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Identification and evaluation of quantitative trait loci associated with soybean cyst nematode resistance in PI437654-derived germplasm

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Soybean Cyst nematode (SCN) is the most damaging pest of soybean worldwide. Damage by SCN costs the North American soybean growers over \$1 billion each year. Growing resistant cultivars together with crop rotation is the most effective way to control SCN; however, using diverse sources of SCN resistance is also essential to avoid the breakdown of resistance over time. To date, about 98% of SCN resistant cultivars in North America are derived from PI 88788 and SCN is already overcoming the resistance in some areas. Developing new SCN-resistant cultivars with different resistant genes may reduce the risk of genetic shift in SCN populations. The main objective of this study was to detect quantitative trait loci (QTL) that underlie new SCN genes in PI 437654-derived germplasm. Two F4-5 recombinant inbred line (RIL) populations derived from crosses between two high yielding Ontario-adapted elite soybeans, OAC Brooke and OAC Calypso, and LD07-3419 that carries SCN-resistance genes from PI 437654 were used for this study. In total, 347 RIL was phenotyped and genotyped in 2017. The RIL populations were evaluated for resistance to SCN HG (*Heterodera glycines*) type 2.5.7 in a greenhouse and genotyped with genotyping-by-sequencing (GBS). The detection and validation of SCN-related QTL analysis along with studying genetic relationships between the QTL and seed yield are projected to facilitate the development of SCN-resistant soybeans with acceptable yield potential using marker-assisted selection.