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Comparison of Gene Expression Changes in Three Wheat Varieties with Different Susceptibilities to Heat Stress Using RNA-Seq Analysis

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[Abstract]

Wheat is highly susceptible to heat stress, which significantly reduces grain yield. In this study, we used RNA-seq technology to analyze the transcript expression at three different time-points after heat treatment in three cultivars differing in their susceptibility to heat stress: Jopum, Keumkang, and Olgeuru. A total of 11,751, 8850, and 14,711; 10,959, 7946, and 14,205; and 22,895, 13,060, and 19,408 differentially-expressed genes (log2 fold-change > 1 and FDR (padj) < 0.05) were identified in Jopum, Keumkang, and Olgeuru in the control vs. 6-h, in the control vs. 12-h, and in the 6-h vs. 12-h heat treatment, respectively. Functional enrichment analysis showed that the biological processes for DEGs, such as the cellular response to heat and oxidative stress—and including the removal of superoxide radicals and the positive regulation of superoxide dismutase activity—were significantly enriched among the three comparisons in all three cultivars. Furthermore, we investigated the differential expression patterns of reactive oxygen species (ROS)-scavenging enzymes, heat shock proteins, and heat-stress transcription factors using qRT-PCR to confirm the differences in gene expression among the three varieties under heat stress. This study contributes to a better understanding of the wheat heat-stress response at the early growth stage and the varietal differences in heat tolerancea.

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