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Analysis of Differentially Expressed Genes Between Leaves and Grain Tissues of Three Wheat Cultivars

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[Abstract]

Wheat is a very important crop as a food source worldwide, but gluten in wheat causes a variety of allergic reactions. Previous studies have developed ω -5 gliadin deleted O-free, known as the central antigen of WDEIA (wheat-dependent exercise-induced anaphylaxis). In this study, we performed RNA sequencing on the grains and leaves of the allergic-reduced species O-free and their cultivars, Keumkang and Olgeuru, to analyze differentially expressed genes (DEG) based on different cultivars and tissues. Tissues of all species were biologically repeated three times. We used bowtie2 version 2.3.5.1 to get sequence data from RNAseq and used cufflinks and Tophat programs to find DEG. When comparing leaf and grain tissues, a total of 1,244 DEGs were found in the leaf tissues while only 563 DEGs were found in the grain tissues. As a result of gene ontology analysis of differentially expressed genes, the leaf tissues were mostly included in the "catalytic activity" part of molecular function, "metabolic process" part of biological process, and "membrane" part of cell component. The grain tissues were mostly included in the "metabolic process" part of biological process, "binding" and "catalytic activity" part of molecular function, and "membrane, cell, cell part" parts of cell component. Based on these results, we present information on the differentially expressed genes of the three cultivars of leaves and grains. This study could be an important basis for studying the characterization of O-free.

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