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Evaluation of Salt Tolerance and Genome-Wide Association Study in 249 Peanut Accessions (*Arachis hypogaea* L.)Kunyan Zou¹, Tae-Hwan Jun^{1*}¹Department of Plant Bioscience, Pusan National University, Miryang 50463, Korea**[Introduction]**

Peanut (*Arachis hypogaea* L.) is considered as a moderately sensitive species to salinity stress, a few reports on salinity tolerance in peanut have been reported. The effects of different salinity concentrations on radicle length can be used to show the salinity effect on seed germination percentage and germination index. The present study was conducted 1) to determine the optimal NaCl concentration to test salinity tolerance at the germination stage, 2) to evaluate salinity tolerance of 249 peanut accessions, and 3) to identify genomic regions related to salinity tolerance by GWAS analysis.

[Materials and Methods]

A total of 249 peanut accessions were used for the study, 74 Korean accessions and 175 core collection from the RDA-GenBank Information Center, South Korea and the US Department of Agriculture, respectively. The Axiom_Arachis array with 58K SNPs was used for genotyping. Ten gradient NaCl solutions from 0.3% to 1.2% w/v were tested to Korean peanut cultivar K-OL to determine the optimal NaCl concentration for salinity-tolerance screening during the germination stage. Ten seeds per accession (5 seeds x 2 reps) were tested and measured for the radicle root length with the selected NaCl concentration. The phenotype data were analyzed using the SPSS 15.0 software, Origin software and Wilcoxon rank-sum (WRS) test in R software. The LASSO package and the compressed mixed linear model (CMLM) of GAPIT package in R software were used to conduct GWAS for the association analysis of the radicle length.

[Results and Discussion]

The salt damage rate showed positive correlation with salinity concentration while germination rate and relative germination index were opposite. The 0.6% NaCl was selected for future test since the concentration could clearly differentiate tolerance or sensitivity to salinity during the germination stage. There was significant difference in the root lengths between Korean accessions and the core collections, and the germination ability of the core collections was stronger than that of Korean at the 0.05 level. A total of 6,003 SNPs were selected for GAPIT and SNP locus AX-176808473 on chromosome Aradu.A03, AX-176823005 on chromosome Araip.B01, and AX-176800655 on chromosome Araip.B05 were significantly related to the radicle length ($P < 0.001$). For LASSO analysis, SNP loci of AX-177639945 and AX-147232746 on chromosome Aradu.A09, AX-176799688 on chromosome Aradu.A05 and AX-177640567 on chromosome Araip.B07 were additionally identified at the strict threshold of 0.569. The use of LASSO and GAPIT methods to conduct association studies is beneficial in (1) boosting confidence in the case where common markers are identified and (2) to maximize the possibility of finding new significant markers associated with a trait of interest. The results of this study about selecting highly tolerant accessions and establishing effective methods for identifying SNP markers related to salinity tolerance could provide a cornerstone of molecular breeding for salinity tolerance in peanut.

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