TRANSCRIPTOME ANALYSIS OF DIFFERENTIAL FUNCTIONAL GENE EXPRESSION IN LARGEMOUTH BASS (*MICROPTERUS SALMOIDES*) AFTER CHALLENGE WITH *NOCARDIA SERIOLAE*

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ABSTRACT

Largemouth bass (*Micropterus salmoides*) are common hosts of an epizootic bacterial infection by *Nocardia seriolae*. In the present study, we conducted transcriptome profiling of *M. salmoides* to understand the host immune response to *N. seriolae* infection, using the Illumina ultra-high-throughput sequencing platform. We generated approximately 4.54 Gb reads in total after Illumina HiSeq next generation sequencing. *De novo* assembly of paired-end reads yielded 47,881 unigenes, the total length, average length, N50, and GC content of which were 49,734,288 bp, 1,038 bp, 1,983 bp, and 45.94%, respectively. Annotation was performed by comparison against non-redundant protein sequence (NR), non-redundant nucleotide (NT), Swiss-Prot, Clusters of Orthologous Groups (COG), Kyoto Encyclopaedia of Genes and Genomes (KEGG), Gene Ontology database (GO), and Interpro databases, yielding 28,964 (NR: 60.49%), 36,686 (NT: 76.62%), 24,830 (Swissprot: 51.86%), 8,913 (COG: 18.61%), 20,329 (KEGG: 42.46%), 835 (GO: 1.74%), and 22,194 (Interpro: 46.35%) unigenes. A significant enrichment analysis of these differentially expressed genes and isogenes revealed major immune-related functions, including toll-like receptor, complement, and coagulation cascades, chemokine signalling, NF-κB signalling, and JAK-STAT signalling. Expression patterns of selected up-regulated genes from control and infected groups were determined with reverse transcription quantitative PCR (RT-qPCR). Together, these results provide valuable insights into the underlying immune mechanisms elicited during bacterial infection in largemouth bass, which may aid in the future development of disease control measures against nocardiosis.

Keywords: Illumina paired-end sequencing, Immune response, Largemouth bass (*Micropterus salmoides*), *Nocardia seriolae*, Transcriptome

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