

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

metabolically active feeding cells, named giant cells. Nematicides, crop rotation, bio-control agents and/or host resistance have not been successfully deployed against nematodes, except in some restrict cases. Plant transformation with genes encoding anti-feeding factors and Cry toxin has initially been tested aiming a biotechnological tool to induce nematode resistance. A new promising tool is gene silencing by RNAi, where GM plants produce dsRNA of nematode gene, when nematodes orally up-take dsRNA, the specific target gene is then silenced, showing different phenotypes according to gene function or RNAi efficiency. In this way, our research group has tested several target genes. Nematode gene were selected, their fragments were isolated, cloned in RNAi binary vector for *Nicotiana tabacum* transformation via *Agrobacterium tumefaciens*. GM tobacco expressing dsRNA of Aspartic, Serine and Cysteine Proteinases, Heat Shock Protein 90 and Isocitrate Lyase genes from *M. incognita* were generated and nematode resistance induction were evaluated. Bioassays on GM tobacco demonstrated 10-70% reduction of egg number per root gram, according target gene and transgenic lines. Indeed, we tested the Splicing Factor as target gene in stable GM soybean. Bioassays at 45 days after inoculation showed 75-95% egg reduction in different transgenic lines. These results presented here increase the list of nematode target genes to expression knock-down as a potential biotechnological tool to induce RKN resistance in GM crops.

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S03T06

Citrus-HLB interaction: what have we learned about this complex pathosystem?

J. Freitas-Astúa^{1,2}, V. Mafrá², M.C. Breton², M.A. Machado²

¹Embrapa Cassava and Fruits, R. Embrapa, s/n, 44380-000, Cruz das Almas, BA, Brazil; ²Centro APTA Citros Sylvio Moreira, CP4, 13490-970, Cordeiropolis, SP, Brazil

Email : Juliana.astua@embrapa.br

Citrus *huanglongbing* (HLB) is considered the most important disease of the crop worldwide and is caused, in Brazil, by *Candidatus Liberibacter americanus* (CaLam) and *Ca. L. asiaticus* (CaLas). Both species are vectored by the Asian citrus psyllid *Diaphorina citri* and are restricted to the phloem of infected plants, where they induce severe imbalance in the translocation of nutrients and other important substances. Several research groups have studied the responses of citrus to HLB, but only for CaLas. Here we present data on the global response of the susceptible genotype Pera sweet orange to CaLam using a customized 385K microarray chip. The analyses detected a significant reprogramming of the citrus transcriptome upon infection, including the induction of zinc transporters, modulation of enzymes related to sugar metabolism, depletion of photosynthesis, induction of several defense-related genes and modulation of enzymes regulating ROS production. We also compare our data with those obtained for CaLas. A time-course RNA-seq transcriptome experiment using tolerant and susceptible citrus genotypes infected with CaLam or CaLas is in progress to investigate the dynamic of expression of important genes during early stages of infection. Finally, we assessed differentially expressed genes from symptomatic leaves and branches infected with CaLas or CaLam by RNA-seq, with the objective not only to better understand the response of citrus to the pathogens, but also to identify candidate genes and phloem-specific promoters that can be used in our citrus transformation program aiming transgenic resistance against HLB.

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S03T07

Biotechnology approaches to overcome biotic stress constraints in soybean production in Brazil

F. C. Marcelino-Guimarães, R. V Abdelnoor, and W. Dias

Embrapa Soybean, Rod. Carlos João Strass, s/n, Acesso Orlando Amaral, Caixa Postal 231, Distrito de Warta, Londrina/ Paraná – Brazil – CEP:86001-970

Email : francismar.marcelino@embrapa.br

Soybean is one of the most important crop in Brazil, being cultivated from the South to the North of the country. The area cultivated surpass 29 million ha while the production overtook 80 billion tons in the last season. Considering that soybean has being cultivated in a large area in the country, and

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that Brazil is a tropical country, consequently the diversity of pathogens that can affect the culture is large too. The Asian soybean rust caused by *Phakopsora pachyrhizi* and diseases caused by nematodes can occur in all major soybean producing areas in Brazil and during all soybean cycle. Besides, both pathogens present high variability and aggressiveness. Based on that, these two diseases have a high potential to cause economic impacts in soybean production. Thus the comprehension of the molecular mechanisms of host resistance and pathogen modulation of the plant innate immunity to enable parasitic infection would contribute to development of a more durable resistance. The aim of our research is to understand the molecular basis of resistance mediated by effectors and PAMPs in soybean and the pathogen strategies to suppress and evade the immune responses. Our strategy is to combine multiple layers of immunity and achieve effective and durable resistance against soybean pathogens.

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