

**GENE ACTION OF AFIS FIBER LENGTH IN UPLAND COTTON****Chris Braden, C. W. Smith and Peggy Thaxton****Texas A&M University****College Station, TX****Eric Hequet****Interantional Textile Center, Texas Tech University****Lubbock, TX****Abstract**

Cotton breeders must be concerned with fiber quality as well as yield if American cotton is to maintain a strong, competitive edge in today's world market. Fiber quality is important to the textile industry because it relates directly to processing performance, productivity, and yarn quality. Improvement in fiber length is important to the textile industry in utilizing high-speed yarn spinning technology and in expanding the array of yarn products. The objectives of this study were to assess the type of gene action, heritability, and estimate the genetic variances of fiber length by weight (FLw) from the Advanced Fiber Information System (AFIS).

Genotypes selected on the basis of their high volume instrumentation (HVI) upper-half mean (UHM) length of fibers and programmatic origins were TAM 94L-25, FiberMax 832, and Tamcot CAMD-E. The two genetic combinations made were: short x near-long staple (CAMD-E/TAM 94L-25 and CAMD-E/FiberMax 832).

Data were analyzed using the proc mixed procedure of SAS with crosses, generations, and years fixed and replications and plants as random effects. The joint scaling test is based on estimating the mean of two lines (m), the additive gene effects (a), and the dominance gene effects (d) from the six generation means by the method of weighted least squares. The additive-dominance model (m, a, d) was fitted and tested for goodness of fit by a weighted chi-square test with three degrees of freedom. When this model proved inadequate, a six parameter model (m, a, d, aa, ad, and dd) was fitted. The genetic parameters were tested for significance using an unpaired t-test.

A significant generation x environment interaction in the analysis of variance required the years to be analyzed separately. The simple additive-dominance model was inadequate for both crosses and years and therefore the six parameter model was used. For CAMD-E x TAM94L-25, the direction of response for the gene effects in 2002 were the same as witnessed in 2001 except for the additive x dominance effect. Additive gene effect estimates were positive and significant for both years, 1.46 and 2.06, respectfully. A significant positive dominance x dominance epistatic effect estimate of 3.21 was obtained in 2002 and this epistatic effect was larger in magnitude than all other effects for both years. In the CAMD-E x FM832, the direction of response across years was different except for additive effect estimates. Additive gene effects estimates were positive and significant both years, 2.78 and 2.00, respectfully. In 2001, a significant negative dominance effect estimate of -6.54 was obtained while a significant positive dominance effect estimate of 9.97 was obtained in 2002. Dominance effect estimates for both years were larger in magnitude than additive effect estimates. In 2001, a significant negative additive x additive effect estimate of -1.40 was obtained while a significant positive additive x additive effect estimate of 4.30 was obtained in 2002. A significant positive additive x dominance effect estimate of 5.63 was obtained in 2001, while a significant negative dominance x dominance effect estimate of -5.50 was obtained in 2002.

The environmental component of variance for the CAMD-E x TAM 94L-25 cross was low in 2001 comprising 19% of the total phenotypic variances while accounting for 30% in 2002. The additive component of variance was larger in 2002 and this is evident in narrow sense heritability estimates of 0.39 in 2001 and 0.70 in 2002. In CAMD-E x FM832, the environmental component of variance was higher for both years, accounting for 68 and 58% of the total phenotypic variance in 2001 and 2002. A negative additive component of variance attributes to the 0 narrow sense heritability estimate in 2001. In 2002, however, we have a narrow-sense heritability estimate of 0.42.

These results show that the importance and significance of gene effects and genetic components of variance for AFIS FLw were dependent upon the particular crossing combination and experimental year and inheritance is the result of many different loci with both additive and dominance effects.