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Genome-wide association analysis reveals a novel QTL for resistance to soybean cyst nematode in soybean

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Soybean cyst nematode (SCN) is the most destructive pest in the USA. Two major resistant loci, *Rhg1* and *Rhg4* on Chromosome (Chr) 18 and 8, respectively have been reported in many sources of resistance to SCN. Of those, PI 88788 (*rhg1*) and 'Peking' (*rhg1/Rhg4*) have been widely used to develop resistant cultivars in the USA. However, shift in SCN races has been resulted from overusing the limited genetic sources. Thus, it is essential to identify new sources of resistance as well as quantitative trait loci (QTL) before the nematodes develop immunity to these resistant sources. In this study, we screened 479 soybean accessions from various origins using a greenhouse bio-assay and genotyped them with three SNPs developed at *Rhg1* and *Rhg4* loci in our lab. Of 479 lines, 49 resistant lines possess 'Peking'-type resistance, while 31 lines carry PI 88788-type resistance, and 60 lines were rated as resistant or moderately resistant do not carry either 'Peking' or PI 88788 resistant alleles. Based on haplotype analysis at these loci assembled with SoySNP50k Infinium Chip data, these lines were grouped separately from PI 88788 and 'Peking'. Using the greenhouse phenotypes and >35,000 SNPs, genome-wide association study identified novel sources with two genomic regions located on Chr 7 and 18, respectively that are significantly associated with SCN resistance. The genomic region on Chr 18 was known to be *Rhg1* locus and the region on Chr 7 is highly significant which was considered as novel. Bi-parent populations are being used to confirm this novel genomic region and incorporate QTL into the elite germplasm pool.