TRANSCRIPTOME CHARACTERIZATION IN MAIZE OPAQUE ENDOSPERM MUTATIONS

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In this study we have assayed the pattern of gene expression in o2, o7, and in the o2o7 endosperm mutants was carried out in our laboratory by profiling endosperm mRNA transcript at 15 DAP and the Zeastar unigene set of selected maize gene sequences. The results revealed distinct, as well as shared, gene expression patterns in these mutants. The o2 mutation has a much greater impact than o7 on gene expression in 15-DAP endosperm, with the o2o7 endosperm mutant, resembling the expression pattern of the o2 gene. For the three endosperm mutants (i.e. o2, o7, and o2o7) 38, 7, and 32 genes, respectively, are upregulated more than 3-fold relative to the wild-type. In agreement with previous observations in the o2 and o2o7 endosperms these genes appeared to function in a number of pathways related to aminoacid and carbohydrate metabolism, signal transduction, protein turnover, transport, and protein folding. By contrast, the expression of 57, 17, and 56 genes are respectively, markedly reduced in the o2, o7, and o2o7 mutant endosperms, compared to the wild-type. In o2 and o2o7 most of the down-regulated genes are involved in zein storage protein synthesis, carbon and carbohydrate metabolism, amino acid metabolism, and signal transduction. In addition, three transcription factors different from o2 appear down-regulated. Collectively, the results may provide a framework for investigating a common mechanism the underlines the opaque kernel phenotype.