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ÔMICAS: do gene ao fenótipo

Transcriptome analysis in *Coffea arabica*, under several abiotic stresses, reveals differentially expressed genes in leaves

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In recent years, *Coffea* ssp. has become subject of increasing research in gene expression analysis, in the quest to find genetic factors associated to abiotic stress responses with special attention to transcription factors such as the DREB family. This focus was due to their involvement in the regulation of many stress-related genes that play an important role in cascading a response to an environmental stimuli. RNA-seq analysis, creates the possibility to s study the transcriptome and to identify differentially expressed genes upon an abiotic stress or any important agronomic trait. The main objectives of this work were to obtain an overview of the transcriptionally active genes in Arabica coffee leaves when subjected to several abiotic stresses and to analyze specific highly expressed candidate genes for environmental-stresses tolerance. After a 3 h exposure period under the different stresses (drought (low relative humidity – 9%), cold 5°C, heat 40°C, photo-oxidative 200 μM m^{-2} s^{-1} and 10^{-5} M abscisic acid (ABA)), leaves were collected for RNA extraction. The preparation of the mRNA library was done via the TruSeq Stranded mRNA Sample Preparation Kit from Illumina. Sequencing was performed on the HiSeq 2500 platform (Illumina) through the SBS (Synthesis By Sequencing) technique by MGX - Montpellier Genomix. Differential expression analysis was performed from the raw read counts using the DESeq2 package. Results presented a total of 17.399 differentially expressed genes between all stresses tested, being 2.217, 812, 4.263, 8.008 and 2.099 for ABA treatment, Cold, Drought, Heat and Photo Oxidative, respectively. Using these data, four candidate genes under the stress conditions tested were selected and their differential expression profiles were confirmed by RT-qPCR experiments. Through the *in silico* and *in vivo* analyzes presented in this work it was possible to identify several candidate genes, responsive to the different stresses applied to coffee, which may help to advance our understanding of the genetic determinism of abiotic stress tolerance in coffee. Furthermore, this work will open new avenues for studies into specific genes and pathways in this species, especially related to abiotic stress, and our data might have a potential value in assisted breeding applications.

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