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MOLECULAR GENETIC DISSECTION OF ROOT -KNOT NEMATODE RESISTANCE IN COTTON

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Abstract only

The root-knot nematode (RKN, *Meloidogyne incognita*) is a serious pest of cotton in the US. Successful management of RKN in cotton will require development of elite cultivars with highly effective nematode resistance. Several approaches are being used to increase understanding of the genetic and molecular basis of RKN resistance in cotton.

In a quantitative genetics approach, 12 genotypes including 7 susceptible (S) lines, 1 moderately resistant (MR) line, 3 highly resistant (R) lines derived from Auburn 634 and F_1 between 33B and Auburn 634 were evaluated in the greenhouse for plant growth, RKN egg reproduction and root galling. RKN egg reproduction was highly positively correlated with galling index and both were highly negatively correlated with plant growth characteristics including plant height, number of leaves, and plant and root weight. Comparison between F_1 and their parents in egg reproduction and galling revealed that the RKN resistance in Auburn 634 was partially dominant. Based on a 9-parent diallel analysis in the greenhouse, the general combining ability played a more important role than the specific combining ability in controlling the RKN resistance. Broad-sense and narrow-sense heritabilities for galling index were 0.82 and 0.65, respectively, indicating a predominant control of RKN resistance by genetic and additive effects. The minimum number of genes for RKN resistance was estimated to be 1 or 2.

Using Mendelian genetics, F_2 populations from crosses with Auburn 634 and its derived resistant line M-240 indicated that the resistance in Auburn 634 is either controlled by one dominant gene or one dominant gene and one recessive gene. Based on genetic and molecular analysis of F_1, F_2, F_3, BC_1F_1 and F_7 recombinant inbred lines from the *Gossypium hirsutum* intraspecific cross of resistant cv. NemX with susceptible cv. Acala SJ-2, resistance was found to be controlled by one major recessive gene with allele dosage effect, named *rkn1*. This gene showed transgressive segregation in NemX crosses with both Acala SJ-2 and Pima S-7 (*G. barbadense*). Using the same segregating progenies of NemX x SJ-2, four AFLP markers and two SSR (microsatellite) markers were found tightly linked to resistance gene *rkn1* in NemX. One of the AFLP markers was converted to a cleaved amplified polymorphic (CAP) marker that segregated with the nematode resistance. By screening segregating progenies from the intraspecific NemX x Acala SJ-2 crosses with additional SSR markers previously mapped in the cotton genome, the *rkn1* locus in NemX was mapped to cotton linkage group A03. By comparing pairs of near isogenic lines (NIL) with or without the Auburn source of resistance, two RGA, two RAPD, and two AFLP markers were identified to be consistently polymorphic between the NIL. The two RAPD markers and one of their converted STS markers classified 23 resistant and 8 susceptible germplasm into three groups that reflected their resistance origins. To determine their utility for marker-assisted selection of nematode resistance in cotton, these RKN resistance-associated markers were screened to test linkage to resistance loci using progenies segregating for the resistance of Auburn source. One RAPD marker and its converted sequence tagged site (STS) marker were tightly linked to the CAP marker associated with the NemX resistance.

Using disease resistance gene analogues (RGA), degenerate primers designed from conserved motifs of known plant resistance gene products amplified genomic DNA sequences from Auburn 634. A total of 165 clones were isolated and sequence analysis revealed 57 clones to be novel nucleotide sequences, many containing the R-protein nucleotide-binding site (NBS) motif. A cluster analysis was performed with RGA nucleotide sequences isolated in this study, in addition to 99 cotton RGA nucleotide sequences already deposited in GenBank. The cotton RGA nucleotide sequences were arranged into 11 groups and 56 sub-groups based on genetic distances. 61 pairs of RGA-STS (sequence-tagged site) sequence primers were designed from these groups and subgroups. A recombinant inbred line (RIL) population of cultivated tetraploid cotton was screened using RGA-STS primers that amplified polymorphic fragments between the two RIL parents. Nine RGA markers were mapped to homeologous chromosomes 12 and 26.