Transcriptional Profiles of Maize lines Differing in Heat Tolerance. (C07-nguyen103517-Poster)

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Abstract:

This study was conducted to obtain transcript profiles in maize leaves in response to heat stress. Gene expression was analyzed using a cDNA micro-array representing 4,570 elements. RNA was isolated from control and heat stressed leaf tissues of B76 (heat tolerant) and B106 (heat susceptible) from various developmental stages and growing conditions. We analyzed the timing, dynamics, and expression of about 150 genes in response to heat stress. Significantly up-regulated genes were primarily heat shock proteins, chaperon, stressed-induced protein sti-1, translation initiation factors, polyubiquitin gene, cytosolic factor protein and other putative proteins. Down-regulated genes were mainly tryptophan synthase beta sub-unit, putative chloroplast proteins, MCM-2 related proteins, protein kinase 3, beta adaptive like proteins and putative DNA polymerase genes. The known differentially expressed genes/proteins were classified into various functional groups and on the basis of time course expression and genotypes. Exploiting the differential response of these genotypes is a viable approach to further elucidate the molecular basis of heat tolerance prior to flowering.

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