

**ABSTRACT**

The improvement of fruit quality is probably the main challenge facing the peach industry nowadays. The volatile organic compounds (VOCs) are a heterogeneous group of substances that are intimately related to peach quality since they entirely define its aroma and in combination with others compounds like sugars and organic acids shape fruit flavor. Among peach VOCs, the lactone-type compounds are those conferring the characteristic peach notes for both aroma and flavor, while others compounds such as esters and terpenoids contributes in a lesser extent by adding specific notes often described as “fruity” and “floral”. Another group of compounds consisting of aldehydes and alcohols, known generically as lipid-derived volatiles, should have a less desirable impact on the flavor of the fruit since they seem to provide notes associated with immature fruit.

Describing in detail the components of this complex group of compounds as well as establishing the genetic and molecular bases that control their synthesis is a prerequisite before undertaking any peach breeding project aimed to increase peach quality with more chances of success.

In the current thesis, the study of the volatile compounds production was addressed holistically by means of a series of "omics" complementary technologies: metabolomics, transcriptomics and genomics.

Initially a high-throughput metabolomics platform for identification and quantification of the VOCs from the fruit was established. Besides the screening of a large proportion of the VOCs from the fruit, this platform enabled, the definition of groups of compounds that share a common regulation.

By a combination of a series of analyzes based on data correlation it was found that the synthesis of volatiles with positive impact in aroma (such as lactones and certain esters) occurs in a coordinated manner. The same happens with negative impact compounds (lipid derived compounds) and other compounds

with less impact (e.g. terpenoids and phenolics). All this suggesting that the peach volatilome is organized into a series of interconnected modules.

The discovery of this regulatory network underlying volatile synthesis was then exploited to propose a number of candidate genes by a functional genomics approach. The gene expression levels were analyzed by microarrays and the volatile contents were profiled in parallel along maturation time course series in the two parental genotypes of our breeding population.

The combined analysis of the co-regulation patterns allowed the identification of different genes whose expression was highly correlated with the levels of lactones, esters, terpenoids, phenolic compounds and lipid derivatives among others, which were proposed as possible candidate genes involved in the synthesis of these aromas.

One of the candidate genes, identified as being associated with the accumulation of lactones and esters, was cloned and by functional analysis showed to be an oleate  $\omega$ -6 desaturase involved in the generation of linoleic acid, a potential precursor peach aromas.

Complementarily, the genetic control of the production of volatile was described by a broad scale QTL analysis. An F1 peach population segregating for fruit aroma was analyzed combining the metabolomics platform developed previously and a high-throughput genotyping platform based on SNPs markers detection. The high organization of the volatiloma in co-regulated modules was reflected in the identification of loci controlling several members belonging to different groups of co-regulation. In this way, three loci that control the synthesis of lactones and some esters were identified in linkage groups 4, 5 and 6 (LG4, LG5 and LG6). Similarly, it was found that the synthesis of monoterpenes is controlled by a single locus located in the upper end of LG4.

The results obtained indicate the presence of important regions in peach genome affecting fruit volatile production and suggest that it should be possible to improve the flavor of the fruits by molecular marker-assisted breeding.

The integration of the results along with the interpretation in light of the existing knowledge allowed the description of the peach volatilome, its regulatory network and the identification of genomic regions controlling their synthesis as well as propose candidate genes involved in the synthesis of the major peach aromas, which could be also used as targets for classical and biotech breeding for flavor and aroma in peach.