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

## BOOK OF ABSTRACTS

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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*

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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

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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

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isolated strains of *Microcyclus ulei*. Genetic mapping revealed unexpected genetic determinisms underlying the observed resistances: whereas a complex genetic determinism implying major resistance genes and several minor QTLs can be bypassed by the pathogen (Le Guen *et al.* 2007), a durable partial resistance appeared to be governed by only 2 major resistance loci (Le Guen *et al.* 2011). To initiate a comprehensive approach of these resistances, eleven cDNA libraries were built, sequenced and annotated from MDF180, Fx3899, PB314 (susceptible) and PB260 (susceptible) genotypes (Garcia *et al.*, 2011). We sequenced 20,493 expressed sequence tags (EST), developed array expression analysis and identified of 212 candidate genes differentially regulated in MDF180 and 30 genes in Fx3899 during the infection process. The integrated analysis of gene expression and systems biology allowed designing a general scheme of major mechanisms associated with durable resistance of MDF180 genotype and susceptibility of PB314 genotype to South American leaf blight. Concomitantly, transcriptomic NGS data give us the possibility to analyze large data set of inoculated and non- inoculated leaves of 3 *Hevea* species, *H. brasiliensis*, *H. pauciflora* and *H. bentamiana*. Comparison of the genes differentially expressed (inoculated vs non-inoculated) indicated few common genes involved in the response to SALB between the genera of *Hevea*. These results, in accordance with genetic mapping, constitute a favorable context for developing a strategy of pyramiding of the resistance.

Work supported by ANR, Michelin, FAPESB, CNPq.

### S01T08

#### **Soybean molecular resistance responses to *Meloidogyne javanica***

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Root-knot nematodes (RKN), encompassing more than 80 species of the genus *Meloidogyne*, are biotrophic parasites to a wide range of angiosperms and cause considerable decrease in crop yield and quality worldwide. Despite the use of management strategies, such as crop rotation with non-hosts, sustainable and long-lasting pest control strategies are in high demand. Therefore resistance in plants is an attractive approach for controlling nematode populations. To perform a large-scale analysis focusing on the infection on soybean (*Glycine max*) we analyzed root cells transcriptome in response to infection with the nematode *M. javanica* into incompatible interaction. The soybean line applied in this work PI 595099 (Accession NPGS/GRIN: G93-9223) is effective against specific strains or races of nematode species including *M. javanica*, *M. incognita*, *M. arenaria* and also for the cyst nematode *H. glycines*. A total of 1,348,738 sequence reads were obtained with 1,123,977 being mapped and aligned to *G.max* reference genome recently sequenced allowing to assay 37,707 transcripts. It was verified that hormone, carbohydrate metabolism and stress related genes were consistently expressed at high levels in infected roots as compared to mock control. Most noteworthy genes include those encoding glycosyltransferases, peroxidases, auxin-responsive proteins and gibberellin-regulated genes. Our data analysis suggests the key role of glycosyltransferases, auxins and components of gibberellin signal transduction, biosynthesis and deactivation pathways in the resistance reaction and their participation in jasmonate signaling and redox homeostasis in mediating aspects of plant growth and responses to biotic stress. Based on this study we suggest a reasonable model regarding to the complex mechanisms of crosstalk between plant hormones, mainly gibberellins and auxins, which can be crucial to modulate the levels of ROS in the resistance reaction to nematode invasion. The model also includes recent findings concerning to the participation of DELLA-like proteins and ROS signaling controlling plant immune or stress responses.

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### S01T09

#### **The contribution of natural genetic variation to adaptative plasticity in *Vitis***

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