ARE *REN^{ARI}* FROM *GOSSYPIUM ARIDUM* AND *REN^{LON}* FROM *G. LONGICALYX* DUPLICATE GENES? David D. Fang Cotton Fiber Bioscience Research Unit, USDA-ARS-SRRC New Orleans, LA Salliana R. Stetina Crop Genetics Research Unit, USDA-ARS Stoneville, MS

Abstract

Reniform nematode (*Rotylenchulus reniformis*) has become a major pest of cotton in the mid-south area of the United States. Resistance genes, Ren^{ari} and Ren^{lon} from *Gossypium aridum* and *G. longicalyx*, respectively, have been identified and introduced into Upland cotton (*G. hirsutum*). We developed an F₂ population of 184 progeny plants by crossing Ren^{ari} –containing plants with a plant having the resistance gene Ren^{lon} . The F₂ plants were evaluated for their resistance to reniform nematodes in a growth chamber. Microsatellite markers BNL2662 and BNL3279 were analyzed to assist the selection of proper parental plants and F₁ progenies, and to study the segregation of the resistance genes in the F₂ population. Our results suggested that Ren^{ari} and Ren^{lon} were duplicate genes with Ren^{ari} residing in chromosome 21, and Ren^{lon} in chromosome 11. F₂ plants containing either Ren^{ari} or Ren^{lon} had significantly fewer nematodes than the susceptible Upland cotton genotype. No significant difference in nematode resistance was found between plants containing Ren^{ari} and Ren^{lon} further enhanced plant resistance to reniform nematodes.