

**PB-55**

## Identification Pre-Harvest Sprouting Tolerance related SNPs in Common Wheat (*Triticum aestivum*) by GWAS Analysis

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### [Introduction]

Pre-harvest sprouting (PHS) is the germination of seeds before harvest, which reduces the yield and quality of grains. This causes economic losses to farmers and is a serious global human problem. The improving PHS wheat is one of the most important breeding target in wheat breeding programs around the world, including Korea. GWAS analysis was performed using the wheat core collection group developed in Korea. PHS-related SNPs were discovered and gene expression was tested for proximal genes.

### [Materials & Methods]

567 lines of wheat (*Triticum aestivum*) belonging to the pre-developed Korean customized wheat core collection were used in this GWAS analysis study. A trait association analysis was performed on 10 trait data. A total of 31,926 SNPs obtained by Axiom genotyping chip were used for genotyping data. Trait association analysis was performed using GAPIT3 and BLINK model. Quantitative real-time PCR was carried out with DAF (Day After Flowering) 35 wheat spikes using Rotor-Gene Q (QIAGEN Hilden, Germany).

### [Results & Discussion]

A total of 510 common wheat accessions used in the GWAS analysis were distributed in each of the six continents. Kinship, cluster, and principal component analysis were performed with 31,926 SNPs which were identified by 35K Axiom wheat SNP chip. The kinship and cluster analysis classified into 8 subgroups from the wheat core collection group 567 lines. In particular, the groups 2 and 4 was composed approximately 90%, 95% for Korean landraces, Korean landrace and Japanese resources, respectively. After the GWAS analysis, 4 SNPs, AX-94771504, AX-94389645, AX-94601848, AX-95255523, were identified as a significantly related with PHS tolerance. The qRT-PCR analysis for the marker proximal genes validated that the expression was changed in accordance with tolerant or susceptible cultivar after PHS treatment. Especially, AX-94389645 which was located in Chromosome 3A was identified as a SNP markers for PHS susceptible cultivars.

### [Acknowledgements]

This research was funded by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIP) (NRF-2020R111A3069901), Republic of Korea.

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