QTL Analysis for Disease Resistance Using F2 and F3 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 F2 and F3 generation-based genetic maps were previously constructed with 318 and 239 marker loci, respectively. Higher map density could be achieved with the F2 map (5.3 cM per locus) as compared to the F3 map (5.7 cM per locus). Quantitative trait loci analysis using multi-environment phenotyping data from F2 and higher generations for disease resistance identified 54 QTL in the F2 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 F3 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 F3 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.

