IDENTIFICATION, ANNOTATION AND COMPARATIVE ANALYSIS OF HSP GENES (HEAT SHOCK PROTEIN 70 AND 90) FROM GILL TRANSCRIPTOME OF THREE FRESHWATER CRAYFISH

Md. Sayeed Abu Rayhan*, Muhammad Yousuf Ali
Fisheries and Marine Resource Technology Discipline
Khulna University, Khulna, Bangladesh
rayhanku15@gmail.com
+8801738868971

Response to environmental stresses, mainly thermal stress are largely maintained by a set of proteins called heat shock protein (HSP) which are encoded by HSP genes. Among those HSP70 and HSP90 play a key role in heat stress regulation. We identified and annotated all these genes from gill transcriptome of three commercially important freshwater crayfish, *Cherax quadricarinatus*, *C. destructor* and *C. cainii*. The sequences were made publicly available to NCBI GenBank. Comparative molecular analysis of these genes across the species were also carried out. The HSP70 obtained from the species *Cherax quadricarinatus*, *C. destructor* and *C. cainii* were named as CqHSP70, CdHSP70 and CcHSP70; and CqHSP90, CdHSP90 and CcHSP90 accordingly. The deduced proteins encoded by CqHSP70, CdHSP70 and CcHSP70 contained 643 amino acids; and those encoded by CqHSP90, CdHSP90 and CcHSP90 were 732, 741 and 742 aa. HSP70 obtained from our study shared high similarity with HSP70s from crabs *Homarus americanus* (96%), *Callinectes sapidus* (93%) and *Scylla paramamosain* (93%) and *Portunus trituberculatus* (93%); with prawn *Litopenaeus vannamei* (94%), *Macrobrachium rosenbergii* (92%); and with shrimp *Penaeus monodon* (94%), *Metapenaeus ensis* (93%). A total of 43 nonsynonymous mutation (amino acid replacement) and 43 synonymous mutations were observed in HSP70s from three crayfish species, while 10 nonsynonymous mutation and 43 synonymous mutation were found in HSP90s across the species. However, all the changes were outside the functional sites. All the active sites in HSP70 and HSP90 were highly conserved across the species suggesting their important conserved functions in response to environmental stress. Findings of the study will assist in further molecular analysis and gene expression study.