

**IDENTIFICATION OF COTTON GERMPLASM AND MOLECULAR MARKERS  
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Drought stress is a major abiotic stress that adversely affects cotton yield and fiber quality. However, there are few drought tolerant cultivars developed and little information about the genetic basis of drought tolerance reported in cotton. The objectives of this project were to screen an interspecific backcross inbred line (BIL) population for drought tolerance and to identify molecular markers associated with drought tolerance. The plant materials utilized were 146 BIL lines generated from an interspecific cross between Upland and Pima cotton. These lines were evaluated in replicated field trials in two locations (Las Cruces and Artesia, NM) in 2008 and 2009 using reduced and normal irrigation treatments. Seedcotton yield, lint yield, lint percentage, boll weight, fiber length, fiber strength, elongation, micronaire, uniformity and short fiber content were determined. Selected BIL lines were also genotyped using molecular markers from the AFLP, cDNA-AFLP, PAAP-RAPD, SSR and STS marker systems. The analysis of variance was performed to partition phenotypic variation into sources due to genotype, treatment, location, genotype x treatment, and genotype x location. A linkage map was constructed and quantitative trait loci (QTL) analysis was performed. The main results were, (1) significant variation existed for genotype, treatment, location, and genotype by location for all traits measured, while genotype by treatment was not detected for many traits including yield, uniformity and fiber strength.; (2) BIL lines with superior drought tolerance were observed within the population; (3) of 543 polymorphic markers, 242 markers were used to construct a linkage map of 41 linkage groups which spanned 842 centiMorgan (cM) and comprised 17% of the cotton genome; (4) 12 QTLs associated with yield and fiber quality traits were detected, in addition to 11 epistatic interactions associated with drought tolerance, yield, and fiber quality traits. Overall, useful introgression of alleles for drought tolerance has been observed in the backcross inbred line population. Further work will be needed to add more markers especially chromosome-anchored SSR markers to the existing linkage map for higher genome coverage and for identification of more QTLs for drought tolerance. The results will lead to the identification and use of superior breeding lines and QTLs for drought tolerance.