

PB-11

## Identification of Pre-harvest Sprouting (PHS) Molecular Mechanism by Transcriptome and Proteome co-profiling of Korean Wheat Cultivars (*Triticum aestivum* L.)

Sang Yong Park<sup>1</sup>, Song-Yi Jeong<sup>2</sup>, Jae Yoon Kim<sup>1\*</sup>

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

<sup>2</sup>167, Chusa-ro, Sinam-myeon, Yesan-gun, Chungcheongnam-do, 32418, Republic of Korea.

### [Introduction]

Wheat (*Triticum aestivum* L.) has long been consumed as a major human food crop worldwide. Wheat production has been damaged by severe drought and rainfall caused by extreme weather, causing instability in food security. In particular, pre-harvest sprouting (PHS) is one of the abiotic stresses caused by frequent and unpredictable rainfall during the harvest season, and PHS reduces the value of wheat. Wheat PHS mechanism studies have been continuously conducted. However, the detailed wheat PHS mechanism has been not fully understood. In this study, we identified candidate genes related to the PHS response and resistance mechanism of Korean cultivars 'Keumgang' (PHS sensitive) and 'Woori' (PHS resistant). To identify differentially expressed genes (DEGs) and differentially expressed proteins (DEPs), RNA-seq and proteomic analysis were performed and co-profiled.

### [Materials & Methods]

The PHS experiment performed by artificial rainfall treatment for 7 days on two cultivars. Samples were obtained before (K0, W0) and after (K7, W7) under PHS treatment. RNA-seq analysis performed on an Illumina. And LC-MS/MS analysis was conducted using an UltiMate 3000 RSLCnano system and an Orbitrap Eclipse Tribrid mass spectrometer.

### [Results & Discussion]

PHS induction experiments were performed on two Korean cultivars. For germination rate analysis, seed germination index was evaluated in 5 spikes of two cultivars. 'Keumgang' (86.65%) and 'Woori' (2.91%) showed similar results to the PHS induction experiment in the previous experiments (Kim et al. 2012; Lee et al. 2021; Park et al. 2022). 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. In particular, DEGs/DEPs functional annotation for each control group showed similar expression in 'spliceosome' related functions and showed an increase in expression by more than 70% in 'Woori' (W7) compared to 'Keumgang' (K7). Representative PHS-related genes were analyzed for gene splicing by PHS induction between the two cultivars using IGV (Integrative Genomics Viewer). *MFT3B1* did not differ in exon between the two cultivars (K0/W0) before PHS induction. However, exon skipping confirmed after PHS induction (K7/W7). This study suggests that differences in PHS sensitivity/tolerance may be related to 'spliceosome' 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.

### [Acknowledgements]

This work was supported by the National Research Foundation of Korea(NRF) grant funded by the Korea government(MSIT)(No. 2022R1A4A1030348).

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