Metabolic and transcriptional regulatory mechanism associated with postharvest fruit ripening and senescence in cherry tomatoes

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Postharvest Biology and Technology, Volume 168, October 2020, 111274

Abstract

Fruit senescence is an inevitable and negative developmental process during postharvest storage of cherry tomato. To characterize the physiological and molecular mechanisms underlying postharvest fruit ripening and senescence, gas chromatography-mass spectrometry (GC–MS) and RNA-Seq were employed to analyze the metabolic and transcriptomic profiles after 7, 14, 21, and 28 d of storage at different temperatures. Several metabolites, such as GABA, proline, fructose, glucose, mannose, and talose, were accumulated in response to senescence stress at ambient temperature (RT). We also observed an outstanding decrease in organic acids (OAs, e.g., citric acid, malic acid, butanedioic acid, *cis*-aconitic acid) under RT, resulting in fruit quality deterioration. The contents of OAs were maintained upon storage at low temperature. Integrated co-expression network analysis combining transcriptome and metabolite data revealed high correlations between OAs and genes involved in primary metabolic pathways (e.g., *PEPC3*, *IDH3*, *PDHA*, *MDH*, *PEPCK1*), plant hormones (especially ethylene and ABA) and transcription factors (e.g., MYB, AP2/ERF, WRKY, NAC). RNA-Seq data indicates ethylene and ABA biosynthesis and signaling genes, including *ACS2/4*, *ACO1/4/5*, *EBF*, *NCED*, *ABA8ox1*, *PYR1/PYL4*, may be key regulators in coordinating postharvest fruit senescence in cherry tomato. In summary, our findings reveal the degradation of OA is an indication of fruit senescence, mainly modulated by a network of ethylene, ABA and transcription factors.