2005 Beltwide Cotton Conferences, New Orleans, Louisiana - January 4 - 7, 2005

RESISTANCE GENE ANALOG (RGA) MARKERS ARE MAPPED TO HOMEOLOGOUS CHROMOSOMES IN CULTIVATED TETRAPLOID COTTON

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Abstract

Degenerate primers designed from conserved motifs of known plant resistance gene products were used to amplify genomic DNA sequences from the root-knot nematode (*Meloidogyne incognita*) resistance genetic source, Upland cotton (*Gossypium hirsutum* L.) cultivar Auburn 634 RNR. A total of 165 clones were isolated and sequence analysis revealed 57 of the clones to be novel nucleotide sequences, many containing the R-protein nucleotide-binding site (NBS) motif. A cluster analysis was performed with resistance gene analogue (RGA) nucleotide sequences isolated in this study, in addition to 99 cotton RGA nucleotide sequences already deposited in GenBank, to generate a phylogenetic tree of cotton R-genes. The cotton RGA nucleotide sequences were arranged into 11 groups and 56 sub-groups based on genetic distances. Multiple sequence alignments were performed on the RGA sequences of each sub-group and either the consensus sequences or individual RGA sequences were used to design 61 RGA-STS (sequence-tagged site) primers. A recombinant inbred line (RIL) population of cultivated tetraploid cotton was genotyped using RGA-specific primers that amplified polymorphic fragments between the two RIL parents. Nine RGA markers were mapped to homeologous chromosomes 12 and 26 based on linkage to existing markers that are located on these chromosomes.