

**PLANT DISEASE RESISTANCE GENE ANALOGUES  
IN COTTON: MAPPING AND EXPRESSION**

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**Abstract**

Diseases cause significant losses in cotton production throughout the Cotton Belt. Growing resistant cultivars can significantly improve cotton yields and effectively reduce production inputs. Disease resistance (R) genes have been isolated in numerous plant species and the R genes with domains of nucleotide binding sites (NBS) and leucine rich repeats (LRR) represent the largest R gene family. The objectives of the present study were, (1) to develop and evaluate a genome-wide R gene profiling system; (2) to map the disease resistant gene analogues (RGA); and (3) to study the expression of the RGA in cotton tissues. Degenerate primers designed based on conserved motifs of R genes were used or in combination with AFLP techniques to analyze RGA in a recombinant inbred line (RIL) population developed from a cross between Pima (*G. barbadense*) 3-79 and the Upland cotton (*G. hirsutum*) line NM24016. 88 polymorphic RGA markers were amplified by 8 pairs of RGA degenerate primers, while 131 polymorphic RGA-AFLP markers were produced using 6 RGA and AFLP primer pairs. Based on SSR markers with known chromosomal locations, 217 RGA and RGA-AFLP markers were assigned to 18 chromosomes using programs Mapmaker and JoinMap. Interestingly, these RGA and RGA-AFLP markers were not evenly distributed among chromosomes in that 189 markers (87%) of them were placed on three "giant" linkage groups (C6, C12, and C15). The results confirm that RGA in cotton tend to cluster together. Our work demonstrates that RGA-AFLP is a powerful DNA marker system for identifying resistance gene analogous with more sequence specificity. Using more RGA and AFLP primer combinations, most, if not all, RGA can be amplified and identified genome-wide in cotton. The identification and mapping of RGA and RGA-AFLP markers should provide a framework to facilitate marker-assisted selection (MAS) for disease resistance in cotton breeding and to understand the genome organization of R genes in cotton. Our preliminary analysis of cDNA indicated that many RGA were expressed. Further work in RGA expression and its relationship with disease resistance will be conducted.