

Metabolome and transcriptome analysis of terpene synthase genes and their putative role in floral aroma production in *Litchi chinensis*

Farhat Abbas¹, Shaoying Guo¹, Yiwei Zhou², Jing Wu¹, and Jiyuan Shen^{1*}, Hui-Cong Wang^{1*}

¹Key Laboratory of Biology and Genetic Improvement of Horticultural Crops - South China/Guangdong Litchi Engineering Research Center, College of Horticulture, South China Agricultural University, Guangzhou, China

²Guangdong Key Laboratory of Ornamental Plant Germplasm Innovation and Utilization, Environmental Horticulture Research Institute, Guangdong Academy of Agricultural Sciences, Guangzhou, China

*Corresponding email: jyshen@scau.edu.cn, wanghc1972@263.net

ABSTRACT

Volatile organic compounds (VOCs) are essential traits of flowers since they attract pollinators, aid in seed distribution, protect the plant from internal and external stimuli, and are involved in plant-plant and plant-environment interactions. Apart from their role in plants, VOCs are used in pharmaceuticals, fragrances, cosmetics, and flavourings. *Litchi chinensis* Sonn. is a popular fruit due to its enticing red appearance, exotic taste, and high nutritional qualities. Litchi flowers bloom as inflorescences primarily on the shoot terminals. There are three distinct flower types, two male and one female, all of which are produced on the same panicle and rely on insect pollination. Herein, we used a comprehensive metabolomic approach to examine the volatile profile of litchi fruit (green pericarp, yellow pericarp, and red pericarp) as well as male and female flowers (bud stage, half open and full bloom). From a quantitative examination of the volatiles in *L. chinensis*, a total of 19, 22, and 21 VOCs were discovered from female flowers, male flowers, and fruits, with the majority of them belonging to sesquiterpenes. Multivariate analysis revealed that the volatile profiles of fruits differ from those of male and female flowers. Three VOCs were unique to male flowers and ten to the fruit, while eight VOCs were shared by both male and female flowers and 11 by both male and female flowers and the fruit. Furthermore, for the first time, we identified and comprehensively studied the *TERPENE SYNTHASE* genes (*TPS*) using the litchi genome and transcriptome database, which revealed 38 *TPS* genes unevenly distributed across the 15

chromosomes. A phylogenetic study showed that *LcTPS* were grouped into TPS-b, TPS-c, TPS-e, TPS-f, and TPS-g subfamilies, with TPS-b having the most genes. The conserved motifs (RR_{x8}W, NSE/DTE, and DD_{xx}D) were studied in *LcTPSs*, and significant variation between subfamilies was discovered. Furthermore, after integrating the metabolome and transcriptome datasets, several VOCs were shown to be development-specific and highly linked with distinct *LcTPS* genes, making them promising biomarkers. Interestingly, *LcTPS17/20/23/24/31* were associated with monoterpene edges, while the rest were connected to sesquiterpene edges, indicating their probable participation in the aroma biosynthesis mechanism of certain compounds.

Keywords: *Litchi chinensis*, Terpenes, Volatile organic compounds, Metabolome, Terpene synthase