# Transcriptomic Analysis of the Head Kidney in Large Yellow Croaker (*Larimichthys crocea*) at Different Stages of *Nocardia seriolae* Infection

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## Abstract

*Larimichthys crocea*, one of the most economically valuable marine fish species in China, faces significant economic losses in aquaculture due to infectious diseases caused by marine bacteria such as *Nocardia seriolae*. The pathogenic mechanisms of *N. seriolae* infection in *L. crocea* and the immune responses elicited by the fish remain poorly understood. We employed transcriptome sequencing to analyze the head kidney tissues of *L. crocea* infected with *N. seriolae* at 1, 3, 7, and 14 days post-infection. KEGG enrichment analysis revealed that differentially expressed genes were primarily enriched in immune and metabolic pathways. These findings enhance our understanding of the defense mechanisms in the head kidney of *L. crocea* against *N. seriolae* infection and the pathogenicity of *N. seriolae*.

## Materials and methods

01 *Larimichthys crocea* *Nocardia seriolae*

02 Infection Experiment

03 HE-stained sections

04 Transcriptomic Analysis

## Results

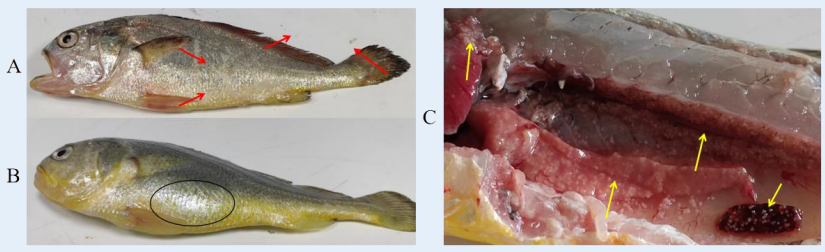


Fig. 1 . A-B: Symptoms of Diseased *L. crocea* on the Body Surface. C: Post-Mortem Symptoms of Diseased *L. crocea* (Red arrows indicate hemorrhagic sites; （black circles denote swollen areas; yellow arrows highlight nodular regions)

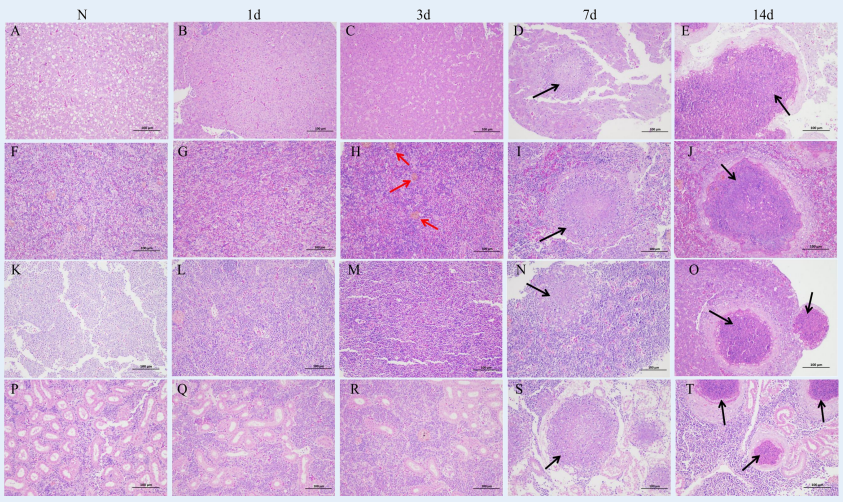


Fig. 2. HE-stained sections of Visceral tissue from *L. crocea.* A-E: liver; F-J: spleen; K-O: head kidney; P-T: trunk kidney (Red arrows indicate hemosiderin deposits, black arrows denote granulomatous nodules).

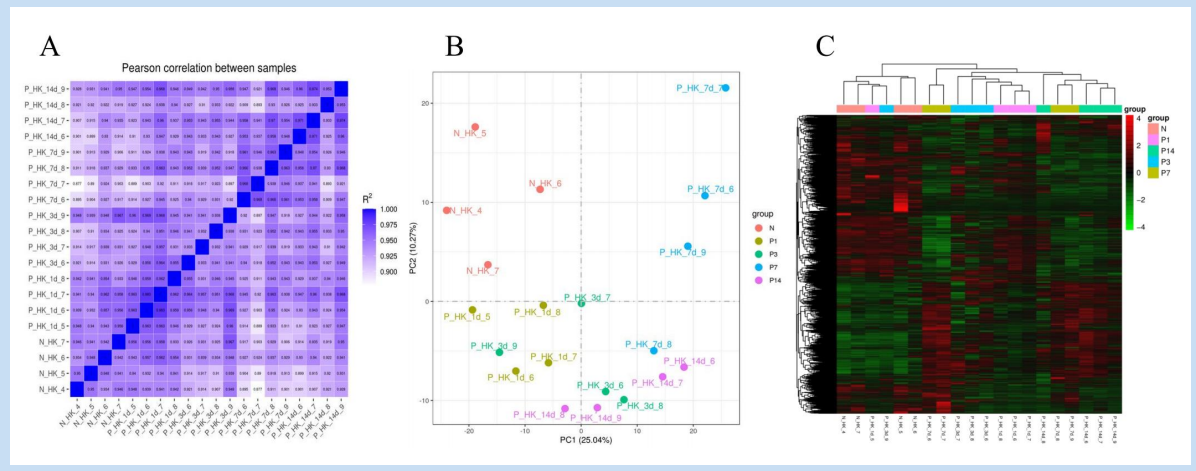


Fig. 3. A: Heatmap of correlation coefficients. B: PCA analysis of gene expression levels. C: Heatmap of differentially expressed genes.

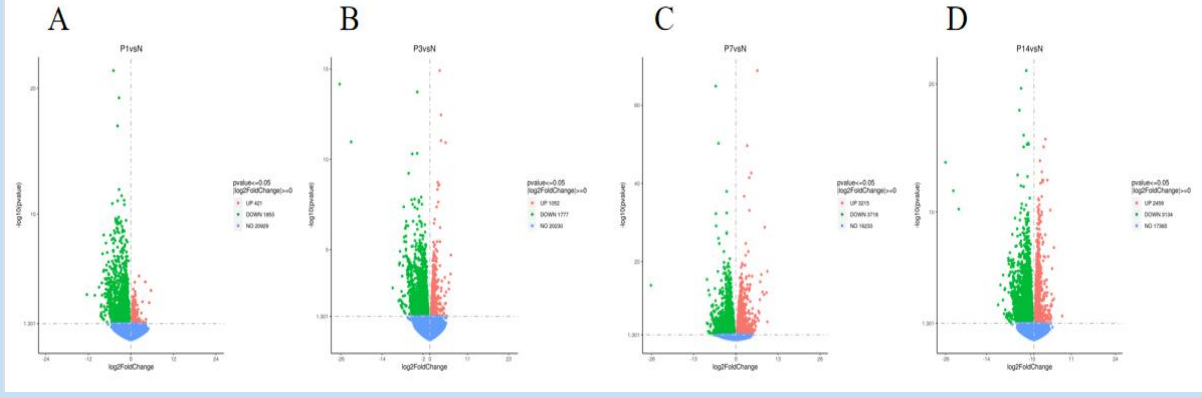


Fig. 4. A: Differentially expressed genes volcano map of P1. B: Differentially expressed genes volcano map of P3. C: Differentially expressed genes volcano map of P7. D: Differentially expressed genes volcano map of P14.

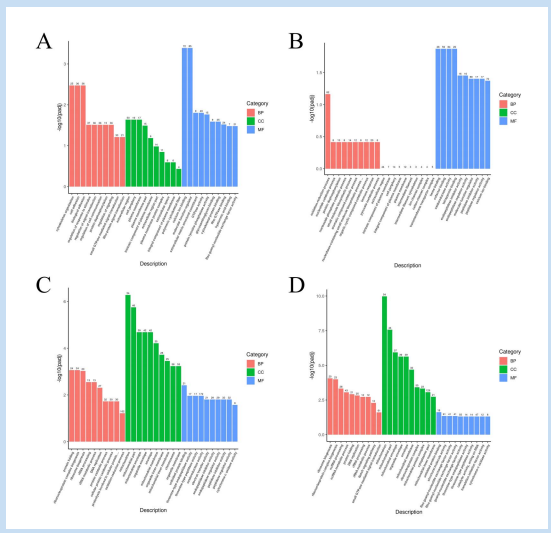


Fig. 5. A: Bar graph of GO entries analysis of P1. B: Bar graph of GO entries analysis of P3. C: Bar graph of GO entries analysis of P7. D: Bar graph of GO entries analysis of P14.

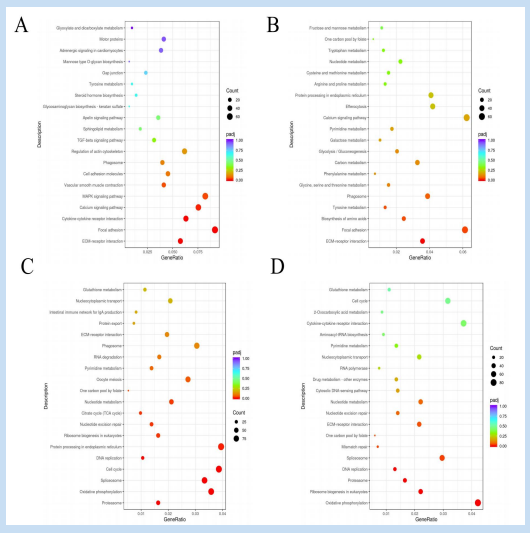


Fig. 6. A: Scatter plot of KEGG enrichment pathway analysis of P1. B: Scatter plot of KEGG enrichment pathway analysis of P3. C: Scatter plot of KEGG enrichment pathway analysis of P7. C: Scatter plot of KEGG enrichment pathway analysis of P14.

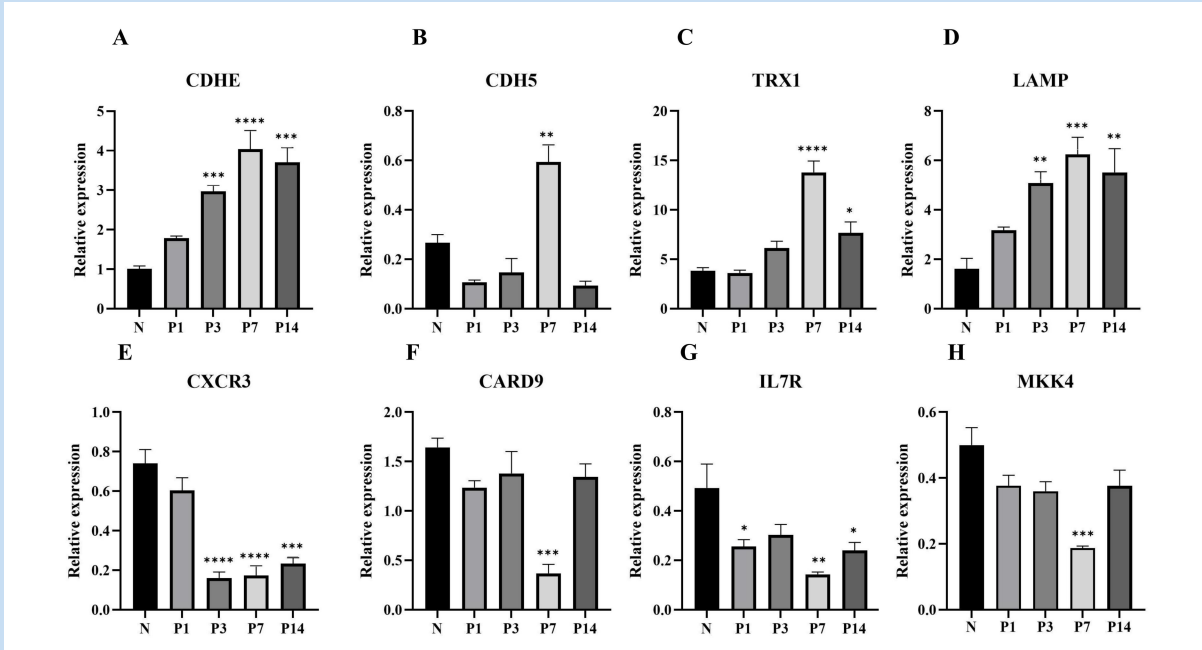


Fig. 7. qPCR validation analysis of immune related DEGs in *L. crocea.*

## Conclusions

In summary, we conducted a transcriptomic study on the head kidney of *L. crocea* infected with *N. seriolae*, identifying differentially expressed genes and enriched pathways in response to infection. Our results indicate that *N. seriolae* infection triggers immune responses and metabolic regulation in *L. crocea*. The significant enrichment of immune pathways, including Toll-like receptor signaling, ECM-receptor interaction, cytokine-cytokine receptor interaction, and focal adhesion, suggests that *N. seriolae* infection elicits an immune response in *L. crocea*. Additionally, the significant enriched metabolic pathways, such as the TCA cycle and oxidative phosphorylation, reveal accelerated ATP synthesis to ensure energy supply during the immune response following infection. Our study provides valuable insights into the molecular mechanisms of fish immune responses to *N. seriolae* infection and may contribute to the development of new strategies for prevention and control in large yellow croaker aquaculture.