

Research report

Marker-assisted breeding for late leaf spot resistance and seed size

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Late leaf spot and early leaf spot are the major fungal diseases plaguing peanut production. Fungicide applications to control these foliar diseases are not only costly to peanut producers but also compromise environmental safety. Host resistance to both diseases is highly desirable to protect peanut yield. GP-NC WS 16 is a derivative from an interspecific hybridization with introgressions from *A. cardenasii*, a wild diploid peanut relative having strong resistance to leaf spot diseases. GP-NC WS 16 was found to have strong resistance to early leaf spot. Florida-07 is a high oleic peanut cultivar susceptible to late leaf spot. In addition, Florida-07 has large seed size and GP-NC WS 16 has small seed size. Increased seed size of recently release cultivars has been an issue due to the market demands for intermediate seed size varieties that has not been met. To investigate QTLs controlling both leaf spot resistance and seed size, recombinant inbred population C1801 (Florida-07 x GP-NC WS16) with 381 lines was genotyped by the *Arachis* Axiom Affymetrix SNP array. A genetic linkage map consisting 26 linkage groups covering a map distance of 1267.9 cM with 1013 markers was constructed. Two to four years of phenotyping data for early, late leaf spots and pod traits were collected for half of the population. Major QTL regions controlling late leaf spot disease resistance were detected on chromosomes B3, A5 and B5. In the meantime, QTL-seq analysis by single nucleotide polymorphism calling between late leaf spot resistant and susceptible bulks revealed QTLs overlapping with genetic mapping analysis. KASPar markers developed from these QTLs were used to select segregating individuals from the half of population that had not been tested for late leaf spot resistance. A leaf spot trial in 2016 indicated that the selected lines were significantly different in response to late leaf spot. These markers allowed for identification of RIL lines with comparable levels of late leaf spot resistance as that in Georganic. These results suggest the usefulness of QTL-seq as a quick and effective method to discover QTLs. QTLs for early leaf spot resistance were identified on chromosomes A3, B3, A5 and B5. These QTLs will be further confirmed by early leaf spot phenotyping data derived from the half of the population not being used for QTL mapping. As for seed size traits, mature double pod weight, double kernel weight and double pod area were mapped to chromosomes A1/B1, A3/B3, A5/B5, A7/B7 and A9. As a yield component, genetic control by multiple QTLs is expected. One of the QTL with a large LOD score of 52 overlapped with the late leaf spot QTL on chromosome A5. Selection of RILs with resistance to both leaf spot diseases pyramided with high oleic and desirable seed size would result in development of new varieties selected for specific market needs.