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## Identification of Wheat Salt Tolerance-related Genes through GWAS

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**[Introduction]**

Abiotic stress is one of the major problems in global agriculture. Salt stress is a major abiotic stress and negatively affects crop growth, development, productivity, and quality. Wheat (*Triticum aestivum* L.) is one of the most important crops. However, wheat is a sensitive crop to salt stress, and salt stress in early growth stages can have a more severe impact on the final yield. Genome-Wide Association Studies (GWAS) connect phenotypic and genetic variants to identify phenotype-genotype associations, providing genomic loci corresponding to target traits. GWAS have contributed to discovering salt tolerance genes in plants. This study was conducted to identify genes acting on salt stress in wheat at the seedling stage using GWAS.

**[Materials and Methods]**

This study was conducted using 566 wheat varieties in the Korean wheat core collection. The wheat 35K SNP array was used for genotyping. The seedling 10 days after germination was treated with water and 200 mM NaCl for 5 days, and the phenotype was measured three times. GWAS was performed using FarmCPU and MLM models. SNPs with a  $-\log(p)$  value of 4.3 or higher were selected in FarmCPU, and SNPs with a  $-\log(p)$  value in the top 3 were selected in MLM, and overlapping SNPs in the two models were finally determined. Associated genes were investigated within  $\pm 250$  kb from the selected SNPs.

**[Results and Discussion]**

The significant differences ( $p$ -value  $< 0.001$ ) were observed between wheat varieties in all traits. The ratios of the NaCl treatment group and the mock control group for each variety were calculated in all traits and used for further analysis. All the phenotype data scored more than 9.5 in the Ryan-Joiner normality test and were used for GWAS. The SNPs detected from both GWAS models were BA00045873 and BA00540391 in root volume, BA00320256 in root average diameter. In BA00045873, a total of 2 associated genes were identified, and one out of the 2 genes was an *indole-3-acetaldehyde oxidase-like* gene involved in the auxin biosynthesis process. In BA00540391, a total of 3 associated genes were identified, and an *indole-3-acetaldehyde oxidase-like* gene was also identified. In BA00320256, 4 associated genes were identified. A *F-box domain-containing protein* gene involved in various plant stress responses by regulating F-box protein expression was identified. The discovered associated genes will be utilized for gene expression and salt stress-related marker development studies.

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