

# Integrated metabolomic and transcriptomic analyses of quality components and associated molecular regulation mechanisms during passion fruit ripening

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## Abstract

Metabolite accumulation and related gene expression were analyzed to elucidate the passion fruit quality and color formation mechanisms during ripening in three stages of maturity: full-green, half-purple (RB), and mature. A total of 488 metabolite compounds were identified in the passion fruit by metabolomics (LC-MS/MS). The metabolite accumulation between fruit peel and pulp was significantly different. Flavonoids mainly increased in fruit peel during ripening and accumulated significantly at the mature stage. Integrated RNA-seq and metabolome analysis revealed that the key enzyme genes (CHI, CHS and F3'H) mainly regulate the synthesis of flavonoids, which are the main factors affecting peel color. In pulp, large amounts of lipids, organic acids, and phenolic acids were significantly reduced during passion fruit ripening. However, sugar alcohols accumulated significantly during ripening and were related to the taste and aroma of passion fruit. Most of the metabolites were significantly changed in the RB stage, suggesting that RB was the key period for passion fruit quality regulation. These results were also verified by qRT-PCR. Our results might be useful for elucidating the molecular mechanisms of coloration and quality formation in passion fruit.