

Construction of High Density Genetic Map and Mapping Quantitative Trait Loci for Growth Habit Related Traits of Peanut (*Arachis hypogaea* L.)

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Plant growth habit is an important and complex agronomic character, which is associated with yield, disease resistance, and mechanized harvesting in peanuts. There are at least two distinct growth habits (erect and prostrate) and several intermediate forms existing in the peanut germplasm. A recombinant inbred line (RIL) population containing 188 individuals was developed from a cross of 'Jihua 5' and 'M130' for genetically dissecting the architecture of the growth habit. A new high-density genetic linkage map was constructed by using specific locus amplified fragment sequencing (SLAF-seq) technology. The map contains 2,808 SNP markers distributing on 20 linkage groups (LGs) with a total length of 1308.20 cM and an average inter-marker distance of 0.47 cM. The QTL analysis of the growth habit related traits was conducted based on 7 environments phenotyping data. A total of 39 QTLs for growth habit related traits were detected on 10 chromosomes explaining 4.55% to 27.74% of the phenotypic variance, in which 6 QTLs were for lateral branch angle (LBA), 8 QTLs were for extent radius (ER), 7 QTLs were for the index of plant type (IOPT), 11 QTLs were for main stem height (MSH), and 7 QTLs were for lateral branch length (LBL). Among these QTLs, 12 were co-localized on chromosome B05 spanning approximately 6kb physical interval in comparison with allotetraploids reference genome of 'Tifrunner'. Analysis of the co-localized genome region has shown that the putative genes are involved in light and hormones, which will facilitate peanut growth habit molecular breeding and study of peanut domestication.