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Gene architecture and expression analyses provide insights into the role of glutathione peroxidases (GPXs) in bread wheat (*Triticum aestivum* L.)

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Abstract

Glutathione peroxidases (GPXs) are redox sensor proteins that maintain a steady-state of H₂O₂ in plant cells. They exhibit distinct sub-cellular localization and have diverse functionality in response to different stimuli. In this study, a total of 14 *TaGPX* genes and three splice variants were identified in the genome of *Triticum aestivum* and evaluated for various physicochemical properties. The *TaGPX* genes were scattered on the various chromosomes of the A, B, and D sub-genomes and clustered into five homeologous groups based on high sequence homology. The majority of genes were derived from the B sub-genome and localized on chromosome 2. The intron-exon organization, motif and domain architecture, and phylogenetic analyses revealed the conserved nature of *TaGPXs*. The occurrence of both development-related and stress-responsive *cis*-acting elements in the promoter region, the differential expression of these genes during various developmental stages, and the modulation of expression in the presence of biotic and abiotic stresses

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