ISOLATION AND CHARACTERIZATION OF DISEASE RESISTANCE GENES FROM COTTON

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Abstract

A PCR-based strategy was used to isolate and clone pathogen resistance genes from cotton. Many plant disease resistance genes encode proteins which contain a conserved NBS (nucleotide binding site) domain. The NBS domains encoded by two resistance genes, the *Arabidopsis thaliana RPS2* gene against *Pseudomonas syringae* and the tobacco *(Nicotiana tabacum) N* gene against tobacco mosaic virus (TMV), share identical conserved amino acid sequences in the kinase-1a motif (GGVGKTT) and the hydrophobic domain (hd) (GLPLAL). Two sets of degenerate oligonucleotides were synthesized on the basis of the conserved amino acid sequences and used as primers in PCR amplification of disease resistance genes in cotton. Six different combinations of the two sets of primers had resulted in totally amplifying six different disease resistance gene homologs. The nucleotide and derived amino acid sequence data indicate that the six cotton resistance genes are highly homologous to other plant disease resistance genes, including two tomato vascular wilt disease resistance genes *12C-1* and *12C-2* against soil-borne fungus *Fusarium oxysporum*, the tomato root know nematode resistance gene *Mi-1.2* against *Meloidogyne incognita*, the *Arabidopsis RPS2* gene, and the two *Arabidopsis* disease resistance gene homologs *pNd11* and *pNd13*. Our results indicated that this PCR-based approach is effective to identify different disease resistance genes against fungi, nematode, and bacteria in cotton.

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