

COMPARATIVE ANALYSIS OF *PIPER* L. CHLOROPLAST GENOME

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Abstract:

Piper aduncum L., *Piper hispidinervum* C.DC and *Piper* aff. *hispidinervum* C.DC are essential oil producing species that are promising alternative sources to obtain the compounds dilapiol, safrol and sarisan, respectively. Due to the high similarity among these species, regarding either morphological or cytogenetic characteristics, they are involved in a taxonomic controversy. Therefore, it is important to assess better resolution genomic information to clarify the taxonomic status of these three Brazilian native species. The aim of this work was to characterize and comparatively analyze the chloroplast genome of them. Chloroplast genomes were assembled in NOVOPlasty, using a data set of paired-end sequences (300 bp) generated in the Illumina HiSeq™ 4000 platform. Annotation was made in GeSeq-CHLOROBOX and circular graphic maps were visualized in OrganellarGenomeDRAW. The genomic alignment for comparative analysis was performed by the MAUVE algorithm. The *Piper* chloroplast genome showed a quadripartite structure, with small single-copy (SSC) region ranging from 18.515 to 18.897 bp (average of 18,554 bp), inverted-repeat regions (IRa and IRb) with same size and ranging from 27.023 to 27.047 bp (average of 27,038 bp) and long single-copy (LSC) region ranging from 88.692 to 88.727 bp (average of 88.705 bp). *P. aduncum* had a chloroplast genome with a size of 161,719 bp, composed of 163 genes, 93 coding sequences of proteins (CDS), 62 transfer RNA (tRNA) genes and 8 ribosomal (rRNA) genes. *P. hispidinervum* and *P. aff. hispidinervum* showed sizes of 161,287 and 161,257 bp, respectively. Both chloroplast genomes were composed of 88 CDS, 34 tRNA genes and 7 rRNA genes. Exclusive and shared genes were identified among species. The chloroplast genomes of *P. hispidinervum* and *P. aff. hispidinervum* were closer to each other, with similarities between the gene regions, and both were more distant from *P. aduncum*, indicating that *P. hispidinervum* is a distinct species from *P. aduncum* and *P. aff. hispidinervum* inherited the chloroplast genome (maternal inheritance) from *P. hispidinervum*.

Palavras-chave: Genome assembly; Quadripartite structure; Maternal inheritance; Long pepper ;

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