In this case study we performed a phylogenetic analysis of peach laccases and characterized specific peach miRs (miR397a and miR408), reported previously as post-transcriptional regulatory elemen ts of laccase genes. Using a bioinformatic approach we identified unique TFBS for abscisic acid (ABA) response elements in promoter regions of both miR and laccase genes. The signaling molecule ABA plays a major role in plant responses to stress. We propose a feed-forward loop motif in the stress response network involving ABA action in peach by integrating the TF-mediated regulation of miR and laccase genes at the transcriptional level with the miR regulation of laccase target genes at the post-transcriptional level.

Genetic dissection of fruit aroma in apple

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The quality of a fruit is represented by a specific set of primary and secondary metabolites which make the fruit edible and desirable. The aromatic "bouqet", in particular, contributes to the final appreciation by consumers, being the last factor non-destructively perceived after appearance. The aroma in apple is controlled by a series of important physiological pathways leading to the formation of key compounds, such as terpenes, alcohols, aldehydes and esters, the latter one the most abundant in the apple aroma.

In order to genetically dissect such complex control, two full sib progenies and two analytical technologies have been employed in this investigation. As phenomics technology for aroma profiling a novel PTR-ToF-MS was employed, in order to fingerprint the VOCs production of the Fuji x Delearly progeny after a postharvest storage. The QTL profile was further compared with the one already available for the C3 population (Discovery x Prima), for which a dataset of volatiles assessed by HS-SPME-GC equipment was already available. The alignment of the two maps allowed the detection of a common set of QTLs, highlighting those positioned on LG2 and co-located with an AAT gene cluster, known to be involved in acetate ester production in apple. Association mapping based on the AAT candidate genes allowed the characterization of a set of markers specifically associated with the ester accumulation in ripe fruit. The results presented here discuss about the utility of these new markers as a valid tool for a molecular breeding towards the creation of new high-quality aromatic apple varieties.