

similar crop load were used to assess physicochemical and sensorial parameters of fruits on both production systems. ORG produced 'Santana', 'Liberty' and 'Golden Delicious' had on the average smaller fruits and more soluble solids (with exception of 'Topaz') and higher flesh firmness (equal in case of 'Golden Delicious'). Higher total phenol content in ORG fruits was found on the average in all investigated cultivars, however only in case of 'Golden Delicious' the difference was statistically significant. The change of phenol content in 'Golden Delicious' might be related to either its higher synthesis or to changes in fruit size. In order to elucidate which classes of phenols were affected by the production management, both ORG and IP cultivars were further analyzed by targeted metabolomics method for multiple classes of phenolics. In conclusion, the sensorial evaluation indicated significant better overall flavor and more acceptable overall appearance of IP produced apples.

AGER Project on Apple Advanced Research. Apple fruit quality in the post-genomic era, from breeding new genotypes to post-harvest: nutrition and health

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International competition and the pressing request of the consumers oblige Italian fruticulture to be at the forefront of innovation. Thanks to the most recent advances on apple "omics" approaches, a wealth of in-field experience, interaction with nutritionists and experts of human health, modern tools for apple orchard management and fruit conservation, six Italian institutions joined in 2010 to implement Italian apple cultivation: A) By developing fundamental technological genetic/genomics tools for apple breeding and technologies and tools for non-invasive fruit quality assessment; B) by elucidating the main structure of the apple fruit metabolome and its relationship with standard fruit quality parameters to improve the knowledge about the molecular bases of fruit quality with emphasis on nutritional and health-related properties. C) By applying the above powerful molecular genetics tools and knowledge to molecular breeding and to the production chain in order to 1) improve apple resistance to pathogens, 2) enhance fruit quality (mainly in terms of nutritional aspects), 3) reduce environmental impacts and increase sustainability, and 4) optimize the production chain.

This proposal has therefore set the following specific objectives:

1. Production of genomic, transcriptomic and metabolomic tools and knowledge to lay the foundation of efficient marker-assisted breeding for varietal innovation and better comprehension, in molecular terms, of the key quality traits of apple fruit.
2. Creation of genetic lines and selections aimed to improve fruit quality and disease resistance.
3. Improvement of the key steps of the pre-harvest production phase, achieved by means of the following actions:
 - Development of new thinning strategies based on environment-friendly chemicals and mechanical methods.
 - Development of new self-thinning cultivars.
 - Water management improvement to control fruit quality.
 - Real time management of crop load.
 - Innovative measuring tools for monitoring the onset and evolution of fruit ripening.
4. Optimization of the production chain, its traceability, and fruit quality assessment, pursued by:
 - New methods to enhance fruit homogeneity.
 - Advanced traceability system.
 - Comparison between instrumental and sensorial fruit quality assessment.
5. Characterization of the key nutraceutical profile and allergenic properties of apple fruit by: A) Identification of bioactive molecules and analysis of their roles as modulators of risk factors for dismetabolic diseases and their anti-neoplastic activity; B) Identification of the master determinants of apple allergenicity and search for hypoallergenic apple cultivars.

The genome sequence of peach, a key diploid tree species, reveals unique patterns of genetic diversity, domestication and genome evolution.

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The plant family Rosaceae is the most important fruit producing clade and its key commercially relevant genera (*Fragaria*, *Rosa*, *Rubus*, *Prunus*) display a broad diversity in growth habit and fruit type as well as compact diploid genomes. Peach [*Prunus persica* (L.) Batsch], a key diploid species, is one of the best genetically characterized deciduous trees. We report the high quality genome sequence of peach obtained from a completely homozygous genotype. A complete chromosome-scale assembly was obtained by Sanger whole genome shotgun methods. We predicted 27,852 protein-coding genes as well as non-coding RNAs. Analyses about the expansion in the peach lineage of gene families related to sorbitol metabolism and to phenylpropanoid network individuated cornerstone features in the evolution of the Spiraeoideae subfamily and a *Prunus*-specific mode of genome evolution likely associated with unique production of the lignified stone in these species. We investigated the path of peach domestication through whole genome resequencing of 14 *Prunus* accessions. The analyses suggest major genetic bottlenecks that have significantly shaped the peach genome diversity.