

(5)Facultad de Ciencias Agronómicas, Departamento de Producción Agrícola, Laboratorio de Genómica Funcional & Bioinformática, Universidad de Chile, Santiago, Chile

Chile is the main exporter of Japanese plum fresh fruit in the world. One of the key issues for the industry is the post harvest conditions of the fruits that allow reaching the market with a good quality product. The fruits are highly perishable and suffer physiological disorders associated to the long time storage under low temperature. One of these disorders is the Internal Breakdown (ID). Toward the identification of genes differentially expressed related to ID in plum fruit, a subtractive suppressive hybridization (SSH) methodology was employed. Two libraries were generated from transcripts obtained from different storage treatments. A set of 387 genes were isolated, sequenced and characterized. BLASTN algorithm and public databases (NCBI and TIGR) were used to determine similarity scores between the cDNA clones and known sequences. Functional categorization was manually determined using the FunCat catalogue from the Munich Information Center for Protein Sequences (MIPS) . Approximately 90% of the partial cDNAs showed significant similarity to proteins registered in databases and 10% presented problems with the sequence therefore were not considered for the analysis. Proteins related to protein fate (folding, modification, destination) were identified when a treatment of two days at 20 °C and storage at 0 °C for 42 days (fruit library T2) was used. Moreover, genes that codify by proteins related to cellular transport, cell-wall-related proteins and transcription factors were identified after a treatment of two days at 10 °C and storage at 0 °C for 42 days (fruit library T4). Four genes were analyzed by qRT-PCR.

This work was supported by fellowship Conicyt 2109018, Tesis de Postgrado en la Industria 78111112, project Fondecyt 11080192 and Consocio Tecnológico de la Fruta SA.

### **Bioinformatic identification of a putative microRNA-transcription factor network motif in the regulation of laccase genes in peach (*Prunus persica*)**

*A.M. Cattaneo*<sup>(1)</sup>, Grzeskowiak L.S.<sup>(1)</sup>, Colaiacovo M.<sup>(2)</sup>, Faccioli P.<sup>(2)</sup>

<sup>(1)</sup>Research and Innovation Centre - Fondazione Edmund Mach, San Michele all'Adige (TN), Italy

<sup>(2)</sup>CRA - Genomics Research Centre, Fiorenzuola d'Arda (PC), Italy

Laccase proteins are multicopper glycoprotein oxidases expressed in plant tissues under biotic and abiotic stress conditions. They are able to catalyze oxidation of a broad range of substrates including phenols and amines. The regulation of expression of such genes is crucial for proper reaction to stress. At the DNA level, this modulation is mediated by the recruitment of specific transcription factors (TF) to suitable transcription factor binding sites (TFBS), usually located upstream of a gene. At the RNA level, the short microRNAs molecules (miRs) interfere with the translation of target proteins through base-pairing with messenger RNAs. Complex regulatory circuits combining those interactions fine-tune protein expression and enhance plant responses to environmental change.

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 elements 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**

*E. Costa*<sup>(1)</sup>, Dunemann F.<sup>(2)</sup>, Cappellin L.<sup>(1)</sup>, Longhi S.<sup>(1)</sup>, Ulrich D.<sup>(2)</sup>, Soukoulis C.<sup>(1)</sup>, Velasco R.<sup>(1)</sup>, Gasperi F.<sup>(1)</sup>, Biasioli F.<sup>(1)</sup>

<sup>(1)</sup>Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige (Trento), Italy

<sup>(2)</sup>Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Quedlinburg, Germany

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 “bouquet”, 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 Delecta 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.