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Molecular characterization of the HSP70 and HSP90 genes in Asian clam (*Corbicula fluminea*) and their expression analysis during heavy metal exposure

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Abstract

The cDNA sequences of *Corbicula fluminea* HSP70/90 (designated as CfHSP70 and CfHSP90, respectively) were cloned in this study. The complete cDNA sequence of CfHSP70 was 2251 bp, including a 1959 bp ORF encoding a 652-amino-acid polypeptide with three HSP70 family signatures. The complete cDNA sequence of CfHSP90 was 2782 bp, including a 2184 bp ORF encoding a 727-amino-acid polypeptide with five HSP90 family signatures. BLAST analysis revealed that the CfHSP70/90 genes were highly homologous to members of HSP70/90 families.

Basal mRNA expression of CfHSP70/90 was found in adductor muscle, foot, gill, digestive gland, gonad, and mantle tissues from *C. fluminea*. The highest expression levels of CfHSP70/90 were observed in the digestive gland. Real-time RT-PCR was used to analyze the mRNA expression of CfHSP70/90 in the digestive gland of *C. fluminea* exposed to heavy metals Cd²⁺, Cu²⁺, and Pb²⁺ for 5, 10, 15, and 20 days. The expression levels of CfHSP70/90 induced by heavy metal gradually, peaked at different times, and then decreased. These results indicate that the CfHSP70/90 genes can be used as sensitive molecular biomarkers of heavy metal pollution in water.

Abbreviations list:

HSP70	heat shock protein 70
HSP90	heat shock protein 90
CfHSP70	heat shock protein 70 of <i>Corbicula fluminea</i>
CfHSP90	heat shock protein 90 of <i>Corbicula fluminea</i>
ORF	open reading frame
UTR	terminal untranslated region

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