

**STATUS REPORT ON INTROGRESSION OF RENIFORM NEMATODE  
RESISTANCE FROM *GOSSYPIUM LONGICALYX***

**A. Forest Robinson and Alois A. Bell**

**USDA-ARS-CPRU**

**College Station, TX**

**Nilesh Dighe and David Stelly**

**Department of Soil and Crop Science**

**Texas A&M University**

**College Station, TX**

**Abstract**

The reniform nematode (*Rotylenchulus reniformis*) is an increasing problem in the central cotton belt of the United States. No cultivars or breeding lines of Upland cotton (*Gossypium hirsutum*) have sufficient resistance to the nematode to suppress populations appreciably in soil. Of six *Gossypium* species where resistant accessions are reported, only *Gossypium longicalyx* is immune and prevents all nematode reproduction. Although *G. longicalyx* is an F-genome diploid that will not cross with *G. hirsutum*, a low incidence (ca 1%) of seed set can be obtained by crossing *G. hirsutum* onto two male-sterile triple-species hybrids developed by A.A. Bell of the USDA. The hybrid denoted HLA has *G. armourianum* as the third species in its background while the hybrid denoted HHL has *G. herbaceum*. On both hybrids, nematode reproduction was undetectable in pots, although low rates (<1%) of maturation of nematodes on roots were apparent in exhaustive root examinations. Both hybrids show morphological traits of *G. longicalyx* as well as their other parents and are presumed to carry a complete F-genome set of chromosomes inherited from *G. longicalyx*, in combination with either a D genome set from *G. armourianum* or an A genome set from *G. herbaceum*. The objective of this research was to evaluate the feasibility of introgressing reniform nematode resistance from these hybrids into *G. hirsutum*, in order to provide breeding lines that can be utilized to develop reniform nematode-resistant cultivars of Upland cotton. We repeatedly backcrossed the hybrids with *G. hirsutum* and selected for nematode resistance at each generation, to obtain more than 1,100 progeny from the hybrids; 96 immune plants with increasing levels of fertility were recovered altogether in first, second and third backcross (BC<sub>1</sub>, BC<sub>2</sub>, BC<sub>3</sub>) generations. Within specific crosses, approximately 25% of backcross progeny were immune, consistent with a single (or linked) dominant gene(s). Transfer of immunity via pollen to the BC<sub>2</sub> and BC<sub>3</sub> was demonstrated and seed obtained by pollinating emasculated Delta and Pineland 458 and Acala NemX flowers with pollen from immune BC<sub>3</sub> plants are ready for testing. Approximately 4,200 cells in 140 plants were cytogenetically analyzed. Eighty BC<sub>2</sub> plants showed chromosome counts of 53-54 in 6 plants, 49-51 in 10 plants, and 52 in 64 plants; thus chromosome numbers typically were at or approaching the normal 52 for *G. hirsutum*. At least 2 of 10 resistant plants analyzed showed evidence of recombination at 10% or more the normal rate. In conclusion, our data on both nematode resistance inheritance and cotton cytogenetics support the feasibility of utilizing existing progeny from the HLA and HHL hybrids to transfer reniform nematode resistance into agronomic types of Upland cotton via conventional plant breeding protocols.