

Title Genomic tools for a better understanding of the fruit ripening process
Author Claudio Bonghi and Livio Trainotti
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Abstract

Purpose of the review: Increased understanding of fruit ripening is feasible with high-throughput methodologies for comprehensive transcriptome analyses. This article reviews main results gained by transcript profiling methods in the identification of genes involved in the regulation of fleshy-fruit ripening, and outlines potential applications of genomic tools developed in model species and already available in some important fruit crops.

Main findings: Global transcript profiling methods allowed the association of newly identified genes, such as some transcription factors, with the ripening syndrome. Furthermore, they helped in the functional characterisation of genes important for quality traits, such as aroma evolution and pigmentation. Comparative genomics carried out by digital analysis of expressed sequence tag repertoires and microarray analyses indicated that groups of genes responsible for regulatory mechanisms are shared between climacteric and non-climacteric fruits.

Direction for the future research: Gene sequences are important for fruit characteristics and can be useful in marker-assisted selection of new varieties. Further information on regulation of fruit ripening requires an extensive analysis of the proteome. Comparative proteomics is an efficient strategy that could be used to achieve this goal. The identification of differentially-expressed protein is becoming easier as a result of the rapid growth of plant DNA databases that allow association of a protein sequence with its cognate gene.