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Earlier transcriptome interaction from resistant and susceptible soybean genotypes under *Pratylenchus brachyurus* infection revealed by RNA-seq

(Transcriptoma da interação inicial de genótipos de soja resistentes e suscetíveis sob infecção de *Pratylenchus brachyurus* revelado por RNA-seq)

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Resumo

Currently, root-lesion nematode (*Pratylenchus brachyurus*) damage has been outstanding every soybean season crops, especially in regions with sandy soils, such as central Brazil. To identify differentially expressed genes (DEG) in a plant-nematode interaction, susceptible (TGM 115 RR) and resistant (BRSGO Chapadões) soybean genotypes were inoculated with the root lesion nematode and RNA-seq libraries were constructed from inoculated roots at 1, 2, 4 e 8 days post-inoculation (dpi). This strategy allowed the monitoring of DEG in plant-pathogen early interaction, including host defense molecular mechanisms. The single-end reads sequences from Genome Analyser plataform were mapped to the soybean genome for identification of expressed genes. Results showed that the total number of DEG corresponds to 3.36% (TMG) and 2.40% (Chapadões) (without redundant in all time treatments) of 73,320 predicted transcripts in soybean by Phytozome displaying significant changes in mRNA levels. The analysis of functional categories revealed many defense-related groups including genes that were previously shown to be induced during other plant–pathogen interactions. Among transcription factors families, it was observed that the largest number of DEG in all resistant cultivar treatments belong to MYB, WRKY and HSF families.