

GLOBAL SCREENING OF MUD CRAB(*SCYLLA* *PARAMAMOSAIN*) INNATE IMMUNITY IN EMBRYOGENESIS

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ABSTRACT

Mud crab (*Scylla paramamosain*) as a vital commercial seafood animal is facing the problem of large scale mortality during early life of development. Large amount of sequence data of mature creatures are available within crustaceans by now, however, little is known about the transcriptional activities underlying mud crab embryonic development. Here with the help of RNA-seq analysis, we employed a time-course transcriptional profiling analysis to gain insight into the immune related events in the embryonic developmental stages. Five embryonic stages and one larva stage covering six different developmental stages (zygote, blastula, gastula, eye pigment, heart beating and zoea) uncovered a dynamic transcriptome profile. Hierarchical clustering revealed the onset and peak of transcripts at different developmental stages and demarcated clusters with distinct expression patterns. It reveals a cohort of genes potentially maternally transferred from the female crab to the offsprings. From the time series, proPO cascade and lectins family were among the most abundant expressed immune related genes. Furthermore, our present work led to the study of the dynamic gene expression profile of antibacterial peptides during embryogenesis. To the best knowledge, our work provide the first comprehensive list of gene expression profile in the early developmental stages of mud crab.

KEYWORDS

Embryogenesis, RNA-seq, *Scylla paramamosain*, Hierarchical clustering, AMPs

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