

Additional files

Elucidating The Mesocarp Drupe Transcriptome of Açaí (*Euterpe oleracea* Mart.), An Amazonian Palm Tree Producer of Bioactive Compounds.

Elaine dos Santos, Hubert Schaller, Artur Silva, Hervé Rogez, Sylvain Darnet*

*Correspondence: Correspondence: Sylvain Darnet shd@laposte.net

Additional file S1: **Table S1.** Quality and completeness statistics of *Euterpe oleracea* transcriptomes obtained during *de novo* assembly optimization. **(A)** Single *k*-mer results. **(B)** Multiple *k*-mer additive approaches. Statistics were calculated using BUSCO pipeline with plant section and Transrate tool with *Phoenix dactylifera* proteome. Read coverage and mapping statistics were obtained using bowtie, SAMtools, and in-house shell scripts. **Table S2.** *Euterpe oleracea* transcripts with functional annotation retrieved from Blast2GO. UniProt database, section *Viridiplantae*, was used to performed BLASTX search with e-value of 1e-3. **Table S3.** Gene Ontology enrichment terms in genes restricted to *Euterpe oleracea*. Gene list restricted to *Euterpe oleracea* is based on singleton category in OMA pipeline. The GO enrichment test was based on Fisher-test performed in Blast2GO, comparing the list of restricted genes and all genes predicted in the transcriptome. An FDR of 5% was considered as the cut-off for enrichment. **Table S4.** Genes of *Euterpe oleracea* with positive selection. The detection was based on all orthologs groups present as single-copy in the *Euterpe oleracea*, *Phoenix dactylifera*, *Arabidopsis thaliana* and *Elaeis guineensis*. The POTION pipeline was used to detect the positive selection with site-models from CodeML/PAML. **Table S5.** Genes from anthocyanin pathway in *Arabidopsis thaliana*, *Vitis vinifera*, *Solanum lycopersicum*, *Euterpe oleracea*, *Phoenix dactylifera* and *Elaeis guineensis*. All orthologs and paralogs of *Arabidopsis thaliana* genes associated with anthocyanin pathways were retrieved using OMA pipeline. Splicing isoforms are marked with an X symbol. **Table S6.** Genes from tocopherol pathway in *Arabidopsis thaliana*, *Vitis vinifera*, *Solanum*

lycopersicum, *Euterpe oleracea*, *Phoenix dactylifera* and *Elaeis guineensis*. All orthologs and paralogs of genes associated with anthocyanin pathways were retrieved using OMA pipeline. Splicing isoforms are marked with an X symbol. **Table S7.** EST-SSRs predicted in *Euterpe oleracea* transcriptome and inter-species transferability to *Phoenix dactylifera* and *Elaeis guineensis*. (A) List of all SSRs positions detected by MISA tool. (B) Primer pair list designed by Primer3 to amplify SSRs with the flanking sequence in the transcripts. (C) List of SSRs found in the three palm trees. **Table S8.** Transcript annotation and classification in OMA groups. The orthology inference was performed using OMA and proteome predicted in *Arabidopsis thaliana*, *Vitis vinifera*, *Solanum lycopersicum*, *Euterpe oleracea*, *Phoenix dactylifera* and *Elaeis guineensis*. For each transcript, the classification in OMA groups, i.e., Hierarchical group (HOG_group column) and Orthologous group (OMA_group column; one-to-one ortholog), was reported. The other information is about the transcript, as organism origin (species), accession number in UniProt (access_number_protein), copy number in HOG group (species and copy_number in HOG, multicopy by species columns), the annotation in UniProt database (description column).

Additional file S2: **Figure S1.** Palm tree and fruit picture of açai (*Euterpe oleracea*). (a) The multi-stemmed tree palm of açai (*E. oleracea*). (b) Ripe black açai bunch. (c-f) Four stages of maturation of black and (g-j) variety white *E. oleracea* fruits. (c) Green fruits, (d) fruits at the beginning of maturation, (e) black fruits and (f) black fruits covered with a wax cuticle. (g) Unripe white açai fruit, (h) greenish yellow fruits, (i) mature fruits and (j) greenish yellow fruits covered with a wax cuticle. **Figure S2.** KEGG annotation of *Euterpe oleracea* transcriptome (a) Global view of classification; (b) categories found in metabolism; (c) Top 10 from “Biosynthesis of other secondary metabolites”

category. All y-axis is in transcript count. **Figure S3.** Distribution of EST-SSRs predicted in *Euterpe oleracea* transcriptome.

Additional file S3: **Data S1.** Orthoxml file with Hierarchical Groups. The inference was predicted by OMA tool and based on proteome comparison among species *Arabidopsis thaliana*, *Vitis vinifera*, *Solanum lycopersicum*, *Euterpe oleracea*, *Phoenix dactylifera* and *Elaeis guineensis*. **Data S2.** Orthoxml file with Orthologous Groups. The inference was predicted by OMA tool and based on proteome comparison among species *Arabidopsis thaliana*, *Vitis vinifera*, *Solanum lycopersicum*, *Euterpe oleracea*, *Phoenix dactylifera* and *Elaeis guineensis*.