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Transcriptome and proteome Co-profiling of Molecular Mechanisms of Pre-harvest Sprouting (PHS) in Common Wheat (*Triticum aestivum* L.)

Sang Yong Park¹, Woo joo Jung², Jae Yoon Kim^{1*}

¹Department of Plant Resources, College of Industrial Science, Kongju National University, Yesan 32439, Republic of Korea.

²Institute of Life Science and Natural Resources, Korea University, Seongbuk-Gu, Seoul, 02841, Republic of Korea.

[Introduction]

Wheat (*Triticum aestivum* L.) is mankind's major food crop consumed worldwide. Food security is emerging issue due to the abnormal climate and global economic instability. In particular, pre-harvest sprouting (PHS) reduces the value of wheat and is one of the abiotic stresses caused by frequent rainfall during the harvest season. The PHS trait in wheat has been studied for a long time. However, the mechanism of PHS is not clearly understood. In this study, molecular mechanisms under PHS were analyzed in two Korean cultivars, 'Keumgang' (PHS-sensitive) and 'Woori' (PHS-resistant). RNA-seq analysis was performed to identify the DEGs associated with the PHS response and tolerance mechanism. Proteomic analysis using LC-MS/MS analysis was also performed in 'Keumgang' and 'Woori' independently, to identify DEPs at the protein level.

[Materials & Methods]

The PHS experiment was performed by artificial rainfall treatment for 7 days on two cultivars, and samples were obtained before (K0, W0) and after (K7, W7) under PHS treatment. RNA-seq analysis was performed on an Illumina NovaSeq6000 platform (Illumina, CA, USA). And LC-MS/MS analysis was conducted using an UltiMate 3000 RSLCnano system and an Orbitrap Eclipse Tribrid mass spectrometer (Thermo Fisher Scientific, MA, USA). During the chromatographic separation, the mass spectrometer was operated in data-dependent mode, automatically switching between MS1 and MS2.

[Results & Discussion]

A PHS induction experiment was performed in two Korean cultivars. In the germination rate analysis, 171 out of 202 'Keumgang' seeds germinated, showing high PHS sensitivity (at 84.65%). On the other hand, in 'Woori', only 6 out of 206 seeds germinated, resulting in high PHS resistance (at 2.91%). A total of 13,154 differentially expressed genes (DEGs) and 706 differentially expressed proteins (DEPs) were identified in four comparison groups between the susceptible/tolerant cultivars. DEGs/DEPs functional annotation for each control group showed similar expression in 'spliceosome' and 'proteasome' related functions, showing an increase in expression by more than 70% in 'Woori' (W7) compared to 'Keumgang' (K7). This study suggests that differences in PHS sensitivity/tolerance may be related to 'spliceosome' and 'ubiquitin-proteasome', which have various effects in response to abiotic stress. In addition, co-profiling analysis between transcriptome and proteasome improved the reliability of transcriptome studies. Our findings contributed to improving basic information and understanding of the PHS mechanism in wheat.

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*Corresponding author: E-mail, jaeyoonkim@kongju.ac.kr Tel. +82-41-330-1203