



Category: Plant Genomics

# Sequencing, De novo Assembly, Functional Annotation and Analysis of *Cardiospermum halicacabum* L. Leaf Transcriptome Using Illumina Platform

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## Abstract

*Cardiospermum halicacabum*, widely known as balloon plant is an affiliate of the family Sapindaceae. It has significant medicinal properties and is traditionally used in the treatment of numerous diseases including arthritis, edema, psoriasis, asthma, etc. In animal studies, it was found to be effective to treat Alzheimer's, Parkinson's, cancer and diabetes. The genomic resources for this plant are highly limited and which in turn limits its medicinal value and pharmacological usage. The present study is aimed to characterize the leaf transcriptome of *C. halicacabum* using high throughput sequencing and advanced genomic tools. To the best of our knowledge, this is the first report on the transcriptome of *C. halicacabum*. *De novo* transcriptome sequencing was performed using Illumina NextSeq 500 platform. We have identified 40,750 unigenes with an average length of 715 bp, among which 4581 are full-length genes. BLAST against Plant Non Redundant database provided annotation for 13525 genes. Kyoto Encyclopedia of Genes and Genomes database deduced 1228 enzymes with 9688 transcripts involved in 140 pathways. Gene Ontology analysis categorized 17422 unigenes under biological process, 17795 in cellular components and 27274 in molecular function. MISA tool has identified 2802 SSR motifs in this plant. There were 414 transcription factors belonging to 46 transcription factor families. We have ascertained that the flavonoids, steroids and carotenoids synthesized by this plant are responsible for their activity. The enzymes involved in the biosynthesis of these secondary metabolites were validated using Reverse transcription PCR. Our study paves the way to comprehend the medicinal properties of *C. halicacabum* making it easy for further study and in the development of new drugs.

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