PREDICTION AND IDENTIFICATION OF MIRNAS IN *ELAEIS GUINEENSIS* JACQ. AND ANALYSIS OF THEIR EXPRESSION IN OIL PALM PLANTS UNDER SALINITY AND DROUGHT STRESS

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Abstract:

Oil palm (*Elaeis guineensis* Jacq.) is an oilseed crop of great economic importance. The oil palm industry has a large-scale production worldwide and uses high efficient extraction and refining processes to obtain palm oil and palm kernel oil. In Brazil, currently, there is an extensive area suitable for oil palm planting outside the Amazon rainforest; however, these areas go through long periods of water scarcity and demand artificial irrigation to be sustainable. One-quarter of the irrigated area in agriculture has a problem with salinity stress. Studies show that microRNAs (miRNAs) play roles in transcription and post-transcriptional regulation of gene expression and are essential molecules in the response of plants to abiotic stress. Our research group performed a comprehensive and large-scale miRNA analysis to characterize the miRNA population in oil palm exposed to drought and saline stresses, aiming to identify putative miRNA target genes in the oil palm genome, and perform an in silico comparison of the expression profile of miRNAs and their putative target genes. Leaf samples collected from young oil palm trees submitted to water deprivation (14 days) or salt stress (12 days). Small RNA-seq datasets underwent rigorous curation and subsequent analysis of differential expression and functional annotation using appropriate software. Seventy-nine and 81 miRNAs appeared in salinity and drought stress, respectively, being 52 known miRNAs and 29 new miRNAs. Those miRNAs with a significant difference in expression (probability $\geq$ 0.95) under saline stress were all down-regulated; on the other hand, under drought conditions, 62 were significantly differentially expressed under drought stress, with five up-regulated and 57 down-regulated. Functional annotation of the differentially expressed putative target genes under saline and drought stress showed several transcription factors. Overexpression or knockout of such genes resulted in tolerance to these abiotic stresses in other plant species. Therefore, our study provides new insights into the early response of young oil palm plants to saline and drought stress and confirms an expected preponderant role of transcription factors along with some long non-coding RNAs (lncRNAs). Furthermore, it points out potential salt and drought-responsive miRNAs and their putative target genes that are candidate genes for producing genetically modified/edited oil palm plants tolerant to these two abiotic stresses.

Palavras-chave: Abiotic stress; tolerance; transcription factor; non-coding RNA; oil palm