

Title Identification of differentially expressed genes potentially associated with apple (*Malus ×Domestica*) superficial scald development

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Abstract

Apple superficial scald is a recurring postharvest physiological disorder with significant economic impact. Elucidating the molecular mechanisms of apple scald development is essential for prediction and prevention. In this study, differentially expressed genes were identified using suppressive subtraction hybridization (SSH) for two types of apple peel samples, i.e., between healthy tissues and tissues with initial scald symptoms. The most apparent up-regulated genes in tissue showing initial scald symptoms were those encoding proteins functioning in oxidative metabolism, including lipoxygenase, oxidoreductase, and polyphenol oxidase. This result is consistent with the hypothesis that development of apple scald is associated with an imbalance in oxidative metabolism. Several pathogenesis-related (PR) proteins encoding genes were also up-regulated, including apple allergens mal d 1/PR protein 10, apple allergens mal d 3/PR protein 14, PR protein 5 and PR-protein 8 in the tissues with initial scald symptoms. Other up-regulated genes included those encoding transporter proteins such as acyl carrier protein, peptide transporter and putative ABC transporter. Also induced were several proteins related to stress responses including heat shock protein, osmotin-like protein and early-response to dehydration protein. Up to 30% of the identified genes were annotated as “unknown function” and or “hypothetical proteins”.