

High-density genetic map using whole-genome re-sequencing for fine mapping and candidate gene discovery for disease resistance in peanut

Running title: Peanut first SNP-based high density genetic map using WGRS

Gaurav Agarwal^{1,2,3,¥}, Josh Clevenger^{4,5,¥}, Manish K. Pandey^{3,¥}, Hui Wang^{1,2}, Yaduru Shasidhar³, Ye Chu⁶, Jake C. Fountain^{1,2}, Divya Choudhary^{1,2}, Albert K. Culbreath², Xin Liu⁷, Guodong Huang⁷, Rupesh Deshmukh⁸, C. Corley Holbrook⁹, David J. Bertioli⁵, Peggy Ozias-Akins⁶, Scott A. Jackson⁵, Rajeev K. Varshney^{3*}, 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), 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 University of Georgia, Department of Horticulture and Institute of Plant Breeding & Genomics, Tifton, GA, USA

⁷ BGI-Shenzhen, Shenzhen, China

⁸ University Laval, Quebec, Canada

⁹ USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA, USA

¥ These authors contributed equally to this work.

Whole genome re-sequencing (WGRS) of mapping populations has facilitated development of high-density genetic linkage maps essential for fine mapping and candidate gene discovery for traits of interest in crop species. Leaf spots, including early leaf spot (ELS) and late leaf spot (LLS), and Tomato spotted wilt virus (TSWV) are devastating diseases in peanut causing significant yield loss. We generated WGRS data on a recombinant inbred line population, developed a SNP-based high-density genetic map, and conducted fine mapping, candidate gene discovery and marker validation for ELS, LLS and TSWV. The first sequence-based high density map was constructed with 8,869 SNPs assigned to 20 linkage groups, representing 20 chromosomes, for the “T” population (Tifrunner × GT-C20) with a map length of 3,120 cM and an average distance of 1.45 cM. The quantitative trait locus (QTL) analysis using high density genetic map and multiple season phenotyping data identified 35 main-effect QTLs with phenotypic variation explained (PVE) from 6.32 to 47.63%. Among major effect QTLs mapped, there were two QTLs for ELS on B05 with 47.42% PVE and B03 with 47.38% PVE, two QTLs for LLS on A05 with 47.63% and B03 with 34.03% PVE, and one QTL for TSWV on B09 with 40.71% PVE. The epistasis and environment interaction analyses identified significant environmental effects on these traits. The identified QTL regions had disease resistance genes including R-genes and transcription factors. KASP markers were developed for major QTLs and validated in the population, and are ready for further deployment in genomics-assisted breeding in peanut.