metabolism of imported sugars in sink cells. Phloem unloading has been studied in various fleshy fruits, but the relationships between growth and sugar metabolism have attracted several studies both in edible and in non-edible organs because, besides their relevance in plant growth and fruit quality, sugars act as essential signaling molecules.
Aim of this study is to elucidate the roles that the three sucrose transporters (named PpSUT1, PpSUT2, PpSUT4 in accordance with Arabidopsis classification), identified in peach genome, play in sucrose partitioning in fruits. Experiments carried out by a phloem mobile symplastic tracer (CFDA) showed the absence of connection between vascular bundles and parenchyma cells in peach mesocarp, in the early and middle phases of fruit development, highlighting the requirement of an active transport driven by specific carriers present in the plasma membrane of phloematic system and parenchyma cells. Consistently with these results, data obtained by real-time PCR allowed to outline the expression pattern of different transporter isoforms in flesh tissues. In detail, transcripts related to PpSUT4 gene exhibited the highest levels in all mesocarp samples collected throughout development (from 57 to 110 days after full bloom, DAFB). In contrast, PpSUT2 and PpSUT1 expression appeared bare ly detected and almost absent, respectively, in samples assayed.
Afterwards, more exhaustive information was obtained taking advantage of Laser Capture Microdissection (LCM) technique, allowing single cell types isolation and then gene expression analysis in selected tissues. This effective approach led to discover that both in the early (57 DAFB) and in the middle-late (92 DAFB) phases of fruit development PpSUT4 was expressed mainly in parenchyma cells, whereas PpSUT2, characterized by low transcript levels when analysis were carried out on the whole fruit, showed high expression levels, limited to vascular bundles. Taken together data provide evidence for a role of PpSUT2 in active phloem unloading and sucrose accumulation in peach fruit.

Identification and characterization of early pathway genes of ellagitannin biosynthesis in strawberry (*Fragaria vesca*)

A. Feller[(1)], Martens S.[(1)]

[(1)]Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 San Michele all'Adige (TN), Italy

Ellagitannins are polyphenolic antioxidants found in certain fruits, trees, tea and medicinal plants. In many fruits, such as strawberries, raspberries, blackberries or pomegranate, ellagitannins, besides anthocyanins, are the most abundant antioxidants. The high amount of antioxidants present in these fruits have been associated with a reduced risk of cardiovascular disease, Diabetes mellitus (type 2) or cancer and these properties, together with the pleasant taste, have made berries one of the favorite fruits on the fresh food market but also as source for nutraceuticals or functional foods.
Due to the previously described bioactivities associated with ellagitannins, studies at the molecular level and identification of genes involved in this biosynthetic pathway are mandatory for further engineering strategies in planta to modulate the amount of metabolites (transgenic strawberry; breeding programmes). We show here the

identification and characterization of four putati ve shikimate dehydrogenase (SDH) encoding genes from strawberry. SDH has recently been shown to convert 3-dehydroshikimate (3-DHS) to gallic acid (GA), the first intermediate in the ellagitannin biosynthetic pathway. Until this finding, SDH was mainly known to catalyze the reversible reduction of 3-DHS to shikimic acid (SA), an essential intermediate for the production of aromatic amino acids. In higher plants the shikimate pathway is present in plastids but has been proposed to exist as a second pathway in the cytoplasm. Both tobacco (N. tabacum) and tomato (L. esculentum) have two SDH encoding genes, one localizes to the chloroplast, where it participates in the production of aromatic amino acid for protein synthesis, and one is localized in the cytoplasm, possibly involved in synthesis of natural products. However, the function of this cytoplasmic SDH is still not completely clear. We propose here that the cytoplasmic SDH is involved in GA formation in strawberry (F. vesc a) and that it catalyzes the first step in the ellagitannin biosynthetic pathway.

Mapping quantitative trait loci for nut quality in almond

A. Fernández i Martí[1], Font i Forcada C.[2], Socias i Company R.[3]

[1]Plant breeding & molecular biology Laboratory. Parque Cientifico Aula dei (PCTAD) Zaragoza Spain
[2]Unidad de Pomología, EEAD-CSIC, Zaragoza, Spain
[3]Unidad de Fruticultura, Centro de Investigación y Tecnología Agroalimentaria de Aragón (CITA), Zaragoza, Spain

Almond breeding is increasingly taking into account kernel quality as a breeding objective. Information on the parameters to be considered in evaluating almond quality, such as protein and oil content, as well as oleic acid and tocopherol concentration, has been recently compiled. The genetic control of these traits has not yet been studied in almond, although this information would improve the efficiency of the almond breeding programs. A map with 56 simple sequence repeat or microsatellite (SSR) markers was constructed for an almond population showing a wide range of variability for the chemical components of the almond kernel. A total of 12 putative quantitative trait loci (QTL) controlling these chemical traits have been detected in this analysis, corresponding to seven genomic regions of the eight almond linkage groups (LG). Some QTLs were clustered in the same region or shared the same molecular markers, according to the correlations already found between the chemic al traits. The logarithm of the odds (LOD) values for any given trait ranged from 2.12 to 4.87, explaining from 11.0 to 33.1% of the phenotypic variance of the trait. The results produced in the study offer the opportunity to include the new genetic information in the almond breeding programs. Increases in the positive traits of kernel quality may be looked for simultaneously whenever they are genetically independent, even if they are negatively correlated. We have provided the first genetic framework for the chemical components of the almond kernel, with twelve QTLs in agreement with the large number of genes controlling their metabolism.