S03O03

Functional characterization of soybean Gm*Hsp*17.6B and Gm*Hsp*22.4 genes in response to *Meloidogyne javanica* infection

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The plant resistance response requires several protein interactions, besides the ones encoded by the R genes, called defense response auxiliary proteins, which include proteins involved in the Reactive Oxygen Species (ROS) generation, kinases and heat shock proteins (HSPs). Frequently, *Hsp*20 genes have been found to be associated with the plant response to nematodes. In resistant (PI 595099) and susceptible (BRS 133) soybean genotypes comparison, Gm*Hsp*17.6B and Gm*Hsp*22.4 genes showed a differential expression profile, being down-regulated in susceptible at 8 days post infection (dpi) by *M. javanica* and up-regulated in the resistant genotype, at the same time and treatment. Besides, these two genes were related to other nematodes species infection and are close to QTLs involved in biotic stress. Thus, we performed experiments with transgenic hairy roots, obtained by *Agrobacterium rhizogenes* infiltration, containing Gm*Hsp*17.6B or Gm*Hsp*22.4 genes under promoter 35S regulation. Samples were collected at 45 dpi, to nematode reproduction factor analyses, and at 8dpi to total RNA extraction. The statistical analyses of variance (ANOVA) followed by Honestly Significant Difference (HSD) Tukey ($p \leq 0.05$) showed significant reduction in *M. javanica* population at roots overexpressing Gm*Hsp*17.6B. Furthermore, to test these genes' influence on defense-related genes, we selected PR1, PR2, and PR5 (Pathogenesis-Related genes) to be evaluated by qRT-PCR. PR2 and PR5 expression was repressed in Gm*Hsp*17.6B-overexpressed roots, while PR1 was repressed in Gm*Hsp*22.4-overexpressed roots. In contrast, the expression of four housekeeping genes was scarcely affected by Gm*Hsp*17.6B or Gm*Hsp*22.4-overexpression. These results suggest that these Gm*Hsp*20 genes may have important influence on nematode infection and play an important role in defense-related genes expression.

This study was supported by the Brazilian agencies Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).

S01O01

Preliminary analysis for integrating transcripts and proteomic profiling of *Coffea canephora* roots subjected to different water conditions

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Coffee is a major agricultural commodity in the world and Brazil is the largest producer and second largest consumer. Drought is one of the main limiting factors to the national coffee production. Plant growth under drought conditions is influenced by changes in photosynthesis, respiration, translocation, ion absorption, metabolism of nutrients and hormones. The aim of this study was to evaluate the gene and protein expression in roots of clones of *C. canephora* grown under control and drought conditions. Clone 22 (drought sensitive) and clones 14, 73 and 120 (drought tolerant), grown under controlled conditions (greenhouse) with (I) and without (NI) irrigation, were used. For each clone and water regime, total RNA and protein was extracted. The profile of the root transcriptome was performed using 454 sequencing, allowing *in silico* analysis of expression among clones and conditions (I *vs.* NI). The proteomic analysis was performed by LC-MS using reverse-phase liquid chromatography coupled to mass spectrometry (MS). Protein identification results were obtained using the software "Protein Lynx". The results obtained by the two integrated analyzes are presented. They showed that differences exist between the techniques used, and the behavior of the clones with respect to stress conditions. The expression analysis by real-time qPCR were performed to validate the gene expression levels obtained by the RNA-seq *in silico* analysis.

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