Saturation of Genetic Maps for Identification of QTLs Controlling Disease Resistance, Oil Quality, and Morphological Descriptors in Peanut (Arachis hypogaea L.).

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The limited DNA polymorphisms have impeded the application of marker assisted breeding in peanut. A high-density genetic linkage map for all chromosomes is necessary for quantitative trait loci (QTLs) analysis and efficient marker-assisted breeding. Peanut is vulnerable to a range of diseases, such as Tomato spotted wilt virus (TSWV), early and leaf spots, and Southern stem rot/white mold, which are constantly posing threat to sustainable peanut production. We developed two genetic mapping populations from Tifrunner × GT-C20 (T population, 248 RILs) and SunOleic 97R × NC94022 (S population, 352 RILs), and the maps with 239 and 172 marker loci for a sub-set lines (158 and 190) of each population, respectively, have been published (Qin et al. 2012. TAG). One genetic map derived from SunOleic 97R × NC94022 (Qin et al. 2012) developed using 190 subset with 172 markers was further advanced with additional polymorphic marker loci on all 352 lines. The saturated genetic map possesses 249 loci distributed on 23 linkage groups with total map distance of 3,433.5 cM. Multiple phenotyping data of all lines on several economically important traits was used for quantitative trait loci (QTL) analysis, resulting in identification of a total of 155 QTLs with phenotypic variance (PVE) ranging from 1.48 to 65.2% and the log-of-odds (LOD) varying from 2.51 to 83.68. One major QTL (16.7% PVE) for Tomato spotted wilt virus (TSWV) resistance, three major QTLs for late leaf spot (12.42 -20.59%), two major QTLs for growth habit (11.90 - 14.05% PVE) while one major QTL each for leaf color (10.43% PVE), pod shape (11.55% PVE) and pod reticulation (14.01% PVE), and four QTLs for seed color (10.12-18.45% PVE) were identified. QTL analysis also revealed that \textit{FAD2B} gene contributes up to 74.03% PVE while \textit{FAD2A} gene could contribute only 11.13% PVE for high oleic/linoleic (O/L) ratio. Interestingly, the A- and B-genome mutations of \textit{FAD2} were also found to contribute to other fatty acids, such as palmitic acid (PVE 21.26 and 27.77%) and gadoleic acid (PVE 13.73 and 10.32%), respectively. The markers linked to major QTLs could be utilized for peanut genetic improvement through molecular marker-assisted breeding. The construction of a saturated genetic map and detailed QTL analysis is still in progress and genotyping of these two full populations are also in progress.


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