

Evolution and Domestication of Plant Specialized Metabolites
Concurrent Speaker - Ana Arruabarrena

Abstract Title: EXPLORING ALLELIC VARIATION FOR KEY CAROTENOID BIOSYNTHESIS GENES IN MANDARINS AND TOMATOES

Primary Author(s) and Institution(s): ANA ARRUABARRENA 1 , LÁZARO E. P. PERES 2 , FERNANDO RIVAS 1 , MATÍAS GONZÁLEZ-ARCOS 1 , SABINA VIDAL 3 , JOANNA LADO 1 1 Estación experimental INIA Salto Grande, Instituto Nacional de Investigación Agropecuaria, Salto, Uruguay 2 Escola Superior de Agricultura "Luiz de Queiroz", University of São Paulo, Piracicaba, Brazil 3 Facultad de Ciencias, Universidad de la República, Montevideo, Uruguay

Abstract

There is an increasing demand for food with a high nutritional value, that can contain bioactive compounds and promote health and prevent diseases. The development of fruits with high amounts of bioactive compounds is of high interest in many research programs. Carotenoids comprise a large group of terpenoid compounds involved in several processes in plants. Some of them are powerful antioxidants. Mandarins and tomatoes are highly consumed worldwide and are major sources of carotenoids. Hence, these crops are good candidates to improve fruit nutritional value for human health. Here we analyzed the key steps of the carotenoid biosynthetic pathway in different mandarin and tomato genotypes throughout their fruit developmental stages. Expression pattern of different PSY and β CHX alleles from several mandarin varieties were characterized. All mandarin genotypes displayed changes in the expression of genes involved carotenoid biosynthesis (PSY and β CHX), which were reflected in carotenoid content during fruit ripening. For tomato, we explored the mRNA accumulation pattern of a putative new phytoene synthase gene in cultivated tomato and in the wild relative *Solanum pimpinellifolium* . We discussed the differences in allelic variation for carotenoid biosynthesis genes and its potential to improve food nutritional value.

Tropical and Mediterranean Plants
Concurrent Chair - Pierre Marraccini

Abstract Title: CREATING NEW COFFEE VARIETIES TO COPE WITH CLIMATE CHANGES: CURRENT KNOWLEDGE AND FUTURE CHALLENGES

Primary Author(s) and Institution(s): P. MARRACCINI¹, S.O. DE AQUINO², L.F. TORRES², G.S.C ALVES², J-C. BREITLER¹, C. CAMPA³, S. LERAN¹, L. VILLAIN¹, F. GEORGET¹, A. de KOCHKO⁴, V. PONCET⁴, A.C. ANDRADE⁵, H. ETIENNE¹, B. BERTRAND¹

¹CIRAD, UMR IPME (Univ. Montpellier, CIRAD, IRD) F-34394 Montpellier, France ²Federal Univ. Lavras (UFLA), 37200 Lavras (MG), Brazil ³IRD, UMR IPME (Univ. Montpellier, CIRAD, IRD) F-34394 Montpellier, France ⁴IRD, UMR DIADÉ (Univ. Montpellier, IRD) F-34394 Montpellier, France ⁵EMBRAPA Café- INCT-Café/INOVACAFÉ, 37200 Lavras (MG), Brazil

Abstract

Like many other crops, coffee production is threatened by climate changes. Therefore, research on coffee adaptation to abiotic stresses as well as alternative faster breeding programs are priorities in

many coffee growing countries. During the last decade, studies have been focused on identifying the physiological, molecular and genetic determinisms of coffee drought-tolerance, mainly on *C. canephora*. By comparing drought-tolerant and -susceptible clones, several candidate genes (like CcDREB1D) were highlighted. Recent studies demonstrated that CcDREB1D promoter haplotypes differentially regulate the expression of this gene under drought (and other abiotic stresses), mainly in leaf guard cells. In order to predict the adaptedness of *C. canephora* populations to climate change, statistical analyses are in progress to associate SNPs found in such candidate genes with climate parameters. Regarding *C. arabica*, new F1 hybrids resulting from conventional varieties crossed with wild Ethiopia accessions were recently created. With high vigor and yield, these hybrids were proved to be better adapted to agroforestry (low light) and full-sun (high light) conditions than traditional cultivated varieties*. Even though the molecular mechanisms of heterosis in these hybrids are largely unknown, preliminary studies suggested higher homeostasis probably linked to a better regulation of genes involved in the circadian clock. *BREEDCAFS (BREEDing Coffee for AgroForestry Systems) project H2020-SFS-2016-2 supported by EU (www.breedcafs.eu)

Tropical and Mediteranean Plants
Invited Speaker - Bjorn Usadel

Abstract Title: Complex tomato genomes: Easy with Nanopores

Primary Author(s) and Institution(s): Bjorn Usadel; RWTH Aachen University, Institute for Biology I

Abstract

Recent updates in Oxford Nanopore technology have made it possible to obtain GBases of sequence data from one single flowcell. It has been demonstrated that this is very beneficial for microbial genome assemblies and can also be used to assemble human genome data. However medium to large plant genomes have been shown to often be recalcitrant to genome assemblies due to their repetitive nature. We therefore set out whether -and if so how- plant genomes can be tackled using long read nanopore data. We comprehensively evaluated different assembly strategies on full (ca. 100x coverage) and subsampled data sets for a genome featuring a size of slightly more than 1.1 Gbase. We showed that excellent N50 values and BUSCO completeness scores can be obtained using long read data alone. We will discussing implications for plant genome assemblies and their analysis.

Tropical and Mediteranean Plants
Concurrent Speaker - Jennifer Smith

Abstract Title: CREATING DROUGHT, HEAT, AND SALT TOLERANT COTTON BY CO-OVEREXPRESSING RCA AND AVP1

Primary Author(s) and Institution(s): JENNIFER SMITH, TEXAS TECH UNIVERSITY NARDANA ESMAEILI, TEXAS TECH UNIVERSITY PAXTON PAYTON, USDA-ARS JOHN BURKE, USDA-ARS HONG ZHANG, TEXAS TECH UNIVERSITY; TexasTech University

Abstract

Abiotic stress is a serious challenge we face in agriculture and our goal as molecular scientists is to create tolerant crop plants to stresses of drought, heat, and salt. Higher yielding crops are urgently