



ISHS INTERNATIONAL SYMPOSIUM

INNOHORT

Innovation in
Integrated & Organic
Horticulture

Avignon, France

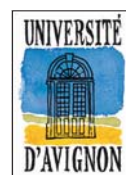
2015

June 8 - 12

PROGRAM
AND ABSTRACT BOOK



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TOPIC 1

The biological dimensions of production (quantity and quality, nutritional and organoleptic): new knowledge to mobilize, from gene to the fresh product

Coordinators: Nadia Bertin & Marc Lateur

Understanding biological processes is an asset in mastering fruit production. This session will address issues such as: desired traits for material adapted to ecologically-based horticultural systems; specifications for cultivars and their interactions with rootstocks and training systems; adaptations (e.g. polygenic) to circumventing and durable resistances; nutrients dynamics and flows and their manipulation to the crop's advantage; components of fruit development and quality as related with environment and technology.

Oral presentations (9th of June, am)

PRODUCTIVITY AND FRUIT QUALITY IN INTEGRATED AND CONVENTIONAL PRODUCTION SYSTEMS OF 2 SPECIES OF AÇAÍ CULTIVATED IN THE BRAZILIAN AMAZON REGION

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The purpose of this experiment was to verify the productivity and fruit quality (organoleptic and functional compounds) of 2 species of açaí produced in a conventional and integrated system in the Brazilian Amazon region. This study was carried out at rural property in the South of Roraima State/Brazil, and the physical-chemical analysis was performed at Food Technology Laboratory, in the Federal University of Roraima. The architecture of the orchards consisted of alternate rows from 4 to 6-year old of *Euterpe oleracea* Mart. and *Euterpe precatoria* Mart., using a 4 x 4 m spacing. Twelve açaí trees of each specie and system were randomly selected and assessed for productivity and fruit quality (organoleptic and functional compounds) during three seasons (2011/12/13). The integrated system showed lower fruit productivity (4.4 to 6.7%) and, berries with 8.2 to 11.5% less of fresh mass and seeds 5.3 to 8.5% heavier, for both species, in comparison with fruits cultivated under conventional production system. For both species, fruits from the integrated orchards showed a more intense purplish color, higher soluble solids content and lower titratable acidity than fruits from the conventional orchard. Fruit from the integrated orchard had higher contents of phenolic, anthocyanins, flavones and vitamin C and higher antioxidant activity (ORAC and DPPH) than fruits of

both species from the conventional orchard. In the organic system the fruits presented higher incidence of rot (5.2 to 13.4% higher). The sensory panel showed the preference for fruits cultivated in the integrated system, taking in consideration taste and flavor parameters, for both species.

Keywords: Roraima State, Amazonia, antioxidant, *E. oleracea* Mart., *E. precatoria* Mart.

DISTRIBUTION OF PHENOLIC COMPOUNDS ACROSS CONTRASTING CITRUS CULTIVARS USING A UPLC-MS APPROACH (PHENOLIC COMPOUND LANDSCAPE IN CITRUS)

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The polyphenol family encompasses several classes of molecules corresponding to different branching points of the biosynthetic pathway. Citrus plants produce large amounts of phenolic compounds, especially flavanones, flavones and coumarins. Some of them are specific to Citrus. In Citrus, these bioactive compounds are involved in fruit quality as well as in plant defense and therefore are a target of breeding programs with some compounds being desired and some others avoided. Many studies have characterized their composition in Citrus. However, few studies reported several classes of polyphenols in a single analysis. In addition,

although phenolic compounds vary strongly with developmental and environmental conditions, these factors are often omitted thus preventing comparative analyses. To overcome these problems, we took care to collect plant organs experiencing similar environmental conditions. This step is essential to link biochemical data to the key steps of the pathway involved in genetic variability or shifts in metabolite biosynthesis in different tissues. Then, we developed a high-throughput procedure that permitted rapid reconstruction of the distribution of main classes of soluble polyphenols in contrasting tissues and genotypes. We evidence that the combination of datasets from contrasting tissues improved cultivar classification based on polyphenol contents. Drawing a map of the distribution of phenolic compounds across cultivars highlights potential regulatory nodes of the biosynthetic pathway. In addition to the steps catalyzed by rhamnosyltransferases, we proposed that the steps catalyzed by phenylalanine ammonia-lyase, the step conducting to 2',4'-dihydrocinnamic acid from p-coumaric acid and the step involving flavone synthase were important regulatory nodes in "Clementine" and "Star Ruby" grapefruit.

Keywords: Phenolic compounds, flavonoids, coumarins, Citrus, UPLC-MS, high-throughput method, phylogenetic relationships, tissular diversity, biosynthetic pathway

VARIABILITY IN FRUIT VOLATILE PRODUCTION. FROM VOLATILE COMPOUNDS TO GENES AND BACK

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We present our current understanding of the mechanisms involved in the biosynthesis of volatile compounds in the ripe tomato fruit and their genetic control, with a focus on those that have a key role in tomato flavour. The progress and difficulties in identifying not only genes or genomic regions but also individual target compounds with actual potential interest for plant breeding will be discussed. The ample variability in the presence or accumulation of different volatile compounds can be observed in experimental populations derived from interspecific crosses and also between heirloom varieties and even commercial hybrids. The identification of Quantitative trait loci (QTLs) for tomato aroma volatiles identified in experimental populations involving different wild tomato species have delivered some intriguing results as (i) the general lack of clear co-localization with structural genes involved the volatile biosynthetic pathways and (ii) the low coincidence on the genomic regions associated among different crosses, indicating that there is huge genetic variability in the control of volatile compound accumulation, giving ample opportunities to alter volatile composition by breeding efforts. Additionally, some genes have been identified as strong candidate genes that may be useful as markers or as biotechnological tools to enhance tomato aroma. Finally, and based on recent reports, the conjugation of volatiles to other metabolites such as sugars will be presented as they seems to play a key role in the modulation of volatile release.

Keywords: tomato, volatiles, fruit quality

GENETIC AND GENOMIC CONTROL OF RESPONSE TO WATER DEFICIT IN CULTIVATED TOMATO

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In the next decade water will be increasingly limiting crop production, in particular in Mediterranean region. Improving plant water use efficiency (WUE) by studying genotype x water regime (G x WR) interactions is of main interest to improve plant adaptation to low water availability. At different degrees, plants can change their phenotypes (molecular, morphological and physiological levels) in response to environmental changes. These modifications relate to phenotypic plasticity. In Tomato (*Solanum lycopersicum* L.), extensively grown in Mediterranean region, first studies have shown genetic variability in the response to water deficit, but very few genes/QTLs have been identified and mostly in wild relative species. Studying water deficit in this fleshy fruit is of particular interest since a well mastered water deficit can stimulate secondary metabolism production, increasing plant defenses and concentration of compounds involved in tomato fruit quality at the same time. In our laboratory, we analyzed 119 recombinant inbred lines (RIL population) and 142 unrelated cherry tomato (*Solanum lycopersicum* L. *cerasiforme*) accessions (GWA population), grown in greenhouse under two watering regimes (WR), in two locations (Morocco and France). Plants were phenotyped for plant phenology, plant vigor and fruit quality traits. We assessed genetic variability and G x WR interactions, for the above traits in the two populations. QTL and GWA analysis were conducted to identify QTL x watering regime (QTL x WR) interactions. The presentation will give a short overview of the research methods available to study genotype by environment interactions in plant and to present the first results of our research project. The possible use of slight water deficit to improve tomato fruit quality in future breeding programs will be investigated.

Keywords: Genotype x Environment interaction, QTL, GWAS, linkage mapping, water deficit, tomato

HOST FACTORS FOR BROWN ROT RESISTANCE IN PEACH FRUIT

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Brown rot in peach fruits caused by the fungi *Monilinia* sp. is a common disease that can provoke as much as 30 to 40% losses of crop. Little is known on the fruit resistance factors and the infection process. The aim of this study is to investigate the factors of resistance of the fruit and their genetic control. This would provide a tool to rationalize genotype x cultural practices combinations in order to reduce brown rot incidence. Physical and biochemical characteristics of fruits (skin conductance, stomatal density, µcracks, surface compounds, epidermis phenolics) potentially linked to *Monilinia* resistance were investigated in cultivars contrasted for their susceptibility. Two segregating populations were phenotyped by infection tests in order to detect QTL