

**GENERATION MEAN ANALYSIS  
OF FIBER QUALITY TRAITS**

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**Abstract**

The modification of a fiber trait through plant breeding approaches requires knowledge of its genetic underpinnings. Little information regarding the mode of gene action of cotton fiber traits is available. Utilizing generation mean analysis, information on the relative importance of additive, dominant and epistatic gene action for five HVI measured fiber traits: micronaire, upper-half mean length, uniformity index, strength (g/tex) and elongation was determined. The parents (Stoneville LA887 and SA565), F1, F2 and backcross generations were evaluated in a completely randomized design in 1997 at the Dean Lee Research Station in Alexandria, LA. Rows were 6m long and plants spaced 10cm apart. Analysis of variance indicated highly significant differences between generations for all five HVI fiber traits. The digenic joint scaling test indicated that the simple additive/dominance model was adequate only for UHM fiber length and for fiber strength. In both cases, the additive variance was significant at the  $p=0.10$  level but dominance variance was not. Epistatic interactions (additive/additive, additive/dominance, dominance/dominance) were not significant for either UHM fiber length or fiber strength. For these two fiber traits there was a close correlation between observed and expected values based upon a simple, digenic model. For micronaire and uniformity index both additive and additive/additive epistatic interactions were significant. For elongation, neither additive, dominant or epistatic interactions were found to be significant. These results imply that developing cotton varieties with improved fiber length and strength should be readily achievable by applying conventional breeding approaches. The presence of epistatic gene action in both micronaire and uniformity index, and the failure of the digenic model for elongation will make improvement of these fiber traits more difficult.