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Haplotype for haplotype compatibility at the Rhg1 and Rhg4 loci identifies new sources of soybean cyst nematode resistance

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Soybean cyst nematode (SCN, *Heterodera glycines* Ichinohe) is the most devastating soybean pest in the United States. Utilizing SCN resistance sources have been proven to be a greatly efficient strategy in SCN disease management. Two genomic loci, the *Rhg*-1 and *Rhg*-4 harboring *GmSNAP18* and *GmSHMT08* genes, respectively, have been identified to underlay SCN resistance. In the present study we analyzed high quality (15x) whole genome resequencing data from 106 diverse soybean lines to identify and characterize allelic variants at the *Rhg*1 and *Rhg*4 locus. Similar to the *Rhg*1 loci, haplotype analysis integrated with comparative genome hybridization, digital-PCR and resequencing identified copy number variation (CNV) at the *Rhg*4 locus. The expression of GmSNAP18 and GmSHMT08 genes positively correlated with CNV and SCN resistance. Further, we identified four haplotypes for the Rhg1 locus (rhg1-a, rhg1-b, rhg1-b1 and rhg1-c) and three haplotypes for the Rhg4 locus (rhg4-a, rhg4-b, and rhg4-c). The interaction between these haplotypes inferred specificity to five races of *H. glycines* infestation, which was supported by protein homology modeling prediction and gene expression profiling. Interestingly, some of the lines do not carry the resistant haplotypes at the *Rhg*1 and *Rhg*4 loci; however, these lines showed resistance to multiple races, suggesting that these lines carry a novel mechanism for SCN resistance. The identification of new source of resistance using genomic assisted haplotype analysis and deployment of broad-resistance would be an effective approach to minimize yield loss under SCN infestation.