In-silico analysis and mRNA modulation of detoxification enzymes GST delta and kappa against various biotic and abiotic oxidative stressors

ABSTRACT

This study reports the comprehensive comparative information of two different detoxification enzymes such as glutathione S-transferases (GSTs) delta and kappa from freshwater giant prawn Macrobrachium rosenbergii (designated as MrGSTD and MrGSTK) by investigating their in-silico characters and mRNA modulation against various biotic and abiotic oxidative stressors. The physico-chemical properties of these cDNA and their polypeptide structure were analyzed using various bioinformatics program. The analysis indicated the variation in size of the polypeptides, presence or absence of domains and motifs and structure. Homology and phylogenetic analysis revealed that MrGSTD shared maximum identity (83%) with crustaceans GST delta, whereas MrGSTK fell in arthropods GST kappa. It is interesting to note that MrGSTD and MrGSTK shared only 21% identity; it indicated their structural difference. Structural analysis indicated that MrGSTD to be canonical dimer like shape and MrGSTK appeared to be butterfly dimer like shape, in spite of four β-sheets being conserved in both GSTs. Tissue specific gene expression analysis showed that both MrGSTD and MrGSTK are highly expressed in immune organs such as haemocyte and hepatopancreas, respectively. To understand the role of mRNA modulation of MrGSTD and MrGSTK, the prawns were inducted with oxidative stressors such as bacteria (Vibrio harveyi), virus [white spot syndrome virus (WSSV)] and heavy metal, cadmium (Cd). The analysis revealed an interesting fact that both MrGSTD and MrGSTK showed higher ($P < 0.05$) up-regulation at 48 h post-challenge, except MrGSTD stressed with bacteria, where it showed up-regulation at 24 h post-challenge. Overall, the results suggested that GSTs are diverse in their structure and possibly conferring their potential involvement in immune protection in crustaceans. However, further study is necessary to focus their functional differences at proteomic level.

Keyword: GST; Prawn; Gene expression; Pathogen; Heavy metal