

Transcriptome sequencing and metabolome analysis reveals the molecular mechanism of drought stress in millet

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Abstract: 【Background】 As one of the oldest agricultural crops in China, millet (*Panicum miliaceum*) has powerful drought tolerance. **【Method】** In this study, transcriptome and metabolome analyses of 'Hequ Red millet' (HQ) and 'Yanshu No.10' (YS10) millet after 6 hours of drought stress were performed. Transcriptome characteristics of drought stress in HQ and YS10 were characterized by Pacbio full-length transcriptome sequencing. **【Result】** The pathway analysis of the differentially expressed genes (DEGs) showed that the highly enriched categories were related to starch and sucrose metabolism, pyruvate metabolism, metabolic pathways and the biosynthesis of secondary metabolites when the two millet varieties were subjected to drought stress. Under drought stress, 245 genes related to energy metabolism were found to show significant changes between the two strains. Further analysis showed that 219 genes related to plant hormone signal transduction also participated in the drought response. In addition, numerous genes involved in anthocyanin metabolism and photosynthesis were confirmed to be related to drought stress, and these genes showed significant differential expression and played an important role in anthocyanin metabolism and photosynthesis. Moreover, we identified 496 transcription factors related to drought stress, which came from ten different transcription factor families, such as bHLH, C3H, MYB, and WRKY. Further analysis showed that many key genes related to energy metabolism, such as citrate synthase, isocitrate dehydrogenase, and ATP synthase, showed significant upregulation, and most of the structural genes involved in anthocyanin biosynthesis also showed significant upregulation in both strains. Most genes related to plant hormone signal transduction showed upregulated expression, while many JA and SA signalling pathway-related genes were downregulated. **【Conclusion】** Metabolome analysis was performed on 'Hequ red millet' (HQ) and 'Yanshu 10' (YS10), a total of 2082 differential metabolites (DEMs) were identified. These findings indicate that energy metabolism, anthocyanins, photosynthesis, and plant hormones are closely related to the drought resistance of millet and adapt to adversity by precisely regulating the levels of various molecular pathways.