

PB-10

GWAS of Salt Tolerance and Drought Tolerance in Korean Wheat Core Collection

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[Abstract]

Abiotic stress is a major problem in global agriculture as it negatively affects crop growth, yield, and quality. Wheat (*Triticum aestivum*) is the world's second-highest-producing food resource, so the importance of mitigating damage caused by abiotic stress has been emerging. In this study, we performed GWAS to search for SNPs associated with salt tolerance and drought tolerance. NaCl (200 mM) treatment was performed at the seedling stage using 613 wheat varieties in Korean wheat core collection. Root length, root surface area, root average diameter, and root volume were measured. Drought stress was applied at the seedling stage, and the above phenotypes were measured. GWAS was performed for each phenotype data using the MLM, MLMM, and FarmCPU models. The best salt-tolerant wheat varieties were 'MK2402', 'Gyeongnam Geochang - 1985-3698', and 'Milyang 13', showing superior root growth. The significant SNP AX-94704125 (BA00756838) were identified in all models. The genes closely located to the significant SNP were searched within ± 250 kb of the corresponding SNP. A total of 11 genes were identified within the region. *NB-ARC* involved in the defense response, *FKSI* involved in cell wall biosynthesis, and putative *BPMI* involved in abiotic stress responses were discovered in the 11 genes. The best drought-tolerant wheat varieties were 'PI 534284', 'Moro of Sind', and 'CM92354-33M-0Y-0M-6Y-0B-0BGD', showing superior root growth. This study discovered SNPs associated with salt tolerance in Korean wheat core collection through GWAS. GWAS of drought tolerance is now proceeding, and the GWAS results will be represented on a poster. The SNPs identified by GWAS can be useful for studying molecular mechanisms of salt tolerance and drought tolerance in wheat.

[Acknowledgement]

This work was carried out with the support of "The RND program for forest science technology (Project No. 2021400C10-2225-CA02)" Korea Forest Service, Republic of Korea.

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