THE GENETICS OF COTTON FIBER INITIATION Rickie B. Turley Stoneville, MS

<u>Abstract</u>

To study the cellular mechanisms involved in fiber initiation, three fiberless lines were crossed with wildtype and fuzzless seed cotton and the F₁, F₂ and BC₁ progeny ratios are presently being evaluated. The three fiberless lines included: MD17 ($N_1N_1n_2n_2$), SL1-7-1 ($N_1N_1fl_1fl_1n_3n_3$) and XZ142w (two genotypes reported, $n_2n_2li_3li_3$ and $n_1n_1n_2n_2li_3li_3li_4li_4$). With two reported genotypes for XZ142w, the first problem is to determine if either genotype is correct. The latter genotype ($n_1n_1n_2n_2li_3li_3li_4li_4$) was dismissed after the evaluation of a proposed modification of genetic functions of the fuzzless seed loci and the lack of lintless, fuzzy phenotypes in the F₂ progeny. The two loci model was evaluated with the F₁ and F₂ progenies of crosses DP5690 X XZ142w and XZFuzz X XZ142w. Both DP5690 and XZFuzz are genotype $N_2N_2Li_3Li_3$. For the DP5690 X XZ142w cross all F₁ progeny had fuzzy seed verifying that XZ142w was homozygous for the recessive fuzzless seed allele n_2n_2 and the F₂ segregated 361F:100N:31fls (F=fuzzy seed, N=fuzzless seed and fls=fiberless) with a X²_{12F:3N:1fls, 2df}=0.8266, P=0.66148. For the XZFuzz X XZ142w cross all F₁ progeny were again fuzzy seed and the F₂ segregated 372F:102N:31fls with a X²_{12F:3N:1fls, 2df}=0.6950, P=0.70643. These data fit the two loci model very well. The BC₁ populations were generated by crossing 143 (n_2n_2) X XZ142w and then crossing the F₁ X 143 with the expected ratio of 100% fuzzless seed was validated by the 167N plants in the population. The F₁ X XZ142w population of 123N:116fls with a X²_{1:1, 1df}=0.2050, P=0.65070. These data indicate that XZ142w has two recessive loci which interact during ovule development to produce a fiberless ovule.