QTL Analysis for Disease Resistance Using F_2 and F_5 Genetic Maps in Peanut (*Arachis hypogaea* L.)

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One mapping population derived from Tifrunner × GT-C20 has shown great potential in developing a high density genetic map and identifying quantitative trait loci (QTL) for important disease resistance, Tomato spotted wilt virus (TSWV) and leaf spot (LS). Both F_2 and F_5 generation-based genetic maps were previously constructed with 318 and 239 marker loci, respectively. Higher map density could be achieved with the F_2 map (5.3 cM per locus) as compared to the F_5 map (5.7 cM per locus). Quantitative trait loci analysis using multi-environment phenotyping data from F_8 and higher generations for disease resistance identified 54 QTL in the F_2 map including two QTL for thrips (12.14–19.43% phenotypic variation explained [PVE]), 15 for TSWV (4.40–34.92% PVE), and 37 for LS (6.61–27.35% PVE). Twenty-three QTL could be identified in the F_5 map including one QTL for thrips (5.86% PVE), nine for TSWV (5.20–14.14% PVE), and 13 for LS (5.95–21.45% PVE). Consistent QTL identified in each map have shown higher phenotypic variance than nonconsistent QTL. As expected, the number of QTL and their estimates of phenotypic variance were lower in the F_5 map. This is the first QTL study reporting novel QTL for thrips, TSWV, and LS in peanut (*Arachis hypogaea* L.), and therefore, future studies will be conducted to refine these QTL.

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