

## 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

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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:

1. Thompson, E., Korani, W., Culbreath, A.K., Bertioli, D., Clevenger, J.P., Guo, B. KHUFU informatics and mutant population to identify gene(s) controlling peanut resistance to early and late leaf spot diseases. Plant and Animal Genome Conference (PAG-30), January 13-18, 2023, San Diego, CA.
2. Gangurde, S.S., Wang, H., Dutta, B., Clevenger, J., Guo, B. Genotyping by whole genome sequencing and KHUFU informatics uncovers spontaneous mutation associated with peanut purple testa color. Plant and Animal Genome Conference (PAG-30), January 13-18, 2023, San Diego, CA.
3. Guo, B., Thompson, E., Cerna, C.D., Wang, H., Gangurde, S.S., Adams, C., Wang, M., Culbreath, A., Clevenger, J. Peanut MAGIC population, a new genetic resource for high-definition trait mapping and breeding. Plant and Animal Genome Conference (PAG-30), January 13-18, 2023, San Diego, CA.