

Characterization and Genetic Mapping of Disease Resistance Genes to TSWV and White Mold and Development of Molecular Markers for Breeding Selection

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The objective of this research was to map the quantitative trait loci (QTLs) for resistance to leaf spots and TSWV in one recombinant inbred line (RIL) mapping population of ‘Tifrunner × GT-C20’ for marker-assisted breeding. Here, we report the improved genetic linkage map with 418 marker loci with a marker density of 5.3 cM/loci, and QTLs associated with multi-year (2010-2013) field phenotypes of foliar disease traits, including early leaf spot (ELS), late leaf spot (LLS), and TSWV. A total of 42 QTLs were identified with phenotypic variance explained (PVE) from 6.36% to 15.6%. There were nine QTLs for resistance to ELS, 22 QTLs for LLS, and 11 QTLs for TSWV, including six, five, and one major QTLs with PVE higher than 10% for resistance to each disease, respectively. Of the total 42 QTLs, 34 were mapped on the A sub-genome and eight mapped on the B sub-genome. This suggests that the A sub-genome chromosomes have more resistance genes than the B sub-genome. This genetic linkage map was also compared with two diploid peanut physical maps, and the overall co-linearity was 48.4% with an average co-linearity of 51.7% for the A sub-genome and 46.4% for the B sub-genome. The identified QTLs associated markers and potential candidate genes will be studied further for possible application in molecular breeding in peanut genetic improvement for disease resistance.

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