION OF THE IMMUNE-RELATED GENES DURING EARLY PHASE OF ACUTE INFECTION WITH FLAVOBACTERIUM OREOCHROMIS IN TAMBAQUI (COLOSSOMA MACROPOMUM)

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RESUMO

The tambaqui (*Colossoma macropomum*) is a fish native to the Amazon basin and is considered the most produced native freshwater species in South America. Infection caused by the bacterium *Flavobacterium oreochromis* is associated with high mortality rates in the early stages of tambaqui production, resulting in considerable economic losses. Understanding the genetic mechanisms that control the immune system of tambaqui in response to this infection is a fundamental factor for the development of its production. The aim of this study was to investigate the genetic effects caused by *F. oreochromis* infection in tambaqui juveniles by comparing gene expression levels between symptomatic (SI) and asymptomatic (AI) individuals. A bacterial challenge was conducted, where tambaqui juveniles were subjected to *F. oreochromis* infection. In parallel, a control group (CTR) was established where individuals were injected with PBS. During the bacterial challenge, 5 skin samples from AI animals and 4 samples corresponding to the SI group were extracted for transcriptome sequencing (RNA-Seq). A pool formed by samples from 5 CTR individuals was also sent for sequencing. Approximately 21 million reads per library were aligned to the tambaqui genome (GCA_904425465.1). A differential expression analysis was performed to compare gene expression levels between AI and SI. To control false discovery rates in the differential expression analyses, p-values were adjusted to q-values < 0.05. A total of 2,470 overexpressed genes and 1,305 underexpressed genes were identified in IS, while 1,358 overexpressed genes and 488 underexpressed genes were generated for AI. Genes overexpressed in both conditions were related to the process of autophagy (*ATG4B* and *ULK2*), as well as genes associated with oxidative stress (*KLF9*, *DDT1*, and *TXNIP*) regulated by the proteasome mechanism. The results suggest that autophagy and oxidative stress are important components of homeostasis and immune defense in tambaqui during the acute phase of *F. oreochromis* infection. We suggest that the progression of efficient immune mechanisms is limited, possibly due to the imbalance of molecular mechanisms. Further studies are needed to better understand the host-pathogen interaction.

PALAVRAS-CHAVE: bacterial challenge, immunogenetics, native fish, RNA-Seq

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