

The International Consortium in Advanced Biology presents:



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

BOOK OF ABSTRACTS

6 to 8 • NOVEMBER • 2013

Cana Brava Resort • Ilhéus - Bahia - Brazil

www.ciba2013.net

supports:



organizing institutions:



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

Cana Brava Resort • Ilhéus-Bahia, Brazil • 6th-8th November 2013

and 1% to the qPCR results. Transcriptomic data obtained by both approaches were consistent, and some specific novel cDNA sequences may be used to unveil the resistance mechanisms acting in *C. arabica*.

Work supported by Embrapa, CAPES and CNPq.

S01T05

Stress tolerance in peanuts: a genomic approach using wild *Arachis*

*ACM Brasileiro*¹, *C Morgante*², *ACG Araujo*¹, *LA Guimaraes*¹, *SC Leal-Bertioli*¹, *D Bertioli*³, *LN Fonseca*¹, *MAP Saraiva*¹, *ACQ Martins*¹ and *Guimarães PM*¹

¹ EMBRAPA Recursos Genéticos e Biotecnologia, Brasília, CP 02372, DF- Brazil,

² EMBRAPA Semiárido, Petrolina, CP 23, PE – Brazil,

³ Universidade de Brasília, Brasília, CEP 70910-900. DF- Brazil.

Email : ana.brasileiro@embrapa.br

Cultivated peanut (*Arachis hypogaea*) has a high morphological but narrow genetic diversity, and understanding the genetic processes of this plant is hindered by the fact that the peanut genome has not yet been sequenced and its genomic resources are still limited. Due to its high genetic diversity and adaptation to a range of environments throughout the evolution course, wild relatives of peanut (*Arachis* spp.) constitute a rich source of allele diversity for resistance to abiotic and biotic stresses. In particular, *A. duranensis* and *A. stenosperma* harbor high adaptability to water stress conditions and root-knot nematode resistance, respectively. In order to identify genes in those wild species that are differentially expressed in response to drought stress and to nematode (*Meloidogyne arenaria*) challenge we conducted comprehensive transcriptome analyses using sequencing data from Sanger, 454 and Illumina HI-SEQ technologies. *In silico* analysis revealed that several genes were significantly up- or down-regulated in the stressed or control conditions. Differentially expressed candidate genes related to abiotic and biotic stresses were further selected for validation through RT-qPCR. Among these, expansin, aquaporin, dehydrin, chaperone, nitrilase, transcription factors, resistance protein MG13, resveratrol synthase genes revealed high levels of differential expression in stressed plants. This data confirms the relationship of these genes with drought stress response or root-knot nematode infection in wild *Arachis* species. The identification of candidate genes for resistance to abiotic and biotic stresses can provide additional resources for peanut breeding and transgenic approaches.

Work supported by Embrapa, CNPq, CAPES, FAP-DF and Generation Challenge Program.

S01T06

Setting up the ground for abiotic stress tolerant crops

Paulo Arruda

UNICAMP-Brazil

S01T07

Combined genetic and genomic approaches to characterize a durable *Hevea* resistance to South American leaf blight

D.M. Koop, L.S. Rippel, M. Déon, A. Berger, R. Rivallan, F. Doaré, V. Le Guen, V. Pujade-Renaud, M. Seguin and D. Garcia

Cirad, UMR-AGAP, 34.398 Montpellier (France)

Email: dominique.garcia@cirad.fr

The South American Leaf Blight (SALB), due to the Ascomycota *Microcyclus ulei*, threatens the world production of natural rubber, based on the cultivation of nearly only one species: the tropical tree *Hevea brasiliensis*. In connection with a breeding program, conducted in Brazil by Michelin and Cirad and aiming to create resistant cultivars of rubber tree, the genetic determinism of three sources of natural resistance to SALB has been analyzed. We developed a classical approach of QTL mapping on a segregating population issued from a crosses implying a quantitative and durable resistant in MDF180 genotype (Le Guen et al., 2008), a quantitative and by-passed resistant in Fx3899 genotype, and a qualitative resistance in Fx2784 genotype. Disease resistance of the progenies was assessed under natural infestation in field trials, in Brazil and French Guyana, or under controlled inoculations with