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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**

Cana Brava Resort
Ilhéus-Bahia, Brazil
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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 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.

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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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Plants employ exogenous abiotic cues, such as light and temperature, to synchronize growth and development to the most favorable environmental conditions, thus, maximizing fitness and adaptation. In woody perennials, the correct timing of the transitions between active growth and dormant developmental programs is critical for plant survival and reproductive success. Genomic regions associated to sensory pathways in association with those coding for members of extensive signaling networks are responsible for the control of environmental perception, signal integration and response elicitation resulting in adaptation. The genus *Vitis* consists of approximately 60 interfertile species, including cultivated *V. vinifera* and wild species that exhibit resistance to several biotic factors. We have employed large scale transcriptome, non structural carbohydrate profiling and morphological analyses of plant growth regions to investigate the responses of *Vitis* genotypes adapted to temperate and tropical conditions to different combinations of daylength and temperature. Temperate cultivated and wild species exhibit a definite temporal sequence of events in response to temperature decrease and daylength shortening. The effects of short days on plant growth were more extreme on wild temperate *Vitis* in comparison to those observed in the cultivated genotype. The transcription of light response and circadian clock associated genes represent a significant portion of the responsive transcriptome not only to changes in the length of the illuminated period but also to temperature. Tropical *Vitis* accession displayed a continuous growth pattern, undisturbed by either photoperiod shortening or temperature reduction. Based on the current results, we hypothesize that a loose coupling between the carbohydrate metabolism and the sensory pathways for temperature and daylength may involved in the maintenance of the continuous growth of the tropical accession under unfavorable environmental conditions. These findings may contribute to candidate gene and genome wide selection strategies for grapevine breeding for tropical conditions.

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S01T10

Cowpea Transcriptomic: looking for genes responding to biotic and abiotic stresses

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The cowpea [*Vigna unguiculata* (L.) Walp] is an extremely valuable legume for the nutrition of people from tropical countries. In Brazil, it also plays a social role, mainly in the North and Northeast regions, as it is grown by family farming. Due to the use of low technology, its yield and productivity are below its potential. The NordEST, a network studying the functional, structural and comparative cowpea genomics, aims to assist the national breeding program by the development and use of new technologies. Thus, with the use of the SuperSAGE methodology, previously selected cowpea accessions were submitted to abiotic or biotic stresses in order to generate expression patterns that allowed the identification of potential genes for breeding. In a salinity assay, 100 mM of NaCl added to the Hoagland solution enabling to stress the roots of both the Pitiuba (tolerant to salinity) and Br14-Mulato (sensitive) accessions, under stress conditions and without it. A total of 4.166.408 SuperSAGE 26 bp tags represented 133,694 transcripts (unitags or different tags). For the drought study, the two tested accessions, Pingo de Ouro (considered tolerant) and Santo Inácio (sensitive), in a hydroponics system, had their roots exposed to air, suffering root dehydration, up to 150 min (six sampling times). The four used libraries generated 26,267,190 tags or 149,305 unitags. During the biotic stress, two viruses were independently studied. The *Cowpea Aphid-Borne Mosaic Potyvirus* analysis using the IT85F resistant accession underwent the following treatments: injuring leaves with abrasive material, followed by virus inoculation (sampling times 30, 60, 90 min and 16 h), leaves without any stress and leaves being only injured but not inoculated. The three first inoculation times were gathered in a single library and the last collection in another one. The four libraries generated 9.075.333 tags (112,505 unitags). For the *Cowpea Severe Mosaic Virus* (CPSMV) study, the assay was done with BR14-mulato resistant accession and three treatments: injured and inoculated leaves (bulks of the sampling times 30 and 90 min), injured and inoculated leaves (sampled at 16 h), and not stressed leaves. A total of 6.834.523 tags was generated (107,161 unitags). The more than 45 million unitags allowed to generate expression profiles of the