

Comparative Transcriptome Profiling in a Segregating Peach Population with Contrasting Juiciness Phenotypes

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Cold storage of fruit is one of the methods most commonly employed to extend the postharvest lifespan of peaches (*Prunus persica* (L.) Batsch). However, fruit quality in this species is affected negatively by mealiness, a physiological disorder triggered by chilling injury after long periods of exposure to low temperatures during storage and manifested mainly as a lack of juiciness, which ultimately modifies the organoleptic properties of peach fruit. The aim of this study was to identify molecular components and metabolic processes underlying mealiness in susceptible and nonsusceptible segregants. Transcriptome and qRT-PCR profiling were applied to individuals with contrasting juiciness phenotypes in a segregating F₂ population. Our results suggest that mealiness is a multiscale phenomenon, because juicy and mealy fruit display distinctive reprogramming processes affecting translational machinery and lipid, sugar, and oxidative metabolism. The candida