RESUMO (POSTER) - RNA E TRANSCRIPTÔMICA

COMPARATIVE TRANSCRIPTOME ANALYSIS OF TWO STREPTOCOCCUS AGALACTIAE STRAINS ISOLATED FROM TILAPIA: ASSESSMENT OF DIFFERENTIAL GENE EXPRESSION OF SEROTYPE IB AND SEROTYPE III STRAINS DURING THE GROWTH CURVE

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Streptococcus agalactiae, the group B Streptococcus (GBS), is known to cause severe infection in humans, cattle, and fish. In the Nile tilapia industry, the second most produced finfish in inland aquaculture worldwide, this bacterial species may lead to high mortality rates and economic losses. Advances in next-generation sequencing and bioinformatic tools allow for a deep investigation of these bacterial pathogens, such as comparing distinct genotypes and conditions. This study aimed to characterize two GBS strains isolated from tilapia in Brazil through RNA sequencing and transcriptome analysis. S. agalactiae SA8-UEL (serotype Ib) and SA10-UEL (serotype III) were cultivated in Tryptic Soy Broth and the cells were collected in three different phases of the bacterial growth curve: late-lag, mid-exponential, and early stationary. RNA was extracted, libraries were prepared using the rRNA depletion approach, and these were sequenced using the Illumina platform. Raw reads were cleaned for adaptors and low-quality reads, and aligned to the genome of each strain. Differential expression analysis among the two strains and the distinct growth phases was performed using the DESeq2 tool. Preliminary results showed that most differently expressed genes, for both strains, were presented during the stationary phase, showing a possible transcript accumulation. Several virulence-related genes were downregulated during exponential and stationary phases, such as adhesins and peptidoglycan-, fibronectin- and albumin-binding proteins. Besides, during the stationary phase, genes related to stress response, CRISPRs, and phages were upregulated. Many genes that compose the carbohydrate phosphotransferase system, the main transport system in bacteria, were upregulated during the stationary phase. Further analyses are being carried out to elucidate the mechanisms both strains use in their development and the distinct genes each serotype uses during growth, making them unique during infection in fish. Characterizing S. agalactiae strains isolated in Brazil may allow a better understanding of the genotypes that impact the tilapia industry in the country, favoring the development of streptococcosis control measures.

Palavras-chave: group b streptococcus; rna-seq; streptococcosis; tilapia farming; virulence.