

Major QTLs for Resistance to Early and Late Leafspot Diseases are Identified in Chromosome 3 and 5 in Peanut (*Arachis hypogaea*)

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Early (ELS) and late (LLS) leaf spots are major foliar diseases that can severely compromise peanut production without intensive fungicide spray programs. Pyramiding host resistance to leaf spots in elite cultivars is a sustainable solution to mitigate the diseases. In order to determine the genetic controls of leaf spot diseases in peanut, a recombinant inbred line population (Florida-07 x GP-NC WS16) segregating for resistance to both diseases was used to construct a SNP-based linkage map consisting of 855 loci. QTL mapping of the four-year LLS disease ratings revealed three consistent QTLs on chromosome A05, B05 and B03 which confirms published results by QTL-seq analysis. *qLLSB03* and *qLLSB05* protected yield loss caused by LLS disease damage. As for early leaf spot, three consistent GP-NC WS 16-derived resistant QTLs were identified on chromosome A03 and B03. *qELSA03 1.1* overlapped with the previously published LLS resistant genomic region in GPBD 4. Flanking markers of these QTLs were used for genotypic selection of the resistant and susceptible pools from the sister RILs of the same population that were not used for genetic mapping. Significant phenotypic difference between the resistant and susceptible pools of RILs was found. Confirmation of the effectiveness of the leaf spot QTLs should lead to integration of these valuable host resistance resources into peanut breeding programs using marker assisted selection.