Linkage-Mapping and Genome-wide Association Study Identified Two Peanut Late Leaf Spot Resistance Loci, PLLSR-1 and PLLSR-2, using a Nested Association Mapping Approach

Sunil S. Gangurde1,2,3, Ethan Thompson1,2, Shasidhar Yaduru1,3, Hui Wang1,2, Jake C. Fountain4, Ye Chu5, Thomas G Isleib6, Peggy Ozias-Akins5, C Corley Holbrook1, Albert K. Culbreath2, Manish K. Pandey3, Baozhu Guo1,*

1USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA, U.S.A.
2Department of Plant Pathology, University of Georgia, Tifton, GA, U.S.A.
3International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana 502324, India
4Department of Plant Pathology, University of Georgia, Griffin, GA, U.S.A.
5Department of Horticulture, University of Georgia, Tifton, GA, U.S.A.
6Department of Crop and Soil Sciences, North Carolina State University, Raleigh, NC, U.S.A.

Identification of genetic markers linked to late leaf spot (LLS) disease resistance in peanut (Arachis hypogaea) has been a focus of molecular breeding for U.S. industry funded peanut genome project. Efforts have been hindered by limited mapping resolution due to low levels of genetic recombination and marker density available in traditional biparental mapping populations. To address this, a multi-parental nested association mapping (NAM) population has been used and genotyped with a peanut 58 K SNP array. LLS severity was evaluated in the field for three years. Joint linkage-based QTL mapping identified nine QTLs with significant phenotypic variance explained (PVE) up to 47.7%. A genome-wide association study (GWAS) analysis identified 13 SNPs consistently associated with LLS resistance. Two genomic regions harboring the consistent QTLs and SNPs were identified from 1,336 Kb to 1,520 Kb (184 Kb) on chromosome B02 and from 1,026.9 Kb to 1,793.2 Kb (767 Kb) on chromosome B03, named as peanut late leaf spot resistance loci PLLSR-1 and PLLSR-2, respectively. PLLSR-1 has 10 NBS-LRR disease resistant genes on B02, and an NBS-LRR disease resistance gene Arahy.VKVT6A was also identified on chromosome A02. PLLSR-2 has five significant SNPs associated with five interesting genes encoding callose synthase, pollen defective in guidance protein, pentatricopeptide repeat (PPR), acyl-activating enzyme, and C2 GRAM domains-containing protein. This study highlights the power of multi-parent populations such as NAM for genetic mapping and marker-trait association studies in peanut. Validation of these two LLS resistance loci will be needed.

Conference Presentations: