Genes related to secondary metabolism and redox status are transcriptionally modulated in *Coffea arabica* leaves by applying hexanoic acid to roots

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Introduction

Hexanoic acid (Hx) is a short, naturally occurring monocarboxylic acid that is a potent natural priming agent against pathogens (Caccalano et al., 2021). The molecular mechanism that rely Hx induced resistance is not fully understood.. We hypothesize that if Hx application can modulate genes related to defense responses, it would be a potential eliciting agent in Arabica coffee.

Materials/Methods

Using RNA-seq, we analyzed the leaf transcriptome of two *Coffea arabica* cultivars, cv. Catuaí Vermelho IAC 144 and Obatã IAC 1669-20, in response to the application of hexanoic acid in an eliciting concentration in nutrient solution. Total RNA was extracted and cDNA libraries were generated using a poly-A selection method and paired-end reads (2 X 150 bp) obtained on the Illumina NovaSeq Platform. RNA-seq analysis used the same rational of Liu et al. (2020). Illumina reads were mapped in the *C. arabica* genome available at NCBI (https://bit.ly/3iB1Ebe).

Table 1: Most abundant Differentially expressed genes in cv. Catuaí leaves. Legend: *Excl Hx = Genes expressed exclusively in Hx-treated plants; **Excl C = Exclusively expressed in controls.

ID C. arabica	BLAST result	log2(fc)
XM_027208730.1	probable glutathione S-transferase	4.95
XM_027210748.1	putative methyltransferase DDB_G0268948	4.92
XM_027229597.1	stamen-specific protein FIL1-like	4.88
XM_027227438.1	cis-abienol synthase, chloroplastic-like isoform X1	3.81
XM_027239490.1	metallothionein-like protein 1	3.67
XR_003449858.1	---NA---	-2.23
XM_027249710.1	endoribonuclease Dicer homolog 2-like isoform X1	Excl Hx*
XM_027250023.1	probable 1-acyl-sn-glycerol-3-phosphate acyltransferase 5	Excl Hx*
XM_027221877.1	ferredoxin--NADP reductase, leaf-type isozyme, chloroplastic	Excl C**
XM_027254981.1	N-(5'-phosphoribosyl)anthranilate isomerase 1, chloroplastic-like	Excl C**
XM_027218799.1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial	Excl C**
XM_027271145.1	RPM1-interacting protein 4-like isoform X2	Excl C**
XM_027222944.1	transcription factor bHLH121-like	Excl C**

Table 2: Most abundant Differentially expressed genes in cv. Obatã leaves.

ID *C. arabica*	BLAST result	log2(fc)
XM_027225327.1	bark storage protein A-like	-4.77
gene-LOC113715020	laccase-15-like [Sesamum indicum]	-4.38
XM_027213576.1	synaptotagmin-5-like	-3.99
XM_027222657.1	LMBR1 domain-containing protein 2 homolog A-like isoform X1	-3.76
XM_027208105.1	acidic endochitinase-like	-3.65
XM_027255085.1	17.4 kDa class I heat shock protein-like	3.83
XM_027242587.1	18.5 kDa class I heat shock protein-like	4.03
XM_027243796.1	small heat shock protein, chloroplastic-like	5.25
XM_027205876.1	serine/threonine-protein phosphatase 5 isoform X1	5.34
XM_027255716.1	pentatricopeptide repeat-containing protein At1g60770-like isoform X1	5.63

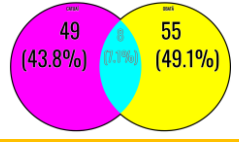

Figure 1. Comparative analysis of differentially expressed genes between cv. Catuaí and cv. Obatã

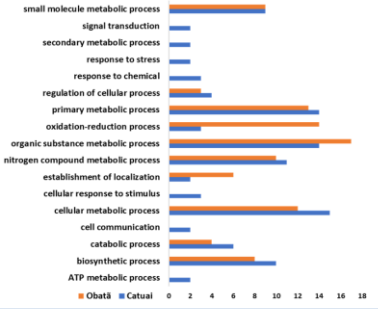

Figure 2. Gene Ontology terms referring to Biological Processes found for differentially expressed genes.

Results/Discussion

Using a publicly available Coffea arabica genome as a reference for mapping RNA-seq data, we identified 57 differentially expressed genes (DEGs) in Catuaí leaves and 63 DEGs in Obatã leaves. A total of eight genes have significant similar transcriptional modulation in both cultivars, including genes related to redox balance, jasmonate signalling and the phenylpropanoid metabolism. Hx significantly repressed only an electron acceptor in chloroplasts in both cultivars. All other genes were upregulated. They include a glycosyltransferase associated to the salicilate-jasmonate signaling crosstalk, an ATPase, aldo keto reductases and genes related to the biosynthesis of hydroxycinnamic acids and terpenoids.

Conclusion/Perspectives

These results demonstrate that Hx application in roots can alter the gene expression patterns of leaves, activating genes involved in redox regulation and synthesis of secondary metabolites. This approach indicate that Hx have a priming effect, modulating genes involved in the establishment of systemic acquired resistance, becoming a promising eliciting substance in *Coffea arabica*. Funding: CAPES (Code 001) and FAPESP (#2016/10896-0).

References:

Caccalano et al. 2021 Journal of Applied Microbiology DOI:10.1111/jam.15125

Liu et al. 2020 Plant Cell Reports DOI:10.1007/s00299-019-02501-2