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Comparative of the complete chloroplast genome and RNA editing of Eucalyptus camaldulensis T5 clone, an elite variety in Thailand

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Abstract. Racharak P, Suttangkakul A, Vuttipongchaikij S. 2023. Comparative of the complete chloroplast genome and RNA editing of Eucalyptus camaldulensis T5 clone, an elite variety in Thailand. Biodiversitas 24: 3774-3784. Eucalyptus camaldulensis, T5 clone, the excellent fast-growing tree plantation in Thailand, was analyzed for the complete chloroplast genome and RNA editing. The complete excellent fast-growing tree plantation in Thailand, was analyzed for the complete chloroplast genome and RNA editing. The complete chloroplast genome revealed a total genome size of 160,204 by that divided into a large single copy (LSC) (88,904 bp) and a small single copy region (SSC) (18,506 bp) by inverted repeat regions (IR) containing 26,397 bp. A circular mapping genome and gene order showed the circle antiparallel mapping gene of 135 genes, including 37 tRNAs, 10 rRNAs, and 1 pseudogene. GC content of the genome was 56.87%. The comparative genomes analysis between the TS clone and *F. camaldulensis* from the NCBI database suggested that the thymine (T) and ademine (A) strongly impacted the indel and transversion process, which could be a point of mutation in the genome. Furthermore, 24 specific genes were used to investigate RNA editing. From all genes, only 11 genes were edited with C to U conversion. Triplet codons, 1UA, UJ, UJg and Ugg were the most frequently edited codon and expressions; the crucial influence of amino acid alterations. Due to RNA editing events, the physicochemical properties of amino acids were changed from polar to nomplete amino acids and from hydropolitic to intropolitie to involution acids. Physicochemical properties conversion is necessary to form complete amino acids and from hydrophilic to hydrophobic amino acids. Physicochemical properties or amino acids and from hydrophilic to hydrophobic amino acids. Physicochemical properties conversion is necessary to form complete amino acid sequences for several essential chloroplast proteins. The event might be the accumulation of amino acid alterations causing phenotypic variation for plant adaptation and evolution.

Keywords: Eucalyptus camaldulensis, complete genome, chloroplast, plastid, RNA editing

INTRODUCTION

Eucalyptus camaldulensis is an important species for Thai economics; it has been renowned extensively for raw materials in wood, pulp, paper industry, and bioenergy. In Thailand, *E. camaldulensis*, a T5 clone, has been improved by the breeding program to enhance growth and development to adapt and grow in unfavorable areas all over Thailand. This species tolerates various biotic and abiotic stresses more than other species imported for the breeding program, for example, E. grandis, E. globulus, E. urophylla, E. pellita, and E. tereticornis. E. camaldulensis, all T5 clones are the most outstanding salt and drought tolerance for abiotic stress compared to the other species. In the same way, for biotic stresses, a T5 clone can be capable of growing throughout in insect stress areas when it is high above 2-3 m from the ground, such as tolerance to a gall wasp in particular genus Leptocybe (Kumar et al. 2015; Mphahlele et al. 2021) Furthermore, they can tolerate to leaf spot, leaf blight, and rust disease. Moreover, E. camaldulensis is excellent for propagation in cutting and in vitro culture (Mendonça et al. 2016; García-Ramírez 2023).

The chloroplast genome contains approximately ±130 genes, and size varies, ranging from 15,553 to 521,168 base pairs (bp) in Asarum minus and Floydiella terrestris, respectively, chloroplast nucleoid copy range from 1,000 to 1,700 copies which highly variable number during the plant growth (Dobrogojski 2020). The chloroplast DNA (cpDNA) structure, inverted repeats (IR), the two identical regions separated by large single copy region (LSC) and small single copy region (SSC), have varied in size from 20,000 to 25,000 bp (Morley et al. 2019). In the *Eucalplus* genus, the first complete chloroplast genome was reported in E globulus (Steane 2005), following E. grandis (Paiva et al. 2011). The complete chloroplast genome of the Eucalyptus 2011) The complete entropiats genome of the Eucarphias genus has been reported in 29 species, including *E. camaldulensis*. The chloroplast genome of *Eucalyptus* comprises 112 individual genes with different genome sizes ranging from 159,257 bp (*E.* oblique) to 161,071 bp (*E. spathulata*). The total RNA mostly contains 45, and 5 genes for total RNA and 6 pseudogene. The total GC contents range from 36.82% to 36.98 %. Exon GC contents range from 39.03% to 39.11%, while intergenic GC contents were 31.28% to 31.61 % (Bayly et al. 2013).

RNA editing is a posttranscriptional event often occurring in plant mitochondria and chloroplast genomes Conversion of cytidine (C) to uridine (U) is the most frequent expression in the chloroplast genome. Furthermore, RNA editing causes the creation of an initial codon, a vital substance for conserving amino acids for protein synthesis, but it is a rare occurrence: for instance, a change in an ATG codon to an ACG codon in the psbL gene. The stop codon from RNA editing probably causes short amino acid

References

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