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RESPONSE OF COMMON COTTON CULTIVARS TO WATER-DEFICIT STRESS

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Abstract

Water-deficit stress is a major limiting factor in cotton *(Gossypium hirsutum* L.) production, but the level of drought tolerance among widely grown cultivars is unknown. Seven cultivars representative of most of the major cotton areas were chosen. These included Maxxa (west), Sphinx (southwest), Fibermax (midsouth), Deltapine Nu33B, Stoneville 474, Sure-Grow 747 (Mississippi River Delta), and Paymaster 1218 (east). An Australian cultivar, Siokra L-23, was included for its known level of drought tolerance. Studies were performed at Fayetteville, Arkansas under both controlled chamber and field conditions. In the growth chambers, at four weeks after planting, half the plants were subjected to water-deficit stress past the point of stomatal closure to full wilt. After full rehydration, osmotic adjustment was measured using end-window thermocouple psychrometry. Means of five experiments indicated a narrow range of osmotic adjustment with the only significant difference being between Maxxa (12%) and Sphinx (44%). Other cultivars ranged between these two extremes. Photosynthesis was also measured 1, 3 and 7 days after stress recovery. Stressed plants of several cultivars showed significant increases in photosynthetic rate three days after stress cessation compared to control plants, especially Siokra L-23 and Sphinx. Leaf epicuticular wax content was significantly higher in all stressed plants, and transpiration rates were inversely related to amount of wax. Stressed Sphinx plants showed the greatest degree of wax accumulation compared to other cultivars. Under field conditions, osmotic measurements mimicked results from the controlled studies. Results indicated a limited amount of drought tolerance in current commercial cultivars. However, there was evidence of enhanced photosynthetic recovery from water-deficit stress in several cultivars. Current research focuses on molecular characterization of drought tolerance. Selected cultivars are being screened for gene expression related to proline and trehalose metabolism.