Addressing fruit quality issues in *Prunus persica* varieties using a deep transcriptomic approach.

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Peach/nectarine varieties exhibit unique features that are the basis for distinctive traits involved in fruit quality. The repertoire of genes that each variety expresses at a given time, is a key issue in acquiring the characteristics that distinguish them. In order to get further insights in the molecular aspects that are important for fruit quality and postharvest life, we carried out a deep transcriptomic analysis of four *Prunus persica* varieties. Two early-season and two late-season varieties were analyzed for different traits such as firmness, color, solid soluble, acidity as well as their susceptibility to mealiness and response to postharvest treatments aimed to control the postharvest disorders. The late season varieties resulted to be more susceptible to chilling injury than the early season varieties. In addition, the comparison between the late-season varieties showed a differential response to treatments such as controlled atmosphere and conditioning. The transcriptomic analysis during ripening, cold storage and postharvest treatments using an Illumina-based RNA-Seq approach, showed clear differences in the repertoire of genes that are expressed among varieties during ripening, cold storage and postharvest treatments. The expressed genes were identified using the Prunus persica reference genome and those differentially expressed were mapped to metabolic networks. Our results indicate that there are set of genes that are differentially expressed in each of the condition analyzed. Their relationship to the traits analyzed in the present study will be discussed.