

**DROUGHT RESISTANCE SCREENING OF TWO BC<sub>1</sub>F<sub>1</sub> populations**  
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**Abstract**

*Gossypium tomentosum* and *G. mustelinum* are tetraploid wild relatives of cultivated cotton, *G. hirsutum*. *G. tomentosum* is native to the Hawaiian Islands and *G. mustelinum* is endemic to northern Brazil. Both species probably share a common AD genome ancestor with upland and sea island cottons. Because they are relatively closely related to upland cotton, we have initiated an introgression effort using these two species to improve agronomic characters and to widen the genetic base of upland cotton. We are pursuing three different introgression methods. The first relies on traditional backcross-inbred populations, which we will advance to the BC<sub>3</sub>F<sub>1</sub>. The second method relies on populations that are random-mated at each level of backcrossing to break undesirable linkages and to allow for the formation of novel epistatic interactions. The third method relies on chromosome substitution lines created by backcrossing to cytogenetic stocks prior to inbreeding. Each method has strengths and weaknesses. We will assess efficacy of the first and second methods using generation mean analysis, while simultaneously selecting individuals for inclusion in traditional cotton breeding programs. Currently greenhouse populations have been evaluated for plant characteristics such as hairiness, flower color, and leaf type and screened with a possible drought tolerance test that we call the wiltiness test. This was a test developed from *Arabidopsis thaliana* for identification of ABA mutants that measures the rate of water loss from excised leaves. Implications of the wiltiness test and future experiments were discussed. We gratefully acknowledge support from Cotton, Inc., TAES, the Texas Food & Fiber Commission (TFFC), and Texas State Support Committee (TSSC).