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Genetic Diversity and Genome-wide Association Study of Seed Aspect Ratio using a High-Density SNP Array in Cultivated Peanut (*Arachis hypogaea* L.) Accessions

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[Introduction]

Peanut (*Arachis hypogaea* L.) is an allotetraploid ($2n = 4x = 40$, AABB) species with two subgenomes (A and B). With the development of the next generation sequencing technology, availability of high-density SNP array with high coverage of whole genome can progress genetic studies and breeding application. This study aimed to evaluation of genetic diversity for 384 peanut germplasms and perform GWAS of seed-related trait using 'Axiom_Arachis' with 58K SNPs..

[Materials and Methods]

A total of 384 peanut germplasms were selected from 160 Korean germplasms and 493 core collections from USDA for genetic diversity analysis. Phenotype seed aspect ratio data were screened by Image J software. A total of 47,837 polymorphic SNPs were identified from the peanut 58K array as genotyping data, 19,554 SNPs have come from A subgenome, 21,876 SNPs from B subgenome and 6,407 SNPs come from scaffold. UPGMA dendrogram and linkage disequilibrium estimation were generated by TASSEL v5.0 software. Population structure and relationship were analyzed by STRUCTURE 2.3.4 software and R software. Genome-wide association study results are summarized by Manhattan plots, quantile-quantile plots and summary tables.

[Results and Discussion]

From the analysis of evolutionary relationships among the 384 peanut individuals, it demonstrated that Korean accessions showed genetic differences from South American accessions. The peanuts individuals from West Asia, East Asia and South Asia are closely related, while the peanuts from East Africa, South Africa and West Africa are closely related. A total of six significant loci showing significant association with seed aspect ratio were identified on chromosome Araip.B08, Araip.B06 and Aradu.A03 with significant P-value < 0.001. The significance of marker-trait associations was determined using false discovery rate (FDR) at a 5% significance level and gene models based on reference genome of *A. ipaensis* genomes, *A. duranensis* genomes and *A. hypogaea* genomes with SNP markers AX-177640938, AX-147218661, AX-176807396, AX-177640219. A number of candidate genes were also identified from the SNP markers. Our results can provide useful tools for molecular breeding programs for various agricultural traits in peanut.

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