

Recombination bin-map facilitates identification of peanut (*Arachis hypogaea*) major QTL on chromosome A01 for resistance to Tomato spotted wilt virus

Running title: Peanut bin-map for major QTL on chromosome A01 and potential resistance genes to TSWV

Gaurav Agarwal^{1,2,3,#}, Josh Clevenger^{4,5,#}, Sandip M. Kale^{3,10}, Hui Wang^{1,2}, Manish K. Pandey³, Divya Choudhary^{1,2}, Mei Yuan⁶, Xingjun Wang⁷, Albert K. Culbreath², C. Corley Holbrook⁸, Xin Liu⁹, Rajeev K. Varshney³, Baozhu Guo^{1*}

¹ USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA, USA

² University of Georgia, Department of Plant Pathology, Tifton, GA, USA

³ International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Center of Excellence in Genomics & Systems Biology, Hyderabad, India

⁴ Mars Wrigley Confectionery, Center for Applied Genetic technologies, Athens, GA, USA

⁵ University of Georgia, Center for Applied Genetic Technologies, Athens, GA, USA

⁶ Shandong Academy of Agricultural Sciences, Biotechnology Research Center, Jinan, China

⁷ Shandong Academy of Agricultural Sciences, Peanut Research Institute, Qingdao, China

⁸ USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA, USA

⁹ BGI-Shenzhen, Shenzhen, China

¹⁰ Present address: The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

#These authors contributed equally to this study.

Abstract

Background: Peanut (*Arachis hypogaea*) cultivars released in recent years are crucial to have some levels of resistance to *Tomato spotted wilt virus* (TSWV), a devastating disease to peanut growers in the Southeastern region of the United States. A recombinant inbred line (RIL) mapping population derived from the cross of SunOleic 97R (a high oleic fatty acid) and NC94022 (high resistance to TSWV), was used in this study to identify the QTLs associated with the resistance.

Results: Whole genome re-sequencing was performed on the parents and 140 RILs. A genetic linkage bin-map was constructed, containing 5,816 bins and 20 linkage groups, which represent 11,106 single nucleotide polymorphism (SNP) markers and 20 chromosomes. Using this bin-map, we identified three QTLs associated with resistance to TSWV, which were all on chromosome A01. One QTL with the largest contribution of 36.51% to the phenotypic variation was within physical distance of 89.5 Kb. This genome region harbors a cluster of genes coding for chitinase family protein, strictosidine synthase-like protein, and LRR receptor kinase. SNPs associated with this QTL were used to develop KASP markers, and the validated KASP markers can be deployed in breeding programs. Therefore, this high-density genetic bin-map and QTL linked to resistance to TSWV lay the foundation for possible functional gene mapping, cloning and marker-assisted breeding selection.

Conclusions: The present study identified the highest number of SNPs among all the studies conducted so far in peanut. This study also demonstrated the use of bin maps for QTL identification in crops with complex genomes like peanut. Presence of chitinase gene clusters and other disease resistance related genes in the identified QTL region strongly suggest their involvement in resistance against TSWV. Markers linked to the QTL can be used as diagnostic markers in breeding applications.