

# Integrated volatile metabolome, multi-flux full-length sequencing, and transcriptome analyses provide insights into the aroma formation of postharvest jasmine (*Jasminum sambac*) during flowering

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Postharvest Biology and Technology, Volume 183, January 2022, 111726

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## Abstract

Jasmine [*Jasminum sambac* (L.) Aiton] flowers usually bloom and release their fragrance at night. However, the underlying regulatory mechanisms of aroma formation during flowering in postharvest jasmine are still poorly understood. Here, we profiled the volatile metabolome, multi-flux full-length sequencing, and transcriptome analysis to investigate volatile biosynthesis and global transcriptomic changes in postharvest flowering jasmine. A total of 102 volatiles were identified. Of these, 16 volatiles were considered key odorants of jasmine flowers. Linalool,  $\alpha$ -farnesene, d-nerolidol, geraniol,  $\alpha$ -cadinol, benzyl alcohol, benzaldehyde, benzyl acetate, benzyl benzoate, 3-hexen-1-ol benzoate, and (*Z*)-3-hexen-1-ol acetate play decisive roles in the typical jasmine fragrance, while benzeneacetaldehyde, benzoic acid, methyl anthranilate, methyl 2-(methylamino) benzoate, and (*E*)-2-hexenal modify the aroma of jasmine. Meanwhile, we built the first reference full-length transcriptome of postharvest jasmine flowers, which had 366,081 non-redundant isoforms. Among them, 280,326 (76.57 %) were annotated with at least one hit in the NT, NR, Swissprot, KEGG, KOG, Pfam, and GO databases. Combined with second-generation transcriptome analysis, we identified 52 differentially expressed transcripts (DETs) involved in terpenoid metabolic pathways and 28 DETs involved in phenylpropanoid/benzenoid metabolic pathway, and 31  $\beta$ -glucosidase transcripts may be related to aroma formation of postharvest jasmine during flowering. In addition, the expression of 42 heat shock protein (HSP) transcripts was positively correlated with the content of 11 key odorants, as revealed by

weighted gene co-expression network analysis (WGCNA). The present results advance the knowledge of the regulatory mechanism of aroma formation in postharvest jasmine during flowering and provide an abundant genetic resource for further studies on gene discovery in jasmine.