

B-146

QTL identification for branching on high-resolution genetic map in soybean (*Glycine max* (L.) Merrill)

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The number of branches is an important factor directly affecting total pod number per plant in soybean. Although a number of quantitative trait locus (QTL) studies for branching has been reported in soybean, identification of candidate genes is still challenging due to low resolution of the markers associated with the previously reported QTLs. In this study, four QTLs for branching were identified based on a high resolution genetic map we constructed through BARCSoySNP6K chip, so that a few candidate genes for branching were able to be identified. Although QTLs for branching and total pod numbers have been reported on the same chromosomes we identified QTLs, the QTL regions were remarkably narrowed down, from 26 Mbp to 460 kbp at most. Four genes, BRANCHED1 (BRC1) gene, which encodes TEOSINTE-BRANCHED1/CYCLOIDEA/PCF (TCP) transcription factor, REVOLUTA (REV) gene, which encodes homeobox-leucine zipper family protein, POUND-FOOLISH (PNF), which encodes BEL1-like homeodomain transcription factor and PETAL LOSS (PTL), which encodes trihelix transcription factor, were detected as candidate genes. Also, it was shown that branching had positive correlation with total pod number ($p < 0.001$, $R = 0.75$). This study will help breeders improve soybean yield by increasing the number of branches using marker assisted selection (MAS) and will facilitate identification of the causative genes for branching in the near future.