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JANTANA WONGSANTICHON: cDNA LIBRARY CONSTRUCTION AND NUCLEOTIDE SEQUENCE CHARACTERIZATION OF SELECTED cDNA CLONES FROM HEMOCYTES OF BLACK TIGER SHRIMP (*PENAEUS MONODON*). THESIS ADVISORS : BURACHAI SONTHEYANON Ph.D., APINUNT UDOMKIT Ph.D., SAKOL PANYIM Ph.D. 110 p. ISBN 974-664-391-6

Shrimp aquaculture are facing devastating viral and bacterial diseases while molecular information regarding crustacean genes in defense mechanism is unavailable. To quickly obtain gene sequences which are expressed in phagocytic cells of the black tiger shrimp, cDNA libraries were constructed and random clones picked up for 5' sequence determination. Directional lambda ZAPII-based cDNA libraries were constructed from mRNA of hemocytes of the black tiger shrimp (*Penaeus monodon*). A few hundred randomly selected plaques were excised into pBluescript phagemids. Each clone was subjected to automated DNA sequencing using dye terminator chemistry. BLAST programs were used to search for sequence similarity with those from online databases. From the first cDNA library, out of 67 ESTs, 32 (48 %) were identified to be of mitochondrial genes, 5 (8 %) were of ribosomal protein genes, 3 (4 %) were of other genes, and 11 (16 %) did not match existing gene data. From the second cDNA library constructed from a larger amount of mRNA, a set of 194 ESTs was determined and analyzed. 123 (64 %) clones showed sequence similarity to previously identified genes and ESTs of many species, 71 (36 %) clones showed no sequence similarity to those of any genes. Frequently found EST identities were mitochondrial genes (14 %), ribosomal proteins (6 %), actin (5 %), and serine proteinase inhibitors (3 %). Several DNA clones for proteins involved in defense mechanism such as serine proteinase inhibitors, and peroxinectin were also found. These two genes were of interest for their involvement in the prophenoloxidase activating system. Some ESTs for protein in signal transduction pathway such as Ran and serine/threonine kinase were also found. In total, over 216 DNA sequences, some complete, have been submitted to Genbank database. The EST data set from our hemocyte cDNA libraries should serve as useful basic information for many fields of biological researches and applications.