

**COMPARATIVE EXPRESSION AMONG COTTON CULTIVARS OF
SELECTED GENES ASSOCIATED WITH WATER-STRESS DEFICIT**
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Abstract

In cotton (*Gossypium hirsutum* L.) production, water deficit is a major limiting factor but the level of drought tolerance among commonly grown cultivars is unknown. After consulting major cotton breeders in the US and abroad, seven cultivars representative of most of the main cotton growing areas of the US were chosen. These included Maxxa (west), Sphinx (southwest), Fibermax (midsouth), Deltapine Nu33B, Stoneville 747, Sure-Grow 474 (Mississippi River Delta), and Paymaster 1218 (east). An Australian cultivar, Siokra L-23, was included for its known tolerance to drought. Physiological characterization under conditions of water-deficit stress indicated a narrow range of osmotic adjustment with the only significant difference being between Maxxa (12 %) and Sphinx (44 %). Several cultivars showed significant increases in photosynthetic rate at three days after stress cessation compared to control plants, especially Siokra L-23 and Paymaster. Leaf epicuticular wax content was significantly higher in stressed plants, and transpiration rates were inversely related to wax content. Based on physiological results, Maxxa, Sphinx, Paymaster 1218, and Siokra L-23 were chosen for molecular characterization. Currently these cultivars are being screened for gene expression related to proline and trehalose metabolism via northern blot analyses. Preliminary northern data indicate an increase in expression of enzymes involved in both catabolism and anabolism of proline under water deficient conditions, suggesting that proline cycling may be an important mechanism in combating water-deficit stress. Expression of several genes involved in trehalose production and degradation was also shown, however additional analyses are required to conclusively establish the expression of this pathway in response to water stress.