

## **Joint Linkage Mapping and GWAS Study Identified Genomic Regions and Candidate Genes Associated with Late Leaf Spots rResistance in Peanut**

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Late leaf spot (LLS) is one of the major reasons for yield loss in peanut. Exploring the multiple alleles using the diverse parental lines widens the possibility to find the resistant genes/quantitative trait loci (QTL). In this study, two nested-association mapping (NAM) populations i.e. NAM\_Tifrunner and NAM\_Florida-07 comprising of 580 and 496 individuals, respectively, were used in joint linkage-based QTL mapping and genome-wide association study (GWAS). The 58K SNP array genotyping data and multi-season phenotyping for LLS in 2015, 2016 and 2017 was used in QTL and GWAS analysis. The joint linkage-based QTL mapping identified 30 QTLs in NAM\_Tifrunner with 4.0 – 65.6 % phenotypic variance explained (PVE) and 32 QTLs in NAM\_Florida-07 with 7.5 – 61.3 %PVE. Eight major QTLs A01 (2 QTLs), A03 (2 QTLs) and B03 (4 QTLs) were detected showing 10-36% PVE with alleles contributed from the interspecific parent. In parallel, GWAS analysis in NAM\_Tifrunner and NAM\_Florida-07 identified 221 significant single nucleotide polymorphism (SNPs) ( $-\log_{10}(P) > 3.0 - 21.1$ ) and 293 significant SNPs ( $-\log_{10}(P) > 3.0 - 58.6$ ), respectively associated with LLS resistance. Integration of QTLs and GWAS results across both populations narrowed down to 27 significant SNPs associated with 26 QTLs for late leaf spots. These significant SNPs upon validation can be used in genomics-assisted breeding programs for LLS resistance in peanut.