

Identification of Peanut Late Leaf Spot Resistance Locus, *pRPP13*-like, using Nested Association Mapping Approach

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Identification of genetic markers linked to resistance to late leaf spot (LLS) in peanut has been a focus of molecular breeding for several years. 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, multi-parental mapping populations including Nested Association Mapping (NAM) populations have been developed along with high-throughput genotyping SNP arrays. Here, we utilized a subset of two NAM populations, NAM_Tifrunner and NAM_Florida-07, which were genotyped with the *Axiom_Arachis* 58K SNP array and phenotyped for three years for LLS severity. These data were used for quantitative trait locus (QTL) and genome-wide association study (GWAS) analyses. Joint linkage-based QTL mapping in NAM_Tifrunner identified 30 QTLs including a major QTL on chromosome A02 with 42.8 - 65.6% phenotypic variance explained (PVE). Similarly, in NAM_Florida-07, 32 QTLs were detected including a major QTL on chromosome A03 with 28.9 - 61.3% PVE. In parallel, GWAS analysis identified 221 and 293 significant single nucleotide polymorphisms (SNPs; $-\log_{10}(P) > 3.0$) in NAM_Tifrunner and NAM_Florida-07, respectively, associated with LLS resistance. Integration of QTL and GWAS results identified 27 significant SNPs associated with 26 QTLs. These markers were associated with several putative resistance genes and pointed to a prominent role for *Recognition of Peronospora Parasitica 13 (RPP13)*-like NBS-LRR R-genes in LLS resistance, here named the *peanut RPP13 (pRPP13)* gene. This gene still requires functional validation and characterization. However, the associated markers are prime candidates for development into selectable markers for molecular breeding. This approach clearly demonstrates the power of NAM populations for marker-trait association in peanut.