

Title Use of genomics tools to study peach fruit postharvest physiology
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Abstract

Peach and nectarine fruit ripen and deteriorate quickly and even at refrigerated temperature their storage life rarely exceeds 4-5 weeks making these fruit types interesting to study in terms of ripening and postharvest physiology. In this context, biochemical and one-to-one-at-a-time gene expression studies are now paralleled by large-scale analyses and genomics approaches using high throughput tools as the first peach microarray (μ PEACH1.0) developed by the Italian Consortium for Genomics Studies in Prunus (ESTree Consortium). μ PEACH1.0 has been used to study the transition from pre-climacteric to climacteric stage and to better characterize the role of ethylene in this fruit species. New genes and basic mechanisms involved in ethylene perception, and in the definition and evolution of quality traits as colour and flesh firmness have been identified. Differently from other fruit species (e.g., apple), 1-methylcyclopropene (1-MCP) has only a limited effect in delaying peach fruit ripening: in order to elucidate the mechanisms responsible for this behaviour, transcriptome analyses have been performed and genes showing differential hybridisations have been grouped according to their expression pattern following 1-MCP treatment. The comparison of transcript profiles in peaches at the transition from immature to mature stage, and following treatment with 1-MCP or exogenous ethylene allowed to identify gene ripening- and/or ethylene-regulated in this fruit species and comparatively assess the influence of ethylene on specific metabolic pathways.