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Identification of the quantitative trait loci (QTL) for seed protein and oil content in soybean.

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Abstract

Soybean is an important economical resource of protein and oil for human and animals. The genetic basis of seed protein and oil content has been separately characterized in soybean. However, the genetic relationship between seed protein and oil content remains to be elucidated. In this study, we used a combined analysis of phenotypic correlation and linkage mapping to dissect the relationship between seed protein and oil content. A $F_{10:11}$ RIL population containing 222 lines, derived from the cross between two Korean soybean cultivars Seadanbaek as female and Neulchan as male parent, were used in this experiment. Soybean seed analyzed were harvested in three different experimental environments. A genetic linkage map was constructed with 180K SoyaSNP Chip and QTLs of both traits were analyzed using the software QTL IciMapping. QTL analyses for seed protein and oil content were conducted by composite interval mapping across a genome wide genetic map. This study detected four major QTL for oil content located in chromosome 10, 13, 15 and 16 that explained 13.2-19.8% of the phenotypic variation. In addition, 3 major QTL for protein content were detected in chromosome 10, 11 and 16 that explained 40.8~53.2% of the phenotypic variation. A major QTLs was found to be associated with both seed protein and oil content. A major QTL were mapped to soybean chromosomes 16, which were designated qHPO16. These loci have not been previously reported. Our results reveal a significant genetic relationship between seed protein and oil content traits. The markers linked closely to these major QTLs may be used for selection of soybean varieties with improved seed protein and oil content.

Keywords: soybean, protein, oil, QTL mapping

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