

Title Identification of genes differentially expressed during development of Braeburn apple internal browning

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Abstract

An assessment of the genetic and physiological origins of Braeburn apple internal browning during storage was the focus of this research. The objective was to identify differences in cortex gene expression in tissues with and without initial symptoms of internal browning. Apples harvested at commercial maturity were held at 20 °C for 7 days, then stored at 0.5 °C in 1 kPa O₂, 3 kPa CO₂ and 95% rH to induce browning. Suppressive subtractive hybridization was used to generate two libraries. The first library was generated with RNA from healthy (tester) and lightly brown (driver) cortex tissues. For the second library, RNA lightly brown cortex (tester) and healthy (driver) cortex was used. For each library, 423 clones were screened and those with >15% difference between subtracted tester and driver were sequenced, ~100 clones for each library. The expression levels were verified using a virtual northern blot. Results indicate genes coding for proteins in a number of metabolic pathways are differentially expressed in tissues with and without internal browning symptoms.