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ARKHOM SAI-NGAM : SCREENING OF TRANSPOSABLE ELEMENT SEQUENCES IN THE GENOME OF BLACK TIGER SHRIMP, *Penaeus monodon*. THESIS ADVISORS : APINUNT UDOMKIT Ph.D., BURACHAI SONTHAYANON, Ph.D., SAKOL PANYIM, Ph.D. 108 P. ISBN 974-663-728-2

Transposable elements have been used as a powerful transformation vector in a number of eukaryotes. Study of transposable elements in the black tiger shrimp, *Penaeus monodon*, could therefore lead to the development of a transformation system that may be useful for genetic improvement of this species in the future. The aim of this study was to identify and characterize transposable elements in the genome of *P. monodon*. Genomic DNA of *P. monodon* was screened in two families of widely spread transposable elements, *hobo/Ac/Tam*3 (*hAT*) and *mariner*-like element (*MLE*), by PCR approach. The degenerate primers used to screen for *hAT* family were designed from two conserved motifs of *hAT* transposase, **T(V/M)DMWT** and **TRWNS**. The degenerate primers used to screen *MLE* family were designed from two conserved motifs of *MLE* transposase, **WVPHEL** and **YSPDLAP**. The PCR approach, although it was able to identify transposable elements in a number of organisms, it was not successful in the amplification of transposable element sequence in *hAT* and *MLE* families from the genome of *P. monodon*. On the other hand, the DNA fragment containing *mariner* sequence could be amplified from the genome of human and *Anopheles dirus* by the same set of primers. The *mariner* DNA fragments of human and *A. dirus* shared 46% identity in their nucleotide sequences. However, the *mariner* sequences of these two organisms were not cross-hybridized to each other nor to the genome of *P. monodon* as demonstrated by Southern blot hybridization experiments. Two full-length *mariner* fragments of *A. dirus* was obtained by PCR using a single primer that was derived from inverted terminal repeats of *mariners* that are conserved in several organisms. The *mariner* of *A. dirus* showed up to 96% identity in nucleotide level to the *mariner* of *C. plorabunda*. The *mariner* of *A. dirus* isolated in this study, however, seemed to be inactive because its coding sequence was interrupted by several stop codons, deletions and frame shifts. Another two clones, PMMAR07 and PMTE10, obtained from the genomic DNA of *P. monodon* by PCR using either MAR or TE primer pairs were homologous to ORF2 for putative reverse transcriptase in several organisms. The hybridization result using these two clones as probe showed that they were present in several copies in the genome of *P. monodon*.

From this study, two possible conclusions could be drawn. Firstly, the genome of *P. monodon* might lack transposable elements in *hAT* and *MLE* families. Secondly, the *hAT* and *MLE* of *P. monodon* might excessively diverge from those of human *and A. dirus* such that they could not be detected by either PCR or hybridization.