

Genome-Wide Association Study of Agronomic and Disease Resistance Traits Using Peanut Nested Association Mapping Populations

B. GUO*, USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA 31793; S. GANGURDE, M. K. PANDEY, and R.K. VARSHNEY, Center of Excellence in Genomics & Systems Biology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad-502324, India; H. WANG, G. AGARWAL, and A. CULBREATH, Department of Plant Pathology, University of Georgia, Tifton, GA 31793; S. HAN and G. HE, Tuskegee University, AL 36088; X. GUO, Heilongjiang Bayi Agricultural University, Daqing, China; X. JI, Ecological Environment Protection Research Institute, Shanghai Academy of Agricultural Sciences, China; Y. CHU and P. OZIAS-AKINS, Horticulture Department, University of Georgia, Tifton, GA 31793; T. G. ISLEIB, Department of Crop Science, North Carolina State University, Raleigh, NC 27695; and C. C. HOLBROOK, USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA 31793.

The U.S. peanut community has developed structured populations with 2 common parents (Tifrunner and Florida 07) and 8 diverse founders which form the basis of 2 nested association mapping (NAM) populations. This NAM approach has great potential for investigating quantitative agronomic traits and finding their genomic control using next generations sequencing. Here, our goal was to demonstrate the utility of peanut NAM populations by using a subset of the available populations (2 x 4) of 1250 RIL lines (Florida 07_NAM with 504 lines and Tifrunner_NAM with 746 lines plus 118 lines from Tifrunner x GTC20 RIL population). These lines were phenotyped for three years including peanut descriptors of leaf length, leaf width, main stem height, plant height, 100 pod weight, and 100 seed weight along with ratings for foliar diseases such as leaf spots and TSWV; and genotyped using the 58K SNP "Axiom_Arachis" Array. Joint inclusive composite interval mapping and genome-wide association analysis (GWAS) were used in this study to identify quantitative trait loci (QTLs) and significant marker-trait associations termed quantitative trait nucleotides (QTNs). Here we report the results of Florida_NAM. A total of 7,672 polymorphic SNPs were identified, and 2,716 SNPs with proper segregation were used for genetic map construction with 2,668 loci spanning 2,393 cM. A total of 162 QTLs were identified through linkage analysis, including 38 for leaf spot resistance (20.1-44.6% PVE), 16 for TSWV resistance (18.8-43.4% PVE), and 108 for the six descriptor traits (16.8-46.6% PVE). Further, 170 QTNs were identified through GWAS using a random effects model, including 92 QTNs for leaf spots resistance (p-value 5-58.6) and 72 QTNs for descriptor traits (p-value 5.2-12.4). Identification of candidate genes for these QTLs/QTNs is still in progress. These results will provide extensive genetic information to dissect the genetic architecture of these traits for the improvement of peanut yield and disease resistance.