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Association Mapping of Soybean Cyst Nematode Tolerance in Soybean

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Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is the major yield-limiting biological factor in soybean production and host genetic resistance has been successfully used to control the pathogen. Because of limited sources of SCN resistance and changes in SCN virulence phenotypes, host resistance in current cultivars has increasingly overcome by the pathogen. Host tolerance has been recognized as an additional tool to manage the SCN. The objective of this study was to conduct a genome-wide association study (GWAS) and identify single nucleotide polymorphisms (SNP) markers for SCN tolerance in soybean. A total of 221 soybean genotypes (lines) were used in this study, with phenotyping conducted in the greenhouse using a completely randomized design (CRD) with four replicates. The tolerance index ($TI = 100 \times \text{Biomass of a line in SCN infested} / \text{Biomass of the line without SCN}$) was used as phenotypic data of SCN tolerance. A total of 4,252 SNPs from the Soy6K SNP Infinium Chips was used as genotypic data. SNP markers were identified to be associated with SCN tolerance at ten regions on ten different chromosomes, including a prominent peak on chromosome 15. This research opens a new approach to use SCN tolerance in soybean breeding and the SNP markers will provide a tool for breeders to select the SCN tolerance through marker-assisted selection (MAS).