

Recombination Bin-Map Facilitates QTL Mapping of Disease Resistance Traits in Peanut (*Arachis hypogaea* L.) Using Whole Genome Re-sequencing

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The availability of peanut (*Arachis hypogaea* L.) reference genome information facilitates the identification and development of useful markers, genes, and improvement of peanut disease resistance and quality. A recombination bin-map strategy based on whole-genome re-sequencing could greatly improve mapping accuracy and resolution. In this study, we report a high-density bin-map developed from 141 recombinant inbred lines (RILs) derived from a cross between SunOleic 97R and NC94022. The parents and RILs were evaluated phenotypically for four years in the field for foliar disease ratings including early leaf spot, late leaf spot, and TSWV, and genotyped by whole genome re-sequencing to a depth >20X and 3-5X, respectively. A total of 11,106 high-quality polymorphic SNPs was identified and used to build the first SNP based bin-map for peanut using a sliding window approach, containing 5,816 bins. The total map length was 2,004 cM with 20 linkage groups, and the average bin density was 2.9 bins per cM. A total of 19 QTLs for resistance to both leaf spots and TSWV were identified and account for 7% to 36.5% of the phenotypic variation. The small intervals of the major QTLs contain a cluster of genes, coding for chitinase family protein, strictosidine synthase-like protein and LRR receptor kinase. A major QTL for TSWV resistance on chromosome A01 was located in the small interval of 89.5 Kb, containing several SNPs that have been used to develop KASP markers. These KASP SNP markers have been validated and could be deployed in genomics assisted breeding. This study has not only paved the path to identify the underlying genes for disease resistance in peanut but also provides a basis for marker assisted selection and map based cloning in further studies.