Transcriptome analysis reveals the metabolisms of starch degradation and ethanol fermentation involved in alcoholic off-flavour development in kiwifruit during ambient storage

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Abstract

Kiwifruit tends to develop alcoholic off-flavour after long-term storage, leading to decreased fruit market value. Actinidia eriantha 'White' and Actinidia deliciosa 'Bruno' are two major cultivated kiwifruits in China. Compared to A. eriantha 'White', A. deliciosa 'Bruno' is prone to developing alcoholic off-flavour associated with ethanol accumulation during storage at ambient conditions without any stresses. In this study, to better understand the complex mechanisms responsible for developing alcoholic off-flavour in kiwifruit during postharvest, transcriptome analysis was used to compare the difference in metabolic pathways between kiwifruits 'white' and 'Bruno' during ripening at ambient storage. Our results indicated that the development of alcoholic offflavour in kiwifruit 'Bruno' might be associated with three metabolic pathways: the respiration and ethylene metabolisms, starch and sucrose metabolism and ethanol fermentation metabolism. In kiwifruit 'Bruno', the higher respiration rate and ethylene production might increase the energy conversion and internal carbon dioxide (CO_2) accumulation. Moreover, the higher expressions of starch phosphorylases (SPs), beta-amylases, UDP-glucose pyrophosphorylases (UGPases), sucrose synthases (SSs) and invertases (INVs) accelerated starch degradation along with soluble sugars accumulation in kiwifruit 'Bruno', which could provide adequate substrates for ethanol fermentation. In addition, the higher activity of ethanol fermentation metabolism associated with higher expressions of pyruvate kinases (PKs), NADP-dependent malic enzymes (NADP-MEs), pyruvate decarboxylases (PDCs) and alcohol dehydrogenases (ADHs) might directly increase the ethanol production.