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Genetic Analysis of Wheat for Plant Height by RNA-seq Analysis of Wheat Cultivars 'Keumkang' and 'Komac 5'

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[Abstract]

One of the most widely grown food crops in the world, wheat, is increasing more lodged since for increased rains and winds caused by abnormal climate. During the Green Revolution, shorter wheat cultivars were bred using many *Rht* genes to increase lodging resistance. However, since only some *Rht* genes were used for breeding shorter wheat, it may have had a limited impact on wheat breeding and reduced genetic diversity. Therefore, it is essential to search for genes that have breeding potential and affect dwarfism in order to increase the genetic diversity of dwarf characteristics in wheat. In this study, we performed the RNA-seq between 'Keumkang' and 'Komac 5' ('Keumkang' mutant) to analyze the difference in plant height. Differentially expressed genes (DEGs) analysis and Gene function annotation were performed using 265,365,558 mapped reads. Cluster set analysis was performed to compress and select candidate gene DEGs affecting plant height, stem and internode. Gene expression analysis was performed in order to identify the functions of the selected genes by condensing the results of the DEG analysis into a cluster set analysis. This analysis of these plant height-related genes could help reduce plant height, improve lodging resistance, and increase wheat yield. Its application to wheat breeding will also affect the increased genetic diversity of wheat dwarfism.

[Acknowledgement]

This research was funded by a "Cooperative Research Program for Agriculture Science & Technology Development (PJ015666)" funded by Rural Development Administration

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