



IV ISGPB

IV INTERNATIONAL SYMPOSIUM ON GENETICS
AND PLANT BREEDING

HOW HAS PLANT BREEDING CONTRIBUTED TO
FOOD SECURITY?



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Anais do IV Simpósio Internacional de Genética e Melhoramento de Plantas

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**Anais do IV International Symposium on
Genetics and Plant Breeding**

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RECURSOS GENÉTICOS



Area of concentration: Genomic Analysis

THE COMPLETE CHLOROPLAST GENOME SEQUENCE OF *Euterpe Precatoria*

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Açaí palm (*Euterpe precatoria*) is an Amazonian tree species and is widely used for food and crafting purposes. Given its economic relevance, there is a wide interest in its conservation and breeding. Despite this interest, little is known about the genomics of *E. precatoria*. In this work we publish the complete chloroplast genome sequence of the species. Chloroplast genomes are known for having a conserved structure and are useful to explore evolutionary questions and to provide markers that unveil the genetic diversity within and between species. Our objective was to assemble and characterize *E. precatoria*'s plastid genome and to perform a comparative analysis to other species within the *Arecaceae* family. Using Illumina reads, the assembly was obtained using the Fast-Plast pipeline. Gene content, as well as tRNA and rRNA sequences were annotated using the GeSeq web interface. Microsatellite loci were identified using MISA. The comparative analysis of the chloroplast genomes of different species of *Euterpe* was carried out using mVISTA. The phylogenomic relationship between the plastid genome of *E. precatoria* and those of other 13 species within *Arecaceae* was also estimated. The final assembly size was 159,282 bp and presented the expected quadripartite structure. A total of 113 genes were annotated, of which 95 were single-copy and 18 were duplicated in the inverted regions. A total of 276 microsatellite loci were identified, the majority of which composed of mononucleotide motifs. The mVISTA analysis confirmed that a major part of plastid genomes is composed of very conserved sequences, especially in gene-coding regions. The phylogenomic tree revealed a closer proximity between *E. precatoria* and *E. oleracea*. Complementing its conserved organization, cpDNA of *E. precatoria* presents the same gene content as of other *Euterpe* species. Our results contribute to open the way for future evolutionary and comparative analysis within *Arecaceae*.

KEYWORDS: Açaí; cpDNA; Genome assembly.