GENE EXPRESSION PROFILING IN RESPONSE TO WATER STRESS IN MAIZE DEVELOPING KERNELS BY DNA MICROARRAY TECHNOLOGY

R. MARINO, L. GIANFRANCESCHI, C. FROVA, M.E. PÈ, M. SARI-GORLA

Department of Biomolecular Sciences and Biotechnology, University of Milano, Via Celoria 26, 20133 Milano (Italy)
mirella.sarigora@unimi.it

gene expression, DNA microarray, drought, Zea mays L.

Drought, like many other environmental stresses, has adverse effects on plant growth and crop yield. As water resources for agronomic uses become more limiting, the development of drought-tolerant genotypes becomes increasingly more important (Bruce et al. 2002). In maize, the early stages of kernel development have been known for long as being very sensitive to dehydration; however, the genetic basis of the cellular response are still not clearly understood. Transcriptome study is a very important tool that allows to simultaneous monitoring the expression levels of numerous genes, thus enabling the identification of sets of genes modulated in a coordinate fashion.

In order to analyze gene expression in response to drought during early phases of maize kernel development under field conditions, DNA array technology has been used to determine transcription profile of thousands of maize sequences, comparing the transcription profile of a maize inbred line susceptible to drought conditions, grown under well watered condition and under water stress conditions. In particular, cDNA microarrays containing several thousand ESTs derived from 10-14 DAP (days after pollination) maize kernels, produced by the University of Arizona, Tucson, were hybridized with labelled cDNA of 10 DAP kernels. Statistical analysis of our results allowed us to identify several sequences putatively regulated in response to drought. Among regulated ESTs were sequences corresponding to genes coding for protein kinases, glycine-rich protein, ribosomal proteins, zeins, heat shock proteins, cadherins and genes responsive to ABA.

In order to refine our analysis, a targeted microarray strategy has been devised, selecting from public data bases 1000 tentative contigs coding for products involved and/or hypothesized to be involved in stress response (RAB, LEA, dehydrins, Hsps), involved in starch synthesis and grain filling, and others (ROS scavenging etc.) Two hundred TC of unknown function, but expressed in developing kernels, were also chosen. From these selected 1000 TC, specific 50-mers were designed and spotted in duplicate onto glass slides (MWG custom service). These oligo DNA arrays are now being utilized to determine transcription profiling of 6 different genotypes (3 highly tolerant and 3 highly sensitive).

References