

**EVALUATION OF FIBER VARIANTS
OF COTTON**
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Abstract

The use of mutants in research has led to numerous discoveries about specific aspects of metabolism. A recent example of this has been the use of *Arabidopsis* or *Petunia* mutants in the elucidation of genes involved in the regulation of gametogenesis. Many of these genes would have likely remained unknown due to the microscopic nature of gametophytic tissues. Using a similar approach, we have collected known fiber mutants (variants) of cotton. These variants include ligo lintless 1 & 2, SL 1-7-1, along with the "clean seed" lines (Mississippi Obsolete Numbers 143 & 243). By using 2-D PAGE, a comparison of protein profiles of SL 1-7-1 and a "normal" fiber producing line (DPL 5690) was made. Five proteins were developmentally unique to the fiber line which accumulated after fiber initiation; these proteins were designated D7, D10, D12, D13, and D14. Partial protein microsequencing has been performed on all but D7. Presently, no functions have been established for any of these D proteins. We have discovered that D12 and D13 are possible members of a multigene family (9 of 11 amino acids are identical on one sequence). Also D10 has some similarity to a protein which is unique to DPL 5690 line designated as V2 (a varietal difference which is present from 3 DBA to 4 DPA). The accumulation pattern of D14 is correlated with the fiber elongation phase. Another comparison, the analysis of protein profiles of the ligo lintless 1 line with TM-1 have been inconclusive. We have also used 2-D PAGE to try to identify proteins which correlate with specific fiber traits. A cross was made with MD51ne X Tamcot HQ95 and 14 DPA fiber was analyzed from the fiber. Seven proteins were found which were associated with specific fiber traits; the correlation occurred when measuring interactions of multiple proteins. Further work needs to characterize these proteins in order to identify clones and possibly make fusion proteins, and thereafter antibodies.