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# GENE EXPRESSION PATTERNS DURING SOMATIC EMBRYO DEVELOPMENT AND GERMINATION IN MAIZE HI II CULTURES

**by**

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## ABSTRACT

Gene expression changes associated with embryogenic callus formation and with somatic embryo maturation and germination were examined in a regeneration-proficient hybrid line of Zea mays, Hi II. 12,060 element maize cDNA microarrays were used to generate gene expression profiles from embryogenic calli induced to undergo embryo maturation and germination. No statistically significant gene expression changes were detected in comparing embryogenic with total callus. On the other hand, over 1,000 genes showed significant time variation during somatic embryo development. In general, a substantial number of genes were downregulated during embryo maturation, largely histone and ribosomal protein genes, which may result from a slow down in cell proliferation and growth during embryo maturation. The expression of these genes dramatically recovered at germination. Other genes upregulated during embryo maturation included genes encoding hydrolytic enzymes (nucleases, glucosidases and proteases) and a few storage genes (zein and caleosin), which are good candidates for developmental marker genes. Germination is accompanied by the upregulation of a number of stress response and membrane transporter genes, and, as expected, greening is associated with the upregulation of many genes encoding photosynthetic and chloroplast components. Thus, some, but not all genes, typically associated with zygotic embryogenesis are significantly up or downregulated during somatic embryogenesis in Hi II maize line regeneration.