

## TRANSCRIPTOMIC INSIGHTS ON FRUIT RIPENING OF TWO VARIETIES OF AMAZON AÇAÍ PALM (*EUTERPE OLERACEA* MART.).

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### Abstract:

Açaí palm (*Euterpe oleracea* Mart.) produces one of the most consumed fruits in the north of Brazil and its production chain has now expanded worldwide, contributing to the Amazon bioeconomy. Our research aimed to sequence the transcriptome of the white and purple fruit in three maturation stages in order to generate knowledge that could be further applied to the açaí production chain. Experiments were designed to compare intra-variety gene expression (purple açaí on phase 2 vs. purple açaí on phase 3; purple phase 3 vs. purple phase 4; white phase 2 vs. white phase 3; white phase 3 vs. white phase 4) and between varieties at the same stage (purple açaí on phase 2 vs. white açaí on phase 2; purple phase 3 vs. white phase 3; purple phase 4 vs. white phase 4). Total RNA was extracted using illustra RNAspin Mini kit (GE Healthcare) and cDNA libraries were sequenced on Ion GeneStudio S5 platform (Thermo Fisher Scientific). Isoforms were *de novo* assembled using Trinity. Reads were mapped against isoforms using FPKM method and differential expression was obtained using DESeq2. Differentially Expressed Genes (DEGs) were determined using Log2FoldChange > 2 and p-value < 0,05. A total of 69,405 gene isoforms were obtained. Our data demonstrated that global gene expression pattern of white and purple açaí in phase 2 were relatively similar compared to the other two phases. Global gene expression starts to change drastically between varieties in phases 3 and 4. The biosynthetic pathway of anthocyanins was of particular interest due to their antioxidant activity and chemical characteristics that give different colors to fruits. Our data showed that during fruit ripening the key flavonoid-producing enzyme chalcone synthase (CHS) was down regulated, suggesting a decrease in the synthesis of these metabolites. The exception occurred between phases 3 and 4 of purple açaí, where the CHS expression remained constant. The same gene expression profile was observed for the second enzyme of the pathway, chalcone isomerase (CHI). Interestingly, the difference in color between the fruits of the two varieties seems to depend on the activity of the enzyme flavonoid 3',5'-hydroxylase (F3'5'H) which, together with the enzyme flavonoid 3'-hydroxylase (F3'H), are responsible for determining the B-ring hydroxylation pattern and consequently the anthocyanin color. The F3'5'H gene was up regulated in the phase 3 of the purple açaí transcriptome and down regulated during phase 4 of the white açaí. This enzyme is responsible for the production of the dark-purple anthocyanin, delphinidin 3-glucoside. It is worth noting that, for some plants, the substrate specificity of the enzyme dihydroflavonol 4-reductase (DFR) influences the anthocyanin chemical composition and fruit pigmentation. However, our analysis found only one DFR isoform thus it is unlikely that its substrate specificity influences more than F3'5'H activity in the production of açaí purple pigmentation. Future genomic analyzes will allow us to assess the influence of other genetic traits on the fruit ripening process such as DNA methylation and SNPs.

**Palavras-chave:** Açaí; Amazon; RNA-Seq; ;

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