

PB-005

Identification of SNPs Related to 19 Phenotypic Traits Using Genome-wide Association Study (GWAS) Approach in Korean Wheat Mini-core Collection

Yuna Kang¹, Yeonjun Sung¹, Seonghyeon Kim¹, Changsoo Kim^{1,2*}

¹Department of Crop Science, Chungnam National University, Daejeon 34134, Republic of Korea

²Department of Smart Agriculture Systems, Chungnam National University, Daejeon 34134, Republic of Korea

[Abstract]

Based on the simple sequence repeat (SSR) marker, a Korean wheat core collection were established with 616 wheat accessions. Among them, the SNP genotyping for the entire genome was performed using DNA chip array to clarify the whole genome SNP profiles. Consequently, a total of 35,143 SNPs were found and we re-established a mini-core collection with 247 accessions. Population diversity and phylogenetic analysis revealed genetic diversity and relationships from the mini core set. In addition, genome-wide association study (GWAS) was performed on 19 phenotypic traits; ear type, awn length, culm length, ear length, awn color, seed coat color, culm color, ear color, loading, leaf length, leaf width, seeding stand, cold damage, weight, auricle, plant type, heading stage, maturation period, upright habit, and degree of flag leaf. The GWAS was performed using the fixed and random model circulating probability unification (FarmCPU), which identified 14 to 258 SNP loci related to 19 phenotypic traits. Our study indicates that this Korean wheat mini-core collection is a set of germplasm useful for basic and applied research with the aim of understanding and exploiting the genetic diversity of Korean wheat varieties.

[Acknowledgement]

This work was supported by the “Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ01315902)”, Rural Development Administration, Republic of Korea.

*Corresponding author: Tel. +82-42-821-5729, E-mail, changsookim@cnu.ac.kr