

Identifying Genomic Regions and Evaluating the Epistasis Controlling Stem Rot Resistance in Cultivated Peanut (*Arachis Hypogaea*)

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Peanut stem rot in peanut (*Arachis hypogaea*) is caused by fungal pathogen *Athelia rolfsii* (*Sclerotium rolfsii*) and can result in great economic loss during production. In this study, a recombinant inbred population with 156 lines from the cross between NC 3033 (stem rot resistant) and Tifrunner (stem rot susceptible) was genotyped by the 58 K peanut single nucleotide polymorphism (SNP) array and phenotyped for stem rot resistance at multiple locations and in multiple years. A linkage map consisting of 1451 SNPs and 73 simple sequence repeat (SSR) markers was constructed. Thirty-three additive quantitative trait loci (QTLs) for stem rot resistance were detected. Among these QTLs, six consistent major QTL regions (qSR.A01-2, qSR.A01-5, qSR.A05/B05-1, qSR.A05/B05-2, qSR.A07/B07-1 and qSR.B05-1) that explained over 10% phenotypic variance were identified. Besides, 12 pairs of QTLs with epistatic (additive × additive) interaction were identified. An additive QTL qSR.A01-2 also with an epistatic effect interacted with a novel locus qSR.B07_1-1 to affect the percentage of asymptomatic plants in a row. One hundred ninety-three candidate genes within 38 stem rot QTL intervals were annotated with functions of biotic stress resistance such as chitinase, ethylene-responsive transcription factors and pathogenesis-related proteins. The identified stem rot resistance QTLs, candidate genes, along with the associated SNP markers in this study, will benefit peanut molecular breeding programs for improving stem rot resistance.