

Title Genomics approaches and tools to study fruit ripening and postharvest quality evolution
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Abstract

The evolution of one-gene-at-a-time approach is represented by genomics studies and tools that are becoming routinely used in many labs aimed at elucidating mechanisms controlling and regulating fruit development. This new approach is based on high-throughput techniques, such as microarrays, that allow a comprehensive transcriptome analysis aimed to identify and dissect the complex genetic networks that underlie processes critical to fruit physiology as fruit ripening. In the model species, tomato, microarrays have been used to better define the role of ethylene in modulating transcriptome profile changes at ripening and further identify ethylene-dependent and ethylene independent genes. In other fruit types such as peaches, specific microarrays analyses have been performed (using the μ PEACH1.0) to study the transition from pre-climacteric to climacteric stage and 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 and described. Large scale analyses have been performed in order to elucidate, at molecular level, mechanisms involved in the responses of peaches to 1-MCP, the antagonist of ethylene that appears to have only limited effects in delaying ripening and prolonging shelf life in peaches and other stone fruits. Genes showing differential hybridizations have been grouped according to their expression pattern following 1-MCP treatment, and specific genes have been identified as potential responsible for the quick recovery of the ripening process during the post-treatment phase. Comparative transcriptome analyses among *Drupoideae* species are also being performed thus providing useful information about shared or specific mechanisms regulating ripening in botanically similar (drupes) but physiologically different (climacteric and non-climacteric) fruits.