Comparative Metabolomics Association between Fruit Ripening and Targeted Metabolites in Two Strawberry Cultivars

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Strawberry fruit ripening is highly linked with the alteration of numerous metabolites during ripening. The objective of this study was to elucidate the comparative targeted metabolomics association between fruit ripening and targeted metabolites in two different strawberry cultivars, ‘Seolhyang’ and ‘Jukhyang’. Fruit were harvested at green, pink, and red maturity stages and left at ambient temperature for 7 days for over-matured ripening stage. Fruit fresh weight and length were higher in ‘Jukhyang’ than in ‘Seolhyang’ at red and over-matured stages. Soluble solids content (SSC) and titratable acidity (TA) were higher in ‘Jukhyang’ than in ‘Seolhyang’. Fructose and glucose contents were higher in ‘Seolhyang’ than in ‘Jukhyang’ but sucrose was lower, regardless of fruit ripening stages. Levels of threonine, serine, glycine, alanine, valine, cysteine, methionine, isoctuline, leucine, β-alanine, proline, and histidine were higher in ‘Jukhyang’ than in ‘Seolhyang’ cultivar, irrespective of fruit ripening stages. Levels of ethyl acetate, acetic acid, ethyl 3-methyl-butanoate, ethyl 3-acetoxybutyrate, phenylmethyl acetate, octyl acetate, ethyl nicotinate, decyl acetate, benzenepropyl acetate, and octyl 3-methylbutanoate were higher in ‘Jukhyang’ than in ‘Seolhyang’ at over-mature stage. Overall, the results indicated that specific amino acids would be strongly linked with certain volatile organic compounds in ‘Jukhyang’ fruit than in ‘Seolhyang’ at over-mature stage.

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