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# Molecular Responses of *Senna tora* to Drought Stress: A Transcriptome Perspective

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Environmental stresses such as drought, intensified by climate change, severely affect plant growth and productivity, and understanding the molecular mechanisms of stress adaptation is a critical challenge in agriculture. *Senna tora* is a representative medicinal plant, and in this study, we investigated transcriptomic changes during drought stress and subsequent recovery to explore its adaptive mechanisms. Plants were subjected to a 7-day drought treatment followed by watering, and leaf and root samples collected at multiple time points were analyzed by RNA-seq. A total of 24,126 genes were differentially expressed and classified into nine expression clusters, including 10,693 genes in leaves and 13,433 genes in roots. Notably, genes associated with drought stress responses such as HSP, oleosin 1, and LEA showed pronounced upregulation. Further analyses, such as GO and KEGG pathway enrichment and transcription factor profiling, are expected to provide deeper insight into the molecular links between drought stress responses and secondary metabolism. This study will provide valuable insights into the stress adaption mechanisms of *S. tora* and contribute to broader understanding of medicinal plant responses to environmental stresses.