

Genome-wide association mapping of bruchid resistance loci in soybean

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Abstract

Soybean is a globally important industrial, food, and cash crop. Despite its importance in present and future economies, its production is severely hampered by bruchids (*Callosobruchus chinensis*), a destructive storage insect pest, causing considerable yield losses. Therefore, the identification of genomic regions and candidate genes associated with bruchid resistance in soybean is crucial as it helps breeders develop new soybean varieties with improved resistance and quality. In this study, 6 multi-locus methods of the mrMLM model for genome-wide association study were used to dissect the genetic architecture of bruchid resistance using 5 traits: percentage adult bruchid emergence (PBE), percentage weight loss (PWL), growth index (GI), median development period (MDP), and Dobie susceptibility index (DSI) on 100 diverse soybean genotypes, genotyped with 14,469 single-nucleotide polymorphism (SNP) markers. Using the best linear unbiased predictors (BLUPs), 13 quantitative trait nucleotides (QTNs) were identified by the mrMLM model, 3 of which, rs16_14976250, rs1_22916615, and rs16_14975721, were associated with more than 1 bruchid resistance trait. As a result, the identified QTNs linked with resistance traits can be employed in marker-assisted breeding for the accurate and rapid screening of soybean genotypes for resistance to bruchids. Moreover, a gene search on the Phytozome soybean reference genome identified 27 potential candidate genes located within a window of 478.45 kb upstream and downstream of the most reliable QTNs. These candidate genes exhibit molecular and biological functionalities associated with various soybean resistance mechanisms and, therefore, could be incorporated into the farmers' preferred soybean varieties that are susceptible to bruchids.

Keywords: *Callosobruchus chinensis*; Glycine max; single-nucleotide polymorphism; GWAS; quantitative trait loci (QTL); candidate genes