

# **GENE EXPRESSION IN DEVELOPING FIBERS AS A MODEL FOR WATER-DEFICIT STRESS**

**Bill L. Hendrix and James McD. Stewart**  
**Dept. Crop, Soil and Environmental Sciences**  
**University of Arkansas**

**Fayetteville, AR**  
**Thea A. Wilkins**  
**Dept. Agronomy and Range Sciences**  
**University of California**  
**Davis, CA**

## **Abstract**

Lockhart (1965) outlined parameters governing plant cell growth. Among these are the mechanisms to control turgor pressure and volumetric extensibility. In cotton, the interplay between turgor pressure and cell wall extensibility is an important biophysical phenomena both in fiber elongation and in water-deficit stress. Though these situations are driven by different stimuli, the metabolic requirements for the two responses would appear to be similar. Accordingly, gene expression profiles may be similar. In this study, *in silico* expression analysis was used to assess the genetic similarity of these two phenomena, and thus the feasibility of using existing fiber-based genomics tools to study cotton gene expression related to adaptation to water-deficit stress. Full-length protein sequences of 124 genes related to water-deficit stress in *Arabidopsis thaliana* were compared to fiber ESTs in the Cotton Pilot Project (CPP) database using the tblastn algorithm. Seventy-nine percent of the genes related to water-deficit stress in Arabidopsis had statistically significant orthologs in the CPP database. The high level of concordance indicates that use of fiber-based microarrays is a feasible approach to study water-deficit stress in cotton.