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ADDRESSING DROUGHT TOLERANCE IN MAIZE BY TRANSCRIPTIONAL PROFILING AND GENETIC MAPPING

R. MARINO*, P. MAHARAJAH*, M.E. PÈ*, C. FROVA*, P. KRAJEWSKI**, M. SARI GORLA*

*) Department of Biomolecular Sciences and Biotechnology, University of Milano, Via Celoria 26, 20133 Milano, Italy – rosanna.marino@unimi.it
**) Institute of Plant Genetics, Polish Academy of Sciences, ul. Strzeszynska 34, Poznan (Poland)

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Drought is among the most important environmental stresses, having adverse effects on plant growth and crop yield. In maize, the early post pollination phase and the grain filling period are very sensitive to this stress, even though the genetic basis of the plant response are still not clearly understood.
The objectives of this study were to: 1) dissect the genetic architecture underlying plant response to water stress and its regulation; 2) develop molecular tools suitable to increase the efficiency of selection for drought tolerance in maize.
For the first objective, DNA array strategy was chosen to simultaneous monitoring the expression levels of a large number of genes. A targeted microarray strategy has been devised, selecting from public data bases 1000 tentative contigs (TC) coding for products involved, or hypothesized to be involved, in stress response, in starch synthesis and grain filling, beside two hundred TC expressed in developing kernels of unknown function. From these TC, specific 50-mers were designed and spotted in duplicate onto glass slides (MWG custom service). Using these oligo DNA arrays we compared transcripts from 10 days after pollination (DAP) kernels of two highly susceptible and two drought tolerant Recombinant Inbred Lines (RILs), grown under well-watered field conditions or under water stress. Statistical analysis of our results allowed the identification of several sequences putatively regulated in response to drought: 252 genes were significantly affected by stress in at least one genotype. Functional analysis of these sequences showed that the more representative class was “Stress/defense response genes”. Comparison of the expression profiling of water stress effects between the four genotypes have pointed that there was a different number of regulated genes in each genotype, and they are different in their transcriptional responses. However 79 genes were differentially expressed in more than one genotype and of these 37% have opposite regulation between the susceptible and tolerant genotypes, while 47% have the same regulation.
About 50 sequences from transcriptome profiling were chosen as candidate genes (CG) to be transformed in molecular markers and localized in our linkage map. This map was previously constructed by genotyping (more than 150 markers) a population of 142 RILs derived from the cross B73 x H99, from which the four genotypes analyzed by DNA microarray have been extracted. This population was previously used in a two-year experiment of linkage analysis for the identification of QTLs involved in the plant response to drought with regard to yield and flowering components. Analyzing single nucleotide polymorphisms (SNPs) found in sequenced CG PCR products, we have designed new 8 CAPS, 1 ARMS-PCR, 16 SSCP markers. Co-segregation of

these new markers with QTLs related to nine phenotypic traits, representing main yield and development components in stressed and control conditions, is at present under study.