# Transcriptomic profiling of wheat grain filling under elevated $CO_2$ and temperature: Discovery of key stress-responsive genes and pathways for climate resilient breeding.

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## Abstract:

Wheat (*Triticum aestivum* L.), one of the world's most vital cereal crops, faces significant challenges from global climate change, particularly elevated $CO_2$ ($eCO_2$) and temperature conditions. Understanding the complex molecular and physiological responses of wheat to these combined stresses is essential for securing sustainable wheat production. In view of this, we performed RNA sequencing analysis of wheat during grain filling to assess gene expression responses to the combined effects of $eCO_2$ and heat stress. A total of 7,051 significant differentially expressed genes (DEGs) were identified, comprising 2542 up-regulated and 4,509 down-regulated genes. Gene Ontology (GO) analysis classified 9,115 DEGs into various functional categories, while KEGG pathway analysis revealed the enrichment of DEGs across various abiotic stress pathways." Transcription factors such as HSP, Rubisco activase 1, WRKY, and DREB2A, along with key regulatory genes including RCA, rbcS, rbcL, GS, PHO, and IRL, which play crucial roles in photosynthesis, nitrogen metabolism, micronutrient assimilation, and yield, were found to be highly abundant among the differentially expressed genes (DEGs). Validation of selected DEGs by RT-qPCR showed expression patterns consistent with the transcriptome data, confirming its reliability. The results of the present study could facilitate further functional validation and exploration of the mechanisms underlying $eCO_2$ and heat stress responses in wheat during grain filling. These findings provide a basis for breeding climate-smart wheat.

Keywords:

Elevated $CO_2$, heat stress, DEGs, Physiological response, Stress tolerance, transcription factors, RT-qPCR.