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RNA-Seq Based Transcriptomic Analysis of Wheat Cultivars for Unveiling of Genomic Variations and Isolation of Drought Tolerant Genes for Genome Editing

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Abstract : Unveiling of genes involved in drought and root architecture using transcriptomic analyses remained fragmented for further improvement of wheat through genome editing. The purpose of this research endeavor was to unveil the variations in different genes implicated in drought tolerance and root architecture in wheat through RNA-seq data analysis. In this study seedlings of 8 days old, 6 cultivars of wheat namely, Batis, Blue Silver, Local White, UZ888, Chakwal 50 and Synthetic wheat S22 were subjected to transcriptomic analysis for root and shoot genes. Total of 12 RNA samples was sequenced by Illumina. Using updated wheat transcripts from Ensembl and IWGC references with 54,175 gene models, we found that 49,621 out of 54,175 (91.5%) genes are expressed at an RPKM of 0.1 or more (in at least 1 sample). The number of genes expressed was higher in Local White than Batis. Differentially expressed genes (DEG) were higher in Chakwal 50. Expression-based clustering indicated conserved function of DRO1and RPK1 between Arabidopsis and wheat. Dendrogram showed that Local White is sister to Chakwal 50 while Batis is closely related to Blue Silver. This study flaunts transcriptomic sequence variations in different cultivars that showed mutations in genes associated with drought that may directly contribute to drought tolerance. DRO1 and RPK1 genes were fetched/isolated for genome editing. These genes are being edited in wheat through CRISPR-Cas9 for yield enhancement.

Keywords : transcriptomic, wheat, genome editing, drought, CRISPR-Cas9, yield enhancement
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