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Genome-wide association study (GWAS) of soybean cyst nematode resistance in soybean

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Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is the most serious yield-limiting pathogen on soybean (*Glycine max* (L.) Merr.) and use of the host genetic resistance is the most effective and environmental friendly method to control the nematode. The objective of this study was to identify quantitative trail locus (QTL) and single nucleotide polymorphisms (SNP) markers for SCN resistance in soybean. A total of 274 USDA soybean germplasm accessions with high levels of resistance and susceptibility to SCN were selected and phenotyped with SCN HG Type 0 (race 3). Genome-wide association study (GWAS) was conducted to identify SCN resistance in the 274 accessions using 29,383 SNPs filtered from the SoySNP50K iSelect SNP beadchip for genotyping. The results showed that three major QTLs were identified in this association panel: SCN-qtl7, SCN-qtl11, and SCN-qtl18. SCN-qtl7 is located at 36,371,468 to 36,428,901 bp region on chromosome (chr.) 7; SCN-qtl11 at 32,788,800 to 33,050,751 bp region on chr. 11; SCN-qtl18 at 1,286,863 to 1,894,078 bp region of chr. 18, which is the region of *rhg1* gene of SCN resistance. Six SNPs in SCN-qtl7, seven SNPs in SCN-qtl11, and five SNPs in SCN-qtl18 were identified to be strongly associated with resistance to race 3. The SCN-qtl7 had the maximum LOD of 50.79, 33.31, and 14.77 with 57.2%, 30.3%, and 26.9% R-squared in single marker regression (SMR), general linear model (GLM), and mixed linear model (MLM), respectively. The SCN-qtl11 had the maximum LOD of 36.16, 20.30, and 8.42 with 45.6%, 20.6%, and 13.6% R-squared in SMR, GLM, and MLM, respectively. The SCN-qtl18 (*rhg1*) had the maximum LOD of 31.23, 16.63, and 7.44 with 40.0%, 16.8%, and 11.9% R-squared in SMR, GLM, and MLM, respectively. The QTLs and SNP markers will provide a tool for breeders to select SCN resistance in soybean breeding programs.