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Identification of molecular biomarkers associated with reniform nematode resistance in soybean

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Reniform nematode (*Rotylenchulus reniformis*) is a yield-limiting pathogen of soybean (*Glycine max*) in the Southeastern region of the United States. Several studies have identified soybean germplasm with resistance to reniform nematode. However, only a few studies have explored the soybean genome for quantitative trait loci (QTL) linked to reniform nematode resistance. Our objective for this study was to identify high resolution single-nucleotide polymorphism (SNP) biomarkers that correlate with reniform nematode resistance in soybean using genotyping-by-sequencing (GBS). A set of 250 recombinant inbred lines developed from a cross between cultivars 'Forrest' and 'Williams 82' was utilized to correlate reduced nematode reproduction to SNP markers, localizing specific QTL regions. The phenotype was determined by growing three replicates of each line in eight-centimeter diameter cups in a growth room maintained at 28°C. Each plant was inoculated with 2000 vermiform reniform nematodes and populations quantified two months after inoculation. Leaf tissue was collected from each line for genotyping. Reduced representation next-generation sequencing techniques were employed to achieve high-density genetic screening through GBS. DNA from each line was digested using specific restriction enzymes *MseI* and *PstI* to prepare gene libraries, then sequenced on the Illumina HiSeq platform and analyzed using *Stacks* software program to generate population genomic summary statistics. We report SNP markers that correlate to the resistant phenotype observed in the developed lines. The characterized genetic markers can be used by soybean breeders in marker assisted selection to enhance their efforts in selecting and employing lines with known resistance to reniform nematode.