



Work Title: Analyses of Cupuassu (*Theobroma grandiflorum*) Transcriptome During Interaction with *Moniliophthora perniciosa*, the causal agent of Witches' Broom Disease

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Key-words: Plant-pathogen interaction, RNA-Seq, apical shoots transcriptional profile, differential gene expression

ABSTRACT:

The cupuassu tree (*Theobroma grandiflorum*) is an important amazonian fruitful species, whose production is hugely affected by the fungus *Moniliophthora perniciosa*, causative agent of the witches' broom disease. To better understand the molecular bases of plant-pathogen interaction, we have analyzed the apical shoots transcriptional profile of resistant and susceptible cupuassu clones inoculated with the fungus. RNA samples at different times after inoculation (0 h, 24 h and 48 h) were sequenced on Illumina platform. Quality reads were mapped to the *Theobroma cacao* V.2 genome sequence using STAR software package followed by HTSeq-Count. Raw number of mapped reads calculated per sample was used as input for EdgeR to produce normalized values accounting for sample-specific effects and to obtain inference of differential gene expression. Gene ontology (GO) enrichment hypergeometric analysis was performed using FUNC software after PFAM and GO terms annotation. A total genotype vs inoculation). The expression pattern of the DEGs in the resistant clone was different from the susceptible clone at 24 h after inoculation, as well as at 48 h. Some GO of 21,442 transcripts were evaluated. 228 differentially expressed genes (DEGs) were identified between the genotypes, and 591 related to the different conditions (categories were enriched in the resistant genotype after inoculation, for example, response to wounding and a variety of enzymatic activity categories. For data validation, some of the DEGs were selected for further qRT-PCR analysis. This is the first cupuassu apical shoot transcriptome described and represents a valuable source for *T. grandiflorum*/*M. perniciosa* interaction studies.

Financial support: Embrapa and Capes