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Genome-wide identification, classification, and expression divergence of glutathione-transferase family in Brassica rapa under multiple hormone treatments

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The GSTs is one of the most important multifunctional protein families which has been playing a crucial role in the different aspects of plant growth. This extensive study about GSTs may establish a solid foundation for the brief functional analysis of BraGSTs in future. In this study, a total of 75 genes were identified in *B. rapa.* Phylogenetic analysis characterized them into eight different sub-classes, while Tau and Phi sub-class being the most numerous. The exon-intron structure and the motif composition of BraGSTs were exhibited accordingly to its sub-classes. Notably, we also investigated 15 tandem paralogous pairs of genes, which highlighted that all the pairs were purifying in nature as their synonymous values were lower than 1.00. Duplication analysis indicated that about 45.33% of genes were mainly occurred through tandem duplication in *B. rapa.* Predominately, the tandem cluster of genes in sub-class Tau was greater than other sub-classes. Furthermore, among eight multiple hormonal treatments (ABA, GA, BR, ETH, IAA, IBA, NPA and JA), most number of BraGSTs were activated by NPA, BR and ABA treatments. This analysis has provided comprehensive information about GSTs family which may assist in elucidating their exact functions in *B. rapa.*

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