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Sommario/riassunto	<p>Fleshy Fruits are a late acquisition of plant evolution. In addition of protecting the seeds, these specialized organs unique to plants were developed to promote seed dispersal via the contribution of frugivorous animals. Fruit development and ripening is a complex process and understanding the underlying genetic and molecular program is a very active field of research. Part of the ripening process is directed to build up quality traits such as color, texture and aroma that make the fruit attractive and palatable. As fruit consumers, humans have developed a time long interaction with fruits which contributed to make the fruit ripening attributes conform our needs and preferences. This issue of Frontiers in Plant Science is intended to cover the most recent advances in our understanding of different aspects of fleshy fruit biology, including the genetic, molecular and metabolic mechanisms associated to each of the fruit quality traits. It is also of prime importance to consider the effects of environmental cues, cultural practices and postharvest methods, and to decipher the mechanism by which they impact fruit quality traits. Most of our knowledge of fleshy fruit development, ripening and quality traits comes from work done in a reduced number of species that are not only of economic importance but can also benefit from a number of genetic and genomic tools available to their specific research communities. For instance, working with tomato and grape offers several advantages since the genome sequences of these two fleshy</p>

fruit species have been deciphered and a wide range of biological and genetic resources have been developed. Ripening mutants are available for tomato which constitutes the main model system for fruit functional genomics. In addition, tomato is used as a reference species for climacteric fruit which ripening is controlled by the phytohormone ethylene. Likewise, grape is a reference species for non-climacteric fruit even though no single master switches controlling ripening initiation have been uncovered yet. In the last period, the genome sequence of an increased number of fruit crop species became available which creates a suitable situation for research communities around crops to get organized and information to be shared through public repositories. On the other hand, the availability of genome-wide expression profiling technologies has enabled an easier study of global transcriptional changes in fruit species where the sequenced genome is not yet available. In this issue authors will present recent progress including original data as well as authoritative reviews on our understanding of fleshy fruit biology focusing on tomato and grape as model species.
