

Understanding microbiome and transcriptome in the early developmental stages of the black tiger shrimp

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Abstract:

Shrimp aquaculture is an important to aquatic animal industry and human nutritional. However, the industry faces numerous challenges, especially disease infections. A high quality of shrimp larva is a crucial key that could help to improve the shrimp production. Here, we examined the bacterial community structures and transcriptomic profiling in four life stages (nauplius, zoea, mysis and postlarva) of black tiger shrimp (*Penaeus monodon*) using 16S rDNA amplicon sequencing and RNA sequencing, respectively. The dominant bacterial phyla were Proteobacteria, Bacteroidetes and Planctomycetes, and these phyla were also found as common bacterial phyla associated though developmental stages. Moreover, bacterial communities associated with black tiger shrimp were different from their rearing water, and bacterial profiles had more similar pattern when shrimp developed to postlarva, suggesting that the differences of shrimp physiology, morphology, diets and immune level could influence on bacterial profiles. Gene enrichment analysis showed that most of transcripts were mainly related to metabolic processes, cell and growth development, and immune system. In particular, several innate immune genes were found in early larval developmental including Toll signaling pathway, pathogen pattern recognition proteins, prophenoloxidase system, antimicrobial peptides, blood clotting system and heat shock protein. Our finding revealed that these immune responses are important for defense mechanisms against invading pathogens in early larval stages.