

**Title** Transcriptomic analyses and postharvest physiology of peaches and nectarines  
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### **Abstract**

A major challenge in modern horticultural science is to characterize the network of genes (and their products) controlling development and modulating quality before and after harvest. In this context, microarray technology is a powerful technique in measuring the level of expression of thousands of genes in a single experiment and is now increase used also for elucidating and studying gene regulation in relation to specific fruit developmental stages (e.g. ripening) and following different postharvest environment conditions, practices and treatments aimed to prolong storage- and taste-life. For peaches and nectarines, specific studies have been performed using  $\mu$ PEACH1.0 (4,806 probes corresponding to the same number of genes expressed in fruit tissues) to elucidate to role of ethylene also through the use of its inhibitor 1-MCP on the physiology of this climacteric species. Analyses have been performed on both melting flesh varieties and ripening mutants such as Stony hard and a slow-ripening phenotype. The results clearly pointed out that the presence of 1-MCP markedly changes transcript profile considering that only 9 genes (instead of 90, in control samples) showed, in comparison to fruit at harvest, significant changes at the end of the 24-hour incubation period, and 102 targets were differently affected when comparing fruit maintained for 24 hours in air and in 1-MCP-enriched atmosphere. A number of these differently expressed targets correspond to genes with a role in hormone (ethylene, but also auxin and ABA) metabolism and regulating transcription. The fast recovery of ripening parameters (softening, in particular) observed 48 hours after the end of the incubation period is the result of a change in the expression of about 50% of the 102 targets, including genes involved in ethylene perception (ETR2) and transcription regulation (EIL1-like). The comparative transcriptiomic approach performed on three *P. persica* genotypes showing altered ripening-associated processes (including ethylene biosynthesis and/or perception) and treated after harvest with exogenous ethylene, allowed to better characterize specific physiological aspects and identify possible key genes involved in the ethylene-mediated response in ripening peaches.