

Title Gene expression associated with apple aroma biosyntheses
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Abstract

A microarray containing over 10,000 gene fragments was used to link changes in gene expression with changes in aroma biosynthesis in ripening apple (*Malus x domestica* Borkh). The microarray was probed with fluorescent-tagged cDNA derived from 'Jonagold' apple skin and cortex tissue representing eight distinct physiological stages spanning 70 days during ripening and senescence. The ripening stages, in chronological order, were 1. early preclimacteric, 2 . late preclimacteric and onset of trace ester biosynthesis, 3. onset of the autocatalytic ethylene and rapidly increasing ester biosynthesis, 4 . half-maximal ester biosynthesis and engagement of the respiratory climacteric, 5. Near maximal ester biosynthesis, peak in respiratory activity, and the onset of rapid tissue softening, 6 . maximal ester biosynthesis prior to its decline, the conclusion of the respiratory climacteric, and the completion of tissue softening, 7 . midpoint in the decline in ester biosynthesis and maximal ethylene biosynthesis, 8 . post climacteric minimum in ester production. Patterns in gene expression reflecting the rise and fall in ester formation were found in some putative genes for beta-oxidation (acyl-CoA oxidase, enoyl-CoA hydratase, and acetyl-CoA acetyl transferase), ester formation (aminotransferase, alcohol dehydrogenase, and alcohol acyl transferase), and fatty acid oxidation (lipoxygenase), but not fatty acid biosynthetic genes. A marked decline coinciding with the onset of ester production was detected in several putative genes for ADH.