



Analysis of quantitative trait loci for main plant traits in soybean

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ABSTRACT. Plant traits are important indices for regulating and controlling yield ability in soybean varieties. It is important to comprehensively study the quantitative trait locus (QTL) mapping for soybean plant traits, cloning related genes, and marker assistant breeding. In this study, 236 F₂ generation plants and a derivative group were constructed by using Jiyu50 and Jinong18, obtained from Jilin Province. A total of 102 simple sequence repeat markers were used to construct a genetic linkage map. With 2 years of molecular and phenotypic data, QTL analyses and mapping were conducted for soybean maturity, plant height, main stem node, main stem branch, seed weight per plant, and more. Five main plant traits were analyzed via inclusive composite interval mapping using QTL IciMapping v2.2. Using one-dimensional scanning, a total of 30 QTLs were detected and distributed across 1 (A1), 4 (C2), and 12 (G). There were 9 linkage groups, including 16 major QTLs. Using two-dimensional scanning, 7 pairs of epistatic QTL interactions for maturity and plant height were detected in the soybean.

Key words: Soybean; Plant trait; SSR; Quantitative trait loci; Inclusive composite interval mapping