

TRANSCRIPTOME CHARACTERIZATION IN MAIZE OPAQUE ENDOSPERM MUTATIONS

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endosperm mutants, gene expression analysis, protein and carbohydrate metabolism

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 amino acid 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.