

Volatile component quantification in combination with putative gene expression analysis reveal key players in aroma formation during fruit ripening in *Carica papaya* cv 'Hong fei'

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Abstract

The purpose of this research was to quantify volatile compound changes during papaya fruit ripening and to identify putative genes that are responsible for aroma synthesis. Volatile compounds at four different stages of fruit ripening were isolated from 'Hong fei' variety by solvent assisted flavor evaporation, then analyzed by gas chromatography-mass spectrometry. In total, 38 different volatile compounds were identified, including terpenes, esters, lactones, ketones, alcohols, aldehydes, volatile acids, S- and N- containing compounds, and volatile phenols. The contents of terpenes, esters, lactones, ketones, volatile acids, and volatile phenols showed general upward trends and reached a maximum at half yellow or full ripe stages, meanwhile most alcohols, aldehydes, S- and N-containing compounds showed downward trends with fruit ripening. The putative aroma biosynthesis genes were quantified by RT- qPCR, and the correlation analysis suggested that *CpLIS1* and *CpP450-2* could be responsible for linalool and linalool oxide biosynthesis, respectively; BITC biosynthesis could be regulated at post-transcriptional, post-translational or enzymatic levels, *CpAAT1* and *CpACX1* could catalyze the formation of some specific esters or lactones. This study offered important clues for further dissection of the molecular mechanisms underlining aroma synthesis in 'Hong fei' during fruit ripening.