



An expression profiling analysis of hybrid millet and its parents at grain filling stage

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ABSTRACT. Heterosis has been widely used in crop breeding and production. However, a shortage of genes known to function in heterosis significantly limits our understanding of the molecular basis underlying heterosis. Here, we report 740 differentially expressed genes (DEGs) in the leaves of the hybrid millet Zhang No.5 and its parents at the grain filling stage determined using Solexa Illumina digital gene expression. Of the 740 DEGs, 546 were from the hybrid and its parents and most were up-regulated in the hybrid. Particularly, a large number of DEGs related to starch and carbohydrate metabolism and 2 DEGs encoding chlorophyll a/b binding proteins were up-regulated in hybrid millet. Moreover, all DEGs were enriched in the biological process and molecular function, and no DEGs were found to be enriched in the cellular component of GO terms. Pathway enrichment using KEGG showed that several DEGs were enriched in the circadian rhythm pathway. Further analysis revealed that the altered circadian rhythm, which mediates photosynthesis and carbohydrate accumulation, may play an important role in heterosis of the hybrid millet.

Key words: Differentially expressed gene; Grain filling stage; Heterosis; Hybrid millet