

High Resolution Genetic and Physical Mapping of a Peanut Spotted Wilt Disease Resistance Locus, *PSWD-1*, to *Tomato Spotted Wilt Virus* (TSWV)

B. GUO*, USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA; C. Zhao, C. Mao, X. Wang, Shandong Academy of Agricultural Sciences, Jinan, China; J.C. Fountain, Mississippi State University, Mississippi State, MS; W. Korani, J.P. Clevenger, HudsonAlpha Institute for Biotechnology, Huntsville, AL; G. Agarwal, H. Wang, E. Ali, A.K. Culbreath, University of Georgia, Department of Plant Pathology, Tifton, GA; M. Wang, USDA-ARS, Plant Genetic Resources Conservation Unit, Griffin, GA.

Quantitative trait loci (QTLs) for resistance to *Tomato spotted wilt virus* (TSWV) in peanut were previously mapped on chromosome A01 in the recombinant inbred line (RIL) mapping population derived from SunOleic 97R X NC94022 using SSR markers and whole genome resequencing. Using the recently released complete genome sequences for both diploid and tetraploid peanut, and the high-density peanut SNP arrays (58K 'Axiom_Arachis_v1' and the haplotype-based 48K 'Axiom_Arachis_v2' arrays), we developed high-resolution genetic and physical maps of the peanut TSWV resistance locus *PSWD-1*. QTL analysis of five years' TSWV disease ratings identified two major QTLs on chromosome A01 explaining 41.43% and 43.69% of phenotypic variance, within 3.7 cM and 0.3 cM in the same region of the genetic maps, respectively, using these two versions of peanut SNP arrays. These QTL intervals corresponded to a 490-kb physical interval. Comparison of the genetic map and the reference genome revealed a 'cold spot' region from 12,040,521 bp to 12,528,768 bp (488 kb) recombination being observed only in two RILs, S1 and S17, which also had clear, contrasting TSWV phenotypes. The recombination "cold spot" was confirmed using re-sequencing data from these two RILs. Therefore, based on the genetic and physical maps we named the resistance locus as the peanut spotted wilt disease 1 (*PSWD-1*) resistance locus. Within this locus there were three candidate genes including an NBS-LRR disease resistance gene, a glutamate receptor, and an MLO-like protein. The strongest candidate resistance gene is the *TIR-NBS-LRR* R-gene with the gene ID *arahy.1PK53M*, which is a prime candidate for future functional characterization and use in genetic improvement of peanut resistance to TSWV.