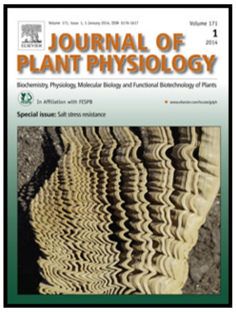

Title: Comparative transcriptome study of hairy and hairless tea plant (*Camellia sinensis*) shoots

Authors: Chuan Yue, Hong-Li Cao, Dan Chen, Hong-Zheng Lin, Zan Wang, Juan Hu, Guo-Yi Yang, Yu-Qiong Guo, Nai-Xing Ye, Xin-Yuan Hao

PII: S0176-1617(18)30407-3
DOI: https://doi.org/10.1016/j.jplph.2018.07.002
Reference: JPLPH 52807

To appear in:

Received date: 9-3-2018
Revised date: 14-7-2018
Accepted date: 14-7-2018

Please cite this article as: Yue C, Cao H-Li, Chen D, Lin H-Zheng, Wang Z, Hu J, Yang G-Yi, Guo Y-Qiong, Ye N-Xing, Hao X-Yuan, Comparative transcriptome study of hairy and hairless tea plant (*Camellia sinensis*) shoots, *Journal of Plant Physiology* (2018), https://doi.org/10.1016/j.jplph.2018.07.002

Comparative transcriptome study of hairy and hairless tea plant (*Camellia sinensis*) shoots

Chuan Yue[a, *], Hong-Li Cao[a], Dan Chen[a], Hong-Zheng Lin[a], Zan Wang[a], Juan Hu[a], Guo-Yi Yang[a], Yu-Qiong Guo[a], Nai-Xing Ye[a, *], Xin-Yuan Hao[b, *]

[a] College of Horticulture, Fujian Agriculture and Forestry University/Key Laboratory of Tea Science in Universities of Fujian Province, Fuzhou, China

[b] Tea Research Institute, Chinese Academy of Agricultural Sciences/National Center for Tea Improvement/Key Laboratory of Tea Plant Biology and Resources Utilization, Ministry of Agriculture, Hangzhou, China

* Corresponding author: E-mail: yccyyx@163.com (C. Yue); haoxy@tricaas.com (X.-Y. Hao); ynxtea@126.com (N.-X. Ye)

Abstract: Trichome (also referred to as ‘háo’ in tea) is a key feature in both tea products and tea plant (*Camellia sinensis*) selection breeding. Although trichomes are used as a model for studying cell differentiation and have been well studied in many plant species, the regulation of trichome formation at the molecular level is poorly understood in tea plants. In the present study, the hairy and hairless tea plant cultivars Fudingdabaicha (FDDB) and Rongchunzao (RCZ), respectively, were used to study this mechanism. We characterised tea plant trichomes as unicellular and unbranched structures. High-throughput Illumina sequencing yielded approximately 277.0 million high-quality clean reads from the FDDB and RCZ cultivars. After de novo assembly, 161,444 unigenes were generated, with an average length of 937 bp. Among these unigenes, 81,425 were annotated using public databases, and 55,201 coding sequences and 4,004 transcription factors (TFs) were identified. In total, 21,599 differentially expressed genes (DEGs) were identified between RCZ and FDDB, of which 10,785 DEGs were up-regulated and 10,814 DEGs were down-regulated. Genes involved in the DNA replication pathway were significantly enriched. Furthermore, between FDDB and RCZ, DEGs related to TFs, phytohormone signals, and cellulose synthesis were identified,