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## Identification of SNPs tightly linked to the QTL for pod shattering in soybean [*Glycine max* (L.) Merr.]

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### Abstract

The pod shattering or dehiscence is essential for the propagation of pod-bearing plant species in the wild, but it causes significant yield losses during harvest of domesticated crop plants. Identifying novel molecular makers, which are linked to seed-shattering genes, is needed to employ the molecular marker-assisted selection for efficiently developing shattering-resistant soybean varieties. In this study, a genetic linkage map was constructed using 115 recombinant inbred lines (RILs) developed from crosses between the pod shattering susceptible variety, Keunol, and resistant variety, Sinpaldal. A 180 K Axiom® SoyaSNPs data and pod shattering data from two environments in 2001 and 2015 were used to identify quantitative trait loci (QTL) for pod shattering. A major QTL was identified between two flanking single nucleotide polymorphism (SNP) markers, AX-90320801 and AX-90306327 on chromosome 16 with 1.3 cM interval, 857 kb of physical range. In sequence, genotype distribution analysis was conducted using extreme phenotype RILs. This could narrow down the QTL down to 153 kb on the physical map and was designated as qPDH1-KS with 6 annotated gene models. All exons within qPDH1-KS were sequenced and the 6 polymorphic SNPs affecting the amino acid sequence were identified. To develop universally available molecular markers, 38 Korean soybean cultivars were investigated by the association study using the 6 identified SNPs. Only two SNPs were strongly associated with the pod shattering. These two identified SNPs will help to identify the pod shattering responsible gene and to develop pod shattering-resistant soybean plants using marker-assisted selection.

**Keywords:** Soybean; *Glycine max*; Pod Shattering; Quantitative Traits Loci; Single Nucleotide Polymorphism; SNP

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