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Biotic and Abiotic Stress Tolerance in Plants: the Challenge for the 21st Century



BOOK OF ABSTRACTS

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Workshop on Biotic and Abiotic Stress Tolerance in Plants:

the Challenge for the 21st Century

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S03P07

Analysis of DREB1D gene sequence in different Coffea genotypes

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In several plant species, the DREB genes play a key role in responses to abiotic stress. Since the development of molecular markers is one of the major goals for accelerating breeding programs, a study was done to evaluate the sequence variability of the DREB1D gene in several Coffea genotypes. The promoter and coding regions of this gene were cloned and sequenced from 16 coffee plants (including 10 from C. arabica and 4 from C. canephora), most of them characterized by different phenotypes (tolerance vs. susceptibility) regarding to drought. This showed that the DREB1D-coding sequence was highly conserved within coffee plants. However, several nucleic polymorphisms ("single nucleotide polymorphism" [SNP] and insertion/deletion [INDELs]) were found in the coffee DREB1D promoter regions. These polymorphisms could explained the differences of DREB1D gene expression levels previously observed in leaves of drought tolerant and susceptible clones of C. canephora. These polymorphisms also allowed the identification of different haplotypes like orthologous sequence variants (OSVs) of C. canephora and C. eugenioides as well as homologous single-nucleotide variants (HSVs) for C. arabica subgenomes (C. canephora and C. eugenioides) that could be used to develop allele and homoeologous specific markers for this locus. Work is now under way to evaluate the capacity of DREB1D promoter regions to control the expression of the uidA reporter gene in transgenic coffee plants.

Work supported by CAPES-COFECUB, Consórcio Pesquisa Café and INCT-Café (CNPq/FAPEMIG).

SUSDUS

Functional analysis of *CcDREB1D* promoter region from two genotypes of *Coffea canephora* through genetic transformation of *Nicotiana tabacum*

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Although some studies in plant physiology resulted in a better understanding of the mechanisms involved in drought tolerance in coffee, knowledge about the metabolic and molecular changes involved in the response of the coffee plant to water deficit conditions is still scarce. Recent studies permitted the identification of several candidate genes presenting differential expression between genotypes contrasting (tolerant vs. susceptible) to this trait. In many higher plants, DREB genes were shown to be involved in the transduction pathways of water stress. Previous results showed that *CcDREB1D* gene expression increased under drought stress in leaves of drought-tolerant clone 14 but not in those of the drought-susceptible clone 22 of *Coffea canephora*. By sequencing the *DREB1D* promoter regions of these clones, several nucleic polymorphisms ("single nucleotide polymorphism" [SNP] and insertion/deletion [INDELs]) were found. In order to know if these polymorphisms could explain the differences of *DREB1D* gene expression observed between the clones 14 and 22 of *C. canephora.*, 5 'deletions of several alleles of the *CcDREB1D* promoter regions were made and cloned in the binary vector pBI101 in order to analyze their ability to control the expression of the *uidA* reporter gene in transgenic tobacco (*Nicotiana tabacum*) plants.

Work supported by CAPES-COFECUB, Consórcio Pesquisa Café and INCT-Café (CNPq/FAPEMIG).

S04P01

Genetic mapping and QTLs detection in a Theobroma grandiflora progeny

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The genus Theobroma covers 22 native species to the Amazon region. Two species are cultivated in Brazil: Theobroma cacao and T. grandiflorum (cupuaçu). T. grandiflora is economically important to the amazonian states of Brazil where it was developed in food and cosmetics with various products manufactured mainly from the pulp of the seed. Both species are susceptible to Moniliophthora perniciosa (Stahel) Singer, the causal agent of witches' brooms disease. 139 SSRs markers (Single Sequence Repeat) from T. grandiflora and 500 SSRs developed by CIRAD in T. cacao, were used to select polymorphic markers and carry out a genetic mapping of a Th. Grandiflora progeny from "174" x "1074" clones, respectively resistant and susceptible to witches' brooms. 145 plants were obtained by Embrapa-CPATU (Belém) today installed in the field at the CEPLAC (Belém) station. Inoculations with the M. perniciosa (from T. grandiflora) were carried out in the progenies and parents to evaluate the resistance. Other observations as vigor or number of ovules per ovary were observed also. We present the first results obtained with the selection of polymorphic specific markers of Th Grandiflora and Cocoa and the first genotying results from 44 SSRs of T. grandiflora including 14 SSRs from expression sequences. In conclusion this study including different teams is ongoing to have at the end of the project: i) the first genetic map of Theobroma grandiflora, ii) identification of QTLs of resistance to witches' broom, and other QTLs and iii) to compare genetic map and QTLs between both species.

S04P02

Advanced Lineages of lettuce type butter heat tolerant

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The aim of this study was to select lineages of lettuce heat tolerant for testing of cultivar competition. Experiments were carried out during two seasons in the dependences of EE Jorge Luiz da Gama Wanderley, belonging to the IPA, located in Vitória de Santo Antão city in Mesorregião of Pernambuco and at the Federal Rural University of Pernambuco-UFRPE, Pernambuco State, Brazil. In the first experiment were evaluated 14 genotypes, being two cultivars, two advanced lines and 10 progenies, in the second experiment 12 genotypes were evaluated, 10 progenies from the first study and two cultivars, these genotypes were evaluated for characteristic post-harvest. In the two trials we evaluated the characters: plant height, head diameter, number of leaves, fresh weight of plant, fresh weight of leaves, stem diameter, stem length, shape of the edge, blade shape and leaves color the character shoulder was evaluated only in the second experiment, for the third experiment, the progeny of the second experiment were evaluated for five days at room temperature. For the first study were selected genotypes AFX-18C-02-23-15-020B-AFX 06-13 and AFX-022B-10-17 as promising genotypes. For the second test were used resulting progenies of selected genotypes. Averages for the characters remained constant for the progenies AFX-18D-02-23-15-01, AFX-18D-02-23-15-02, AFX-18D-02-23-15-03, AFX-18D-02-23-15-04 and AFX-18D-02-23-15-06, these being selected as lineages able to participate in trials of cultivars.

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S04P03

Advanced Lineages of lettuce type butter resistant to Meloidogyne incognica race 1

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The aim of this study was to select advanced lineages of lettuce type butter resistant to *M. incognita* race 1 root-knots. The experiments were carried out during March to April 2013, in the dependences of Federal Rural University of Pernambuco-UFRPE, located in Recife, Pernambuco State,