

Public Abstract

First Name:Md

Middle Name:Sariful

Last Name:Islam

Adviser's First Name:David

Adviser's Last Name:Sleper

Co-Adviser's First Name:

Co-Adviser's Last Name:

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Title:Molecular Characterization of Genetic Resistance to Soybean Cyst Nematode in Soybean Line SS97-6946

Soybean cyst nematode (SCN) *Heterodera glycines* Ichinohe is the most yield reducing pest of soybean and estimated yield losses are 1.5 billion dollars annually in USA. Breeding resistant cultivars is the most efficient means to control SCN, but the nematode has adapted and overcome resistance of developed soybean cultivars due to narrow genetic base. Resistant genes for different nematode HG types have been genetically mapped in several soybean accessions, but most of them have common quantitative trait loci (QTL). However, *H. glycines* populations are enormously variable and have broken down resistance ability of cultivars. Eventually cultivars become less effective in reducing yield losses. Hence, it is essential to explore new soybean SCN resistant sources for discovery of new genes that confer resistance to SCN field populations to offer long-lasting resistance. Soybean line SS97-6946 is resistant to different SCN HG types and could have novel genes for SCN resistance. Objectives of this study were to investigate the genetic basis of resistance to SCN populations of HG types 2.5.7, 1.2.5.7, 0 and 1.2.7 (corresponding to races 1, 2, 3, and 5, respectively) and determine the QTL associated with resistance to SCN populations of HG types 2.5.7, 1.2.5.7, 0 and 1.2.7 (corresponding to races 1, 2, 3, and 5, respectively) in SS97-6946. PI 567476, moderately susceptible to SCN races was crossed with SS97-6946 to produce F1. One hundred sixty F2 and F2:3 families were developed to investigate the reaction to specific SCN HG types in the greenhouse. Three, two, 24, and seven F2:3 families were categorized as resistant ($FI \leq 10$) to SCN races 1, 2, 3, and 5, respectively. On the other hand 157, 158, 136, and 153 individuals showed susceptible ($FI > 10$) reaction to these four SCN races, respectively. Ratio of resistant to susceptible F2:3 families fitted a three-gene model of inheritance. It was speculated that a genotype with three recessive genes (rhg, rhg, and rhg) for races 1 and 2; two dominant and one recessive (Rhg, Rhg, and rhg) for race 3; one dominant and two recessive (Rhg, rhg, and rhg) for race 5 existed. Some F2:3 families had broad-spectrum resistance to multiple SCN races due to all tested SCN HG types being highly correlated. Three-hundred forty-seven out of 547 (<63%) SSR primer pairs were found polymorphic between PI 567476 and SS97-6946. These selected 347 polymorphic primer pairs covered all 20 linkage group of soybean to screen 160 F2 families derived from the cross PI 567476 X SS97-6946. Phenotypic and genotypic data were analyzed to identify markers associated with resistant QTL to SCN by using MapQTL software. Markers SUIC 100-8K, Satt268, and Satt610 were mapped on linkage groups (LGs) A2, E and G (chromosome no. 8, 15 and 18), respectively, and were found to be associated with resistance to SCN race 1 and accounted for 29.1 % of the total phenotypic variance. One resistant QTL was detected in LG A1 (Chromosome no. 5) associated with marker Sat_368 and accounted for 18.8% of total phenotypic variance of race 2. Markers SUIC 100-8K, Satt610, and Satt551 on LGs A2, G, and M (chromosome no. 8, 18 and 7), respectively were discovered to be associated with resistance to SCN race 3 and shared 30.5% of total phenotypic variance. Markers Sct_187 and Satt610 on LG G (chromosome no. 18) together with markers Sat_368, Satt 665, Sat_287, Sat_121, and Satt173 on LG A1, B1, B2, M, and O (chromosome no. 5, 11, 14, 7 and 10), respectively, were shown to be linked with SCN resistance to race 5 and accounted for 58.9% of total phenotypic variance. Resistance QTL detected in LGs A1, A2, G, M and O could come from resistant parent SS97-6946. Other QTL identified in LGs B1, B2, E could come from PI 567476.