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## A Combination of a Genome-Wide Association Study and a Transcriptome Analyses in the Response to Salt Stress in Peanuts

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### [Introduction]

Salinity stress is one of the important abiotic stresses in crops. Although peanut (*Arachis hypogaea* L.) is considered as a moderately sensitive species to salinity stress, however a few reports on salinity tolerance in peanut have been reported.

### [Materials and Methods]

A total of 300 peanut accessions with 58K SNPs Axiom\_Arachis array were used for the genome-wide association study (GWAS) by the enriched compression mixed linear model (ECMLM) of GAPIT package. Transcriptome analysis was performed with roots of each salinity tolerance and susceptible accession with 200 mM NaCl at 0h, 12h and 24h after salt treatment. Gene differential expression analysis was performed using edgeR software. The screening criteria for DEGs distinguishing two samples were  $|\log_2 \text{fold change}| > 2$  and adjusted P-value  $< 0.05$ . Quantitative real time PCR (qRT-PCR) was performed using the ABI Real-Time PCR system and Applied Biosystems SYBR Green Kit. The relative gene expression level was calculated using the  $2^{-\Delta\Delta CT}$  method with a reference gene.

### [Results and Discussion]

We identified 33 SNPs as being significantly associated with salt stress in GWAS analysis, and the 105 candidate genes significantly related to sodium ion content were detected. A total of 973 differentially expressed genes (DEGs) were identified, of which 342 were down-regulated and 631 were up-regulated genes, assigned to 233 GO terms and 29 KEGG groups. These 973 DEGs included candidate genes that are known to be involved in tolerance to salinity stress: transporters, MAPK signaling pathway and Cytochrome P450, etc.

The study was conducted to identify genomic regions related to salinity tolerance by GWAS and transcriptome analyses. The results from this study will provide a cornerstone of molecular breeding for salinity tolerance in peanut.

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