STRUCTURAL AND FUNCTIONAL ANALYSIS OF STRESS-RESPONSIVE GENES AND THEIR SELECTED PROMOTERS FROM YOUNG OIL PALM (*ELAEIS GUINEENSIS*) UNDER TWO ABIOTIC STRESSES

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Abstract:

The biomass production and manufacturing system has been affected on a regional, national and global scale due to population growth and climate change. Two abiotic stresses that most threaten agriculture are drought and soil salinity. Transcriptomics consists of portraying the gene expression profile of an organism under contrasting conditions (control and specific situation) via RNA Seq, also known as full-shotgun sequencing of the transcriptome. This technology allows the identification of genes expressed at a given stage, measuring the transcriptional expression levels. Total RNA samples were subjected to RNA-Seq using an Illumina HiSeq platform at the GenOne Company (Rio de Janeiro, RJ, Brazil), using the paired-end strategy. The raw data analyzed in this study are available in the Sequence Read Archive (SRA) database of the National Center for Biotechnology Information - BioProject PRJNA573093, BioSample SAMN12799239. After *in silico* determination, the gene expression profile must undergo *in vivo* validation employing the qPCR technique. This study aimed to prospect, annotate and validate genes and their stress-inducing promoters differentially expressed in the leaves of oil palm (*Elaeis guineensis*) plants under drought or salinity stresses. The strategy used by the study employed RNA-Seq followed by time-course differential expression analysis. In addition, a quantitative and qualitative comparison study attempted to validate the *in silico* results using qPCR. The total RNA was used as a template for reverse transcription to obtain cDNA using the commercial kit SYBR® GreenER™ qPCR SuperMix Universal (Invitrogen®). The gene named EgEfMPOB00119 40S ribosomal protein S23 mRNA, complete cds, mRNA sequence present in *E. guineensis*, was chosen as a positive control (constitutive gene). The qPCRs were carried out in optical 96-well plats in a 7500 Real-Time PCR System, following the manufacturer's instructions. Besides, the selected genes underwent structural and functional annotation. To investigate the tertiary structure of the proteins, the Software RaptorX was used. The NCBI Conserved Domain Search was used to search for functional domains in proteins. When comparing the expression profiles of the quantitative PCR technique with those of the RNA-seq technique, some inconsistencies appeared, confirming the importance of the *in vivo* validation. Based on the oil palm reference genome, 1,000 bp upstream sequences of the selected genes were acquired. PlantCARE was used to analyze them, with the default parameter. Several of the cis-acting elements found in the promoter sequences of the selected genes are known to be involved in various abiotic stresses. Several of the selected genes coded for uncharacterized proteins, which family membership were not predicted by InterPro. On the other hand, some of the genes coded for transcription factors, and known enzymes (transferases, translocases, and dehydrogenases). The results of this study allowed us to generate a database of genes and promoters with potential use as biotechnological tools to develop plants tolerant to these two abiotic stresses via genetic modification/edition.

Palavras-chave: Abiotic stress; Salinity; Drought; Transcriptomics; Stress-Responsive Genes

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