

Characterization of the glutathione S-transferase gene family in Mollusca

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Motivation and Aim: Glutathione S-transferase (GST) is one of the critical proteins in xenobiotic metabolism and a cellular protector under various stress factors as intoxication, hypoxic condition, infection, etc. It is known cytosolic, mitochondrial and microsomal subfamilies of GST [1]. The cytosolic subfamily has a lot of gene classes, representing which differs in various organisms. Each of GST classes may lead to a different expression profile depending on the negative factor or the type of tissue [2]. This should be considered when analyzing gene expression during toxicological and ecological studies. However, there are very few studies on GST encoding genes in marine invertebrates. This study aimed to determine all genes encoding glutathione S-transferases in Mollusca and classify them based on genome data.

Methods and Algorithms: To date the genome assemblies are available for 81 Mollusca species in NCBI. All GST genes for each species were identify through mapping Mollusca GSTs from non-redundant protein sequence and SwissProt databases on genomes. The total RNA was extracted from different tissues of *Mytilus galloprovincialis* for investigation of tissue-specific GSTs expression profile. The beta-actin as a housekeeping gene was used as a reference. All reactions were performed with three replicates. The relative expression levels of each targeted gene were counted by using the $\Delta\Delta C_t$ comparative method.

Results: All classes of GST for each mollusk were characterized and their exon-intron structure analyzed based on genome data. For many species, these classes have been identified for the first time. It is shown that some classes have duplications in the genome (alpha, sigma, pi, omega, and mu). In addition, the expression of each gene under hypoxic conditions was investigated for *M. galloprovincialis*. It is worth noting that increased expression was found only for omega and sigma GST classes, confirming the assumption that the expression profile depends on the stress factor. The possible tissue specificity of the GST gene family in *M. galloprovincialis* was also analyzed.

Conclusion: The obtained results suggest a greater representation of different GST classes in Mollusca than previously thought. Probably such diversity of GST in the genome is some mechanisms of adaptation evolution resulting in the occurrence of an effective system of cellular detoxification. This question requires further investigation.

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References

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