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PII: S0378-1119(17)30662-5
DOI: doi: 10.1016/j.gene.2017.08.013
Reference: GENE 42119

To appear in: *Gene*

Received date: 4 January 2017
Revised date: 8 July 2017
Accepted date: 23 August 2017

Please cite this article as: Feng Liu, Yu Wang, Zhaotang Ding, Lei Zhao, Jun Xiao, Linjun Wang, Shibo Ding , Transcriptomic analysis of flower development in tea (Camellia sinensis (L.)), *Gene* (2017), doi: 10.1016/j.gene.2017.08.013

Transcriptomic Analysis of Flower Development in Tea (*Camellia sinensis*(L.))

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Abstract

Flowering is a critical and complicated process in plant development, involving interactions of numerous endogenous and environmental factors, but little is known about the complex network regulating flower development in tea plants.

In this study, *de novo* transcriptome assembly and gene expression analysis using Illumina sequencing technology were performed. Transcriptomic analysis assembles gene-related information involved in reproductive growth of *C. sinensis*. Gene Ontology (GO) analysis of the annotated unigenes revealed that the majority of sequenced genes were associated with metabolic and cellular processes, cell and cell parts, catalytic activity and binding. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis indicated that metabolic pathways, biosynthesis of secondary metabolites, and plant hormone signal transduction were enriched among the DEGs. Furthermore, 207 flowering-associated unigenes were identified from our database. Some transcription factors, such as *WRKY*, *ERF*, *bHLH*, *MYB* and MADS-box showing up-regulated in floral transition, which might play the role of progression of flowering. Furthermore, 14 genes were selected for confirmation of expression levels using quantitative real-time PCR (qRT-PCR). The comprehensive transcriptomic analysis presents fundamental information on the genes and pathways which are involved in flower development in *C. sinensis*. And our data provided a useful database for further research of tea and other species plants.

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