

Heat Stress Related Gene Expression in *Gossypium hirsutum* L.

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Abiotic stress is a major limiting factor to crop productivity, and heat stress is one of the important elements for reduced crop production. Plants respond to heat stress at molecular and cellular levels as well as physiological level. Heat stress alters expression patterns of numerous genes in plants. At the molecular level, most of the information for heat stress response was obtained from model plants such as *Arabidopsis thaliana*, *Medicago truncatula*, and, *Oryza sativa*, but little molecular research has focused on heat stress response in cotton. Our knowledge is insufficient on heat stress response of cotton at molecular level. To improve our understanding of how cotton responds to heat stress at molecular and cellular levels, we intend to carry out our research on heat stress changed gene expression with upland cotton (*Gossypium hirsutum* L.), which is one of the most important cash crops in Turkey and the world. In this study, differential display technique was used to identify heat stress related genes in cotton. For this purpose, we exposed cotton to heat stress at 38°C and 45°C, and heat stressed cottons were compared with control cottons at mRNA expression level. By using this technique, we identified 160 different band patterns on the gels. Among them 8 ESTs were down-regulated, 23 were up-regulated, 32 were completely suppressed, and 97 ESTs were newly expressed when plants were exposed to heat stress. 25 ESTs were isolated, cloned, and sequenced. Sequences of cloned ESTs were searched in gene banks and EST banks for determination of their homology to known genes and ESTs from cotton and other organisms. After sequence alignment search, we determined that 10 ESTs had homology to known genes, but 15 ESTs were not similar to any known genes. The 15 sequences related to unknown genes showed significant similarity with cotton ESTs. Our future research will focus on amplification of full length ESTs, determination and characterization of unknown sequences, and characterization of ESTs which are similar to the known genes.