

RESEARCH SUMMARY

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 of cotton germplasm for resistance to reniform nematode; and evaluation of cotton germplasm for resistance to abiotic stresses, particularly heat and drought. We have evaluated over 200 experimental lines (developed by two methods of inbreeding: pedigree and single-seed descent) during 2005 and 2006 for yield and fiber properties. Preliminary analysis showed inbreeding method to have no effect on yield or fiber quality with few exceptions. Negative correlations among traits, particularly between lint yield and fiber strength, and lint yield and fiber length, continue to exist and be problematic in adapted germplasm, underlying the difficulty in selecting for improved yield and fiber properties simultaneously. Other negative correlations exist. Several of these lines showed excellent yield potential however, and will be advanced to regional cooperative tests (Regional Breeders Testing Network) for testing in 2007. We have also cooperated in this test for the past four growing seasons. After extensive evaluation of 2000 cotton genotypes, we have identified seven that were considered moderately resistant to reniform nematode. These are considered only moderately resistant because they support roughly 30% of the nematode reproduction of a check cultivar. However, these genotypes are very poorly adapted (will not flower or produce yield in Alabama) and the incorporation of genes for resistance into adapted types will be a long-term process. Similarly, we have evaluated the same set of 2000 genotypes for reaction to heat during vegetative growth, and have identified several that tolerate heat better than a check cultivar in the growth chamber. 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.