

Sequencing and analysis of transcriptome in *Gleditsia sinensis*

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G*leditsia sinensis* Lam. is one of the alleged 50 fundamental herbs used in traditional Chinese medicine. *G. sinensis* has been used as a medicinal herb in China and Korea and have antitumor properties. The thorns of *G. sinensis* (Leguminosae) have been used in traditional medicine for the treatment of inflammatory diseases including swelling, suppuration, carbuncle and skin diseases. However, the basic biology on *Gleditsia sinensis* Lam. is relatively weak, especially the molecular mechanism of the formation of the thorns has not been reported, which seriously restricts the exploration of key gene resources, the metabolic mechanism of secondary metabolites and the genetic improvement of *G. sinensis*. With the increasing perfection and maturity of high-throughput sequencing technology and the cross-application of bioinformatics and molecular biology, high-throughput sequencing technology has become the

mainstream means of transcriptome sequencing and gene expression research. In this study, the shoots of a specific plant without thorns and the shoots and tender thorns of a normal tree were used as the experimental materials. The transcriptome sequencing of *G. sinensis* was done by high-throughput sequencing technology and the results were systematically analyzed for the biological information, laying a genetic foundation for digging out the genes related to the thorn formation of *G. sinensis*. Comparing all-Unigene with KOG database, 25 different functional annotations were obtained. All-unigene was further predicted and analyzed for transcription factors and CDS. The main transcription factors are MYB, bHLH and WRKY family which are closely related to secondary metabolism. Sixteen genes involved in regulating the formation of thorns were screened.

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