

## RESEARCH REPORT

Title: Breeding Cotton for Yield and Quality in Alabama

Project Number: 02-172-AL

Principle Investigator: David B. Weaver

There are three major aspects to this project: Development of cotton germplasm or cultivars with improved yield and fiber properties; evaluation and development of cotton germplasm for resistance to reniform nematode; and evaluation and development of cotton germplasm for resistance to abiotic stresses, particularly heat and drought. For the first objective, experimental breeding lines from seven different cotton populations were developed using bulk and pedigree methods. In 2007, we evaluated 280 experimental lines (roughly 40 lines/population) for yield and fiber properties at two locations, Tallassee and Prattville. Plots were two rows, 6.1 m in length, with a spacing of 1 m between rows, replicated 3 times. Data were collected by sampling 50 bolls from each plot for determining lint percentage, boll size, lint weight per seed, and fiber quality. Fiber quality was analyzed by HVI at Cotton, Inc., Cary, NC. The entire plot was spindle-harvested to determine seed and lint yield. No data were collected at Prattville due to extreme drought. Supplemental irrigation, plus some very timely rainfall late in the season resulted in good data from Tallassee, however, and fiber analysis is in progress. Five advanced lines were evaluated in the Regional Breeders Testing Network at 12 locations across the cotton belt. These are the first entries from the Auburn program since its inception. All locations have not reported, however, the top performing line at the Tallassee location (29 entries plus 3 checks) was an Auburn experimental line (Au04-6207, from the cross Miscot 8001 × Suregrow 747), with a lint yield of 1371 lb/A. Test average was 1123 lb/A. Fiber quality of this line was good, with 42.7 % lint, micronaire of 4.4, 50% span length of 1.12 inches, and strength of 29.25 g/tex. Other Auburn lines are performing well at other locations, but all data have not been submitted. We have cooperated in this test for the past five growing seasons. Further work is being done to develop new populations for generating experimental cotton lines for future testing.

We have made significant progress developing advanced populations from crosses between four adapted lines (FM966, SG747, PM1218, and DeltaPearl) and two germplasm lines (TX245 and TX1419) identified as having a moderate level of resistance to reniform nematode. Three types of populations have been developed: Adapted × resistant accession ( $F_{2:3}$  lines); (adapted × resistant accession) × adapted ( $BC_{1:2}$  lines); and (adapted × resistant accession) × resistant accession ( $BC_{1:2}$  lines). We have a total of 1200 lines representing 25, 50 and 75% adapted germplasm, and these lines are ready for evaluation for nematode resistance in 2008. Evaluation and incorporation of genes for resistance into adapted types will be a long-term process.

We are continuing along the same path in development of similar type populations using genotypes identified as heat tolerant. We have identified seven accessions as having significantly greater vegetative heat tolerance than Deltapine 90. Development of these populations is progressing more slowly, due to the difficulty of crossing with these materials. These lines are photoperiodic, with long juvenile periods and can take over a year between planting and flowering. We were unable to make crosses in the winter nursery in 2007, and lines

also failed to flower in the field during 2007. However, plants that were planted in the greenhouse in spring of 2007 are now flowering, and we are making crosses with the adapted Deltapine 90. We hope to have F<sub>2</sub> populations developed by fall, 2008, however it is highly probable that the F<sub>1</sub> hybrids will also have a long juvenile period, so it may take until 2009 before F<sub>2</sub> populations are available for evaluation. During the upcoming year, we will continue to work with these lines to determine the level of expression of this trait and hope to identify genes that are responsible.