

Fine Mapping and Identification of Candidate Genes in Chromosome A01 of Peanut for Resistance to TSWV.

CHUANZHI ZHAO, HUI WANG, G. AGARWAL, YADURU SHASIDHAR, JAKE C. FOUNTAIN, A. CULBREATH, University of Georgia, Department of Plant Pathology, Tifton, GA; J. CLEVINGER, Mars-Wrigley Confectionery, University of Georgia, Athens, GA; YADURU SHASIDHAR, M.K. PANDEY, R.K. VARSHNEY, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; CHUANZHI ZHAO, XINGJUN WANG, Shandong Academy of Agricultural Sciences, Jinan, China; **B. GUO***, USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA.

Completion of peanut reference genomes facilitates development of peanut tools and identification of useful markers and traits/genes for improvement of peanut disease resistance and quality. TSWV (*Tomato spotted wilt virus*) causes severe yield loss in the Southeastern US and management of TSWV disease severity increases the cost of peanut production. We developed a recombinant inbred line (RIL) population from SunOleic 97R and NC94022, and first identified a major QTL for TSWV (PVE 35.8%) in chromosome A01 in 2012, which was improved in 2016, using SSR markers. The QTL was mapped between the markers Ah126 and GNB842, and the nearest marker GNB555 was in the region of 20 Mb to 30 Mb of A01. Recently in 2018, this QTL was further mapped within 89.5 Kb physical interval at about 9.5 Mb using whole genome resequencing. In the current study, the goal is to fine-map this QTL for potential candidate gene identification and cloning. We used the first version of peanut SNP array, *Axiom_Arachis* 58 K SNP Array, and identified a major QTL (PVE 36%) at about 9.2 Mb, the closely linked SNP (A01:9205209). With further fine-mapping, we narrowed the potential candidate gene(s) at about 0.5 Mb, the distal region of chromosome A01, in which nucleotide-binding–leucine-rich repeat (NB-LRR)-encoding genes are of interest. In summary, we focus on the 10 Mb in the upper arm of A01, in which there are twelve NBS-LRR genes.