2004 BELTWIDE COTTON CONFERENCES, SAN ANTONIO, TX – JANUARY 5-9

# CHARACTERIZATION OF RESISTANCE GENE ANALOGUES (RGAS) ISOLATED FROM UPLAND COTTON: ORIGIN, FUNCTION, AND EVOLUTIONARY RELATIONSHIPS

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## Abstract

Degenerate primers designed from conserved motifs of known plant disease resistance genes were used to amplify genomic DNA sequences from upland cotton (*G. hirsutum* L.). Amplification products were compared between two near-isogenic lines of upland cotton that were resistant or susceptible to the sedentary endoparasite root-knot nematode (*Meloidogyne incognita*). A total of 145 clones were isolated from the resistant upland cotton cultivar Auburn 634RKR. Sequence analysis revealed 65 novel nucleotide sequences, many of which share a high degree of homology to RGA nucleotide sequences previously isolated from *Gossypium hirsutum* and *Gossypium barbadense*. A cluster analysis was performed with RGA nucleotide sequences isolated in this study, in addition to 100 cotton RGA nucleotide sequences present in Genbank. The cotton RGA nucleotide sequences clustered into 9 groups and 55 subgroups. Multiple sequence alignments of each subgroup generated consensus sequences that were used to design RGA-specific primers. Diploid cotton genomes are currently being screened using the RGA-specific primers. The presence or absence of the RGAs in diploid cotton species, as well as nucleotide sequence divergence, will allow inferences concerning the evolution of resistance genes in cotton. Genomic DNAs from four pairs of near-isogenic lines of upland cotton were screened using the RGA-specific primers, and 2 putative polymorphic DNA markers were identified only in the root-knot nematode resistant lines. The polymorphic DNA markers will be used to screen mapping populations of upland cotton to determine genetic distance from the root-knot nematode resistant locus or loci.