High or low fructose? Consequences for sugar metabolism in peach fruit

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Fruit taste is largely affected by the content of sugars and acids. Fructose is the sweetest tasting sugar. In commercial peach fruit, sucrose is the main sugar, followed by fructose and glucose which have similar levels. Interestingly low fructose accessions have been described in wild peaches. Two hypotheses can explain this fructose deficiency: reduced synthesis or increased degradation. Through an extensive profiling of metabolites and enzymatic activities, this study aims at i) describing sugar metabolism in peach fruit at different developmental stages and ii) comparing two genotypes with contrasted fructose/glucose ratios. We have measured 12 metabolites and 12 enzyme activities during fruit growth, for two genotypes over two years. Genotypic and year effects were observed for some metabolites, whereas the enzyme activities were stable between genotypes and years. More specifically, we did not detect any difference in the activities of the enzymes responsible for s ynthesis or degradation of fructose. Finally, our results show a highly regulated system in which a major perturbation in a central compound has only slight repercussions on sugar metabolism. Further explanations for the low fructose phenotype are discussed, such as different substrate affinities between iso-enzymes, limited fructose storage resulting in higher degradation or a differential consumption of the two hexoses for respiration, cell wall or synthesis of other carbon compounds.

Candidate gene functional profiling during fruit development and ripening in apple

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The physiological process of fruit development and ripening is the result of a functional gene interplay governing the formation of the features characterizing the fruit quality properties. Among the several physiological processes, the modifications occurring in the cell wall are the most relevant and important, for their impact in the maintenance of the general fruit quality as well as the management of the postharvest storage. Beside

the specific gene activation over the fruit cycle, also the particular genetic constitution can play important controlling roles.
To investigate the functional machinery involved in the control of fruit texture and ethylene production during fruit ripening, two different cultivars, such as Golden Delicious and Granny Smith, were selected and a specific set of samples were collected, processed and hybridized over an ad hoc designed custom microarray platform. The specific regulation of approximately 3800 genes involved in fruit ripening and regulatory process, together with their relative anchoring on a set of QTL intervals, will allow the simultaneous analysis of the genes differentially regulated among the different samples and their putative genetic control on these fruit quality traits. This study can thus represent a step forwards into the comprehension of the several mechanisms underlying the apple fruit quality, offering new opportunity for supporting the constitution of the most favourable apple ideotypes.

Identification of a cell number regulator (CNR) gene family in *Prunus*

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In natural and breeding cross populations fruit size varies continuously, behaving as a typical quantitative trait with multiple loci incrementally contributing to and largely influenced by environmental conditions. However, in some cases, a high proportion of the phenotypic variation can be explained by a few quantitative trait loci (QTL), corresponding to genomic regions that likely contain one or more major genes with a significant effect on fruit size. A gene known to regulate fruit size, tomato fw2.2, and two of its maize homologs, named CNR (Cell Number Regulators), have been shown to exert their effect on organs size by modulating cell number. In the present study, the CNR gene family in the recently released peach (Prunus persica) genome was characterized. A total of 23 CNR gene sequences, spanning the eight Prunus chromosomes were identified and their sequences were compared to the 13 CNR gene family members identified in maize. Moreover, two of the Prunus CNRs l ocate in close proximity of two known cherry (P. avium) fruit size QTLs, one of which has been shown to be associated with differences in mesocarp cell number. Even though the functional characterization of CNR genes in Prunus is still at the beginning, they provide a set of candidate genes of great interest for understanding the genetic bases underlying important traits related to plant and organ (e.g. fruit) size.

QTLs for brown spot resistance in European pear

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