

Genetic dissection of peach fruit quality traits

R. Pirona⁽¹⁾, Pacheco I.⁽²⁾, Chietera G.⁽³⁾, Eduardo I.⁽⁴⁾, Da Silva C.⁽²⁾, Troglio M.⁽⁵⁾, Banchi E.⁽⁵⁾, Dondini L.⁽⁶⁾, Tartarini S.⁽⁶⁾, Pozzi C.⁽⁵⁾, Vecchiotti A.⁽⁷⁾, Rossini L.^(1,2)

⁽¹⁾Parco Tecnologico Padano, Lodi, Italy

⁽²⁾Department of Agricultural and Environmental Sciences - Production, Landscape, Agroenergy, University of Milan, Milan, Italy

⁽³⁾INRA, Versailles, France

⁽⁴⁾IRTA, Center for Research in Agricultural Genomics CSIC-IRTA-UAB-UB, Barcelona, Spain.

⁽⁵⁾Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, Italy.

⁽⁶⁾DCA, Department of Fruit Tree and Woody Plant Science, University of Bologna, Bologna, Italy

⁽⁷⁾Monsanto Vegetable Seeds Division, Bergschenhoek, The Netherlands

Genetics and genomics approaches are integrated to dissect key quality and agronomic traits in peach, such as fruit weight, composition of Volatile Organic Compounds (VOCs), resistance to pathogens and maturity date (MD). 213 peach accessions and five biparental populations were genotyped with advanced SNP platforms such as the 9K Illumina peach SNP array providing an ideal basis for GWAS and QTL analyses.

Here, we report results from QTL analyses of VOCs in an F1 cross between two peach cultivars differing in their aroma profiles, Bolero and OroA. Based on gas chromatography-mass spectrometry (GC-MS) analysis of fruit essential oil, 43 QTLs were uncovered for 23 different VOCs and candidate genes were identified for two major QTLs. In parallel, to gain insight into gene expression differences that might be associated with the aroma profiles of Bolero and OroA, a novel microarray (uPEACH2.0) was specifically designed: transcriptomic comparisons at three developmental stages allowed the identification of 12 genes putatively involved in VOC biosynthesis. Due to the strong impact of MD on a number of fruit quality traits, we also report progress on QTL analysis in three different populations segregating for MD: in addition to the Bolero x OroA cross, F2 populations derived from Contender x Ambra and NJ Weeping x Bounty were used to map QTLs providing a robust framework for genetic analysis of MD. Analysis of genetic variations in some CG will be discussed.