

Nested Association Mapping (NAM) Population-based Joint Linkage Mapping and GWAS for Identification of Consistent QTLs/QTNs for Disease and Pod Traits in Peanut.

S. YADURU*, H. WANG, J.C. FOUNTAIN, A.K. CULBREATH, Department of Plant Pathology, University of Georgia, Tifton, GA, 31793; S. GANGURDE, P. SONI, M.K. PANDEY, R.K. VARSHNEY, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana, India; C. ZHAO, Shandong Academy of Agricultural Sciences (SAAS), Jinan, Shandong, China; B. GUO, USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA, 31793.

Incorporation of greater levels of allele diversity among parental lines in developed populations increases the power of quantitative trait loci (QTLs) and association studies to identify and map key genes and markers for traits of interest. To maximize and demonstrate this for disease and descriptor traits in peanut, we used two nested-association mapping (NAM) populations comprising of 496 and 570 recombinant inbred lines (RILs) derived from common parents Florida-07 (NAM-Florida) and Tifrunner (NAM-Tifrunner), respectively. These NAM populations were genotyped with a 58K SNP array and phenotyped for leaf spots (LS), *Tomato spotted wilt virus* (TSWV), 100 seed weight (100SW), and 100 pod weight (100PW) in 2015, 2016, and 2017. Joint QTL linkage mapping analysis produced maps with 2,668 loci (NAM-Florida) and 3,341 loci (NAM-Tifrunner). QTL analyses identified 162 QTLs with phenotypic variance explained (PVE) ranging from 18.8 – 46.6% for NAM-Florida, and 80 QTLs with 5 – 44% PVE for NAM-Tifrunner. In addition, GWAS based on 7,672 SNPs identified 145 significant quantitative trait nucleotides (QTNs) of which 92 (p-values 10^{-5} – 10^{-59}) were detected for leaf spot, 11 (p-values 10^{-5} – 10^{-8}) for 100PW, 17 for (p-values 10^{-5} – 10^{-13}) for 100SW in NAM-Florida. For NAM-Tifrunner, GWAS based on 11,520 SNPs identified 47 (p-values 10^{-3} – 10^{-19}) significant QTNs for LS, 12 (p-value 10^{-3}) for TSWV, 24 (p-values 10^{-3} – 10^{-15}) for 100SW and 26 (p-values 10^{-3} – 10^{-8}) for 100PW. Chromosomes A05 and B05 for in particular were strongly associated with significant QTLs and QTNs for 100SW while A02 and A03 were significantly associated with LS QTLs and QTNs. These significant QTLs and QTNs were also found to be associated with genes likely to function in disease resistance or physiological development in peanut. Markers developed from these studies may be useful for selection in peanut breeding programs.