

**TRANSGRESSIVE SEGREGATION IN UPLAND COTTON****Benjamin Beyer****C. W. Smith****Texas A&M University****College Station, TX****Gregory L. Berger****Virginia Tech University****Blacksburg, VA****Steve Hague****Texas A&M University****College Station, TX****Abstract**

The United States traditionally markets upland cotton, *Gossypium hirsutum*, with a High Volume Instrument (HVI) upper half mean length (UHML) of 1.06 in. although international trade requires a minimum of 1.09 in. Strains and cultivars have been developed that exhibit UHML of approximately 1.26 in. that are referred to as long staple uplands (LSU). Further improvement in fiber length could provide the opportunity for the U.S. to produce a unique fiber type that could be instrumental in maintaining global competitiveness. Breeders often cross a parent exhibiting one extreme of a trait with a parent exhibiting the opposite extreme in order to evaluate the combining ability and heritability of the trait. The objectives of this research were to determine [1] the parental and F<sub>2</sub> associated fiber length parameters among LSU / LSU, LSU / short staple upland (SSU), ELSU / LSU, ELSU / MSU, and ELSU / ELSU, and [2] transgressive segregation in each combination. TAM 94L-25 (Smith, 2003), a LSU, was crossed with three LSU and one short staple upland (SSU) phenotypes. Parents and their F<sub>2</sub> generations were grown in a randomized complete block design at College Station, TX in 2001 and 2002. Two extra long staple upland (ELSU) genotypes, TAM B182-39 (unreleased breeding line) and TAM C155-22 (PI 654366; Smith et al., 2009) were intercrossed and each crossed with Deltapine 491 (PVP 200100159, PI 618609), a LSU, and Deltapine 50 (PI 529566), a medium staple upland (MSU) cultivar. These parents and their F<sub>2</sub> populations were grown at Weslaco, Texas in 2008. Hand harvested seedcotton from individual plants of parents and F<sub>2</sub>s were ginned on a laboratory gin, and HVI and Advanced Fiber Instrument System (AFIS) fiber properties determined. Transgressive segregates were found in all F<sub>2</sub> populations.