Genome-Wide Association Study on Peanut Water Deficit Stress Tolerance Using the U.S. Minicore to Develop Improvement for Breeding

C. SUNG*, Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409; M. BALOTA and S. SARKAR, Virginia Tech University, Suffolk, VA 23437; R. BENNETT and K. CHAMBERLIN, USDA-ARS, Stillwater, OK 74075; N. WANG, Oklahoma State University, Stillwater, OK 74078; P. PAYTON and J. MAHAN, USDA-ARS-CSRL, Lubbock, TX 79415; J. CHAGOYA, Texas A&M AgriLife Research, Lubbock, TX 79403; M. D. BUROW, Texas A&M AgriLife Research, Lubbock, TX 79403, and Department of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409.

Global climate change has resulted in large variations in weather, exacerbating the drought situation around the world. This can result in decreased crop yield, which may lead to severe outcomes such as food crisis. Peanut is one of the most important crops in the world and has been widely planted in many semi-arid areas. Therefore, it is important to develop peanut varieties that are tolerant to water deficit stress. Genetic studies can assist by identifying specific genes or markers for selection. In this research, we included 104 minicore accessions. We extracted 125 DNA samples from peanut seeds harvested in 2017 and sent them for SNP chip analysis on the Affymetrix platform for genotyping. A total of 8,189 SNPs were included in this analysis. Data related to water deficit stress tolerance were collected from the field in TX, OK, and VA in 2017. We used STRUCTURE to perform the linkage disequilibrium analysis and estimate the population structure (Q matrix) with a putative number of populations. GWAS was performed first using SPAGeDi to estimate kinship (K matrix), then association mapping was performed using TASSEL using a mixed linear model (GLM+Q+K). We have identified 120 SNPs (P-value = 10^{-4}) and 558 SNPs (P-value = 10^{-3}) significantly associated with the phenotypic data. Of these, 71 SNPs are significantly associated with more than one trait (44 SNPs associated with 2 traits, 26 SNPs associated with 3 traits, and 1 SNP associated with 4 traits). Overall, 163 SNPs are considered the most reliable SNPs, significantly associated with traits over different locations, or associated with multiple traits, or both. We will validate these significant SNPs again by using phenotypic data collected in 2018 and 2019. These SNP markers are important for future use such as marker-assisted selection (MAS) in peanut breeding. The SNP data can be used for identifying marker trait associations (MTAs) including water deficit stress tolerance and other important traits.