



cDNA-AFLP transcriptional profiling reveals genes expressed during flower development in *Oncidium* Milliongolds

X. Qian*, M.J. Gong*, C.X. Wang and M. Tian

Research Institution of Subtropical Forestry, Chinese Academy of Forestry,
Fuyang, Zhejiang Province, China

*These authors contributed equally to this study.

Corresponding author: M. Tian

E-mail: tmin115@163.com

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ABSTRACT. The flower developmental process, which is crucial to the whole lifecycle of higher plants, is influenced by both environmental and endogenous factors. The genus *Oncidium* is commercially important for cut flower and houseplant industry and is ideal for flower development studies. Using cDNA-amplified restriction fragment length polymorphism analysis, we profiled transcripts that are differentially expressed during flower development of *Oncidium* Milliongolds. A total of 15,960 transcript-derived fragments were generated, with 114 primer sets. Of these, 1248 were sequenced, producing 993 readable sequences. BLASTX/N analysis showed that 833 of the 993 transcripts showed homology to genes in the NCBI databases, exhibiting functions involved in various processes, such as signal transduction, energy conversion, metabolism, and gene expression regulation. The full-length mRNAs of *SUCROSE SYNTHASE 1 (SUS1)* and *LEAFY (LFY)* were cloned, and their expression patterns were characterized. The results showed that the expression levels of *SUS1* and *LFY* were similar during flower development. To confirm the function of *SUS1* in flower buds,

carbohydrate content and sucrose synthase activity were determined. The results showed that changes in sucrose content and sucrose synthase activity reflected *SUSI* expression levels. Collectively, these results indicate that *SUSI* influences flower development by regulating *LFY* expression levels through changing the sucrose content of flower buds.

Key words: Flower development; cDNA-AFLP; *Oncidium* orchid; Transcript-derived fragment; Semi-quantitative RT-PCR