

## OA-03

**Study on Traditional and Molecular Breeding for Pre-harvest Sprouting (PHS) Resistance in Korean Wheat**Sang Yong Park<sup>1</sup>, Chang Hyun Choi<sup>2</sup>, Kyung Hoon Kim<sup>2</sup>, Woo joo Jung<sup>3</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>National Institute of Crop Science, Rural Development Administration, Wanju 55365, Republic of Korea<sup>3</sup>Institute of Life Science and Natural Resources, Korea University, Seongbuk-Gu, Seoul, 02841, Republic of Korea.**[Introduction]**

Wheat (*Triticum aestivum*) is consumed main food crop for humankind worldwide without regional restrictions. However, food security is not stable due to the unpredictable climate and unstable international economy. In particular, pre-harvest sprouting (PHS) is one of the factors that frequently occurs due to irregular climates and damages the value of wheat. In this study, PHS induction experiments were conducted on PHS-sensitive 'Keumgang' and PHS resistance mutations line 'Jeonju 377'. DEGs analysis and functional annotation were conducted to identify candidate genes and understand mechanisms for germination and dormancy based on RNA-seq results.

**[Materials & Methods]**

'Keumgang' and 'Jeonju 377' were grown for 35 days in DAF (Day after fertilization) and watered for an average of 12 hours per day for 7 days to maintain rainfall conditions for PHS induction. RNA-seq analysis was constructed using the TruSeq™ RNA library preparation kit (Illumina, CA, USA). 100-bp paired-end sequencing was performed on an Illumina HiSeq™-2500 platform (Illumina, CA, USA).

**[Results & Discussion]**

RNA-seq conducted experiments on 'Keumgang' and 'Jeonju 377', which show clear differences in PHS, and conducted genetic functional annotation and DEG analysis on the obtained samples using 234,131,980 raw reads data. KOG (Eukaryotic Orthologous Groups) and KEGG (Kyoto Encyclopedia of Genes and Genomes) analysis was performed on transcripts assembled through *de novo* assembly, and it was confirmed that starch and sugar decomposition metabolism, carbohydrate metabolism, energy supply in seeds, and germination mechanism. In the comparative combination of K1 vs KM1 and K7 vs KM7, the group that showed high expression before PHS was conducted. GO term analyzed a total of 1,036 related DEGs expressed as 49 in Biological Process (BP) and 12 in Cellular Component (CC) and Molecular Function (MF) respectively. The selected candidate DEGs group tested expression in the PHS condition sample through differential expression analysis. As a result, it is predicted that 18 DEGs are related to seed germination and dormancy. It seems that additional functional tests should be conducted.

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