

GENE EXPRESSION OF GUAYULE FIELD PLANTS UNDER DROUGHT STRESS: A COMPARATIVE RNA-SEQ STUDY

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Guayule (*Parthenium argentatum* A. Gray) is a perennial desert shrub native to the southwestern United States and northern Mexico and represents a potential commercial source of natural rubber (NR, *cis*-1,4-polyisoprene), a strategic raw material necessary for national defense, modern transportation, and medicine. Previous studies have shown that rubber yield in guayule increases under various environmental stresses, including drought stress, under which guayule is naturally native habituated. At the molecular level, drought stress results in differential expression of genes regulating various metabolic pathways. To elucidate drought stress responses in rubber biosynthesis pathways as well as identify drought stress related genes in guayule, transcriptome data were generated from stembark tissues harvested in two-year-old guayule field plants following high and low irrigation treatments. A comprehensive transcriptome database was built using genome-guided and *de novo* RNA-seq assembly, yielding 230,554 unique transcripts with a N50 of 1,638 bp. Putative functions could be assigned to 70.15% of the transcripts based on BLAST searches against several public protein and transcription factor annotation databases. A total of 1475 differentially expressed genes (DEGs) were identified when comparing the two irrigation treatments, with 796 and 679 up regulated and down regulated, respectively, under water limiting conditions. Candidate secondary metabolite genes related to rubber synthesis, rubber particle associated genes, and genes related to drought stress response were experimentally validated for their expression using q-PCR analysis. Rubber and resin yield were quantified and plants subjected to drought conditions were found to produce more rubber. Yield results were used to study correlations of secondary metabolic pathway gene expression to rubber biosynthesis in guayule. In conclusion, we report the identification of a large set of guayule cDNA unigenes from stembark tissues, providing insights into the genetic and molecular basis of rubber production and response to drought stress in guayule.

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