ABSTRACT

Ananas comosus var. erectifolius (L.B. Smith) Coppens & Leal, a tropical plant from Bromeliaceae family, has immense applications, especially for fiber production of excellent quality. The lack of available chloroplast (cp) genome information limits its breeding and application. Here, we assembled its complete cp genome using Illumina high-throughput sequencing technology. The cp genome size is 159,983 bp, with 37.4% GC content, including a large single copy region (LSC) of 87,787 bp, a small single copy region (SSC) of 18,606 bp, and a pair of inverted repeat regions (IRs) of 26,795 bp. It encodes 89 protein-coding, 38 tRNA and 8 rRNA genes. Phylogenetic analysis showed that A. comosus var. erectifolius was close to Ananas comosus. The complete cp genome sequences could provide valuable information for variety breeding and genetic analysis of agronomic and economic traits in A. comosus var. erectifolius.

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Ananas comosus (Accession number: AP014632.1) was used as the reference. Finally, the assembled complete cp genome was annotated by via PGA software (Qu et al. 2019). The complete chloroplast genome was submitted to GenBank with Accession no. MZ457322.

The total length of A. comosus var. erectifolius cp genome is 159,983 bp, with 37.4% GC content, comprising a pair of IRs 26,795 bp, separating the LSC region of 87,787 bp and SSC region of 18,606 bp. There were 135 genes, including protein-coding genes, 8 rRNA genes, and 38 tRNA genes. Among of them, 15 genes (trnK-UUU, rps16, trnG-GCC, atpF, rpoC1, trnL-UAA, trnV-UAC, petB, petD, ndhB, trnL-GAU, ycf68, trnA-UGC, ndhA) contained one intron, two genes (clpP and ycf3) contained two introns, while one gene (rps12) underwent trans-splicing.

Phylogenetic analysis was performed based on complete cp genomes of A. comosus var. erectifolius and other 20 related species reported in the Commelinids clade, Arabidopsis thaliana as outgroup. The chloroplast genome sequences were aligned with MAFFT 7.407 with default parameters (Nakamura et al. 2018), and then the maximum-likelihood tree was constructed by IQ-TREE 1.6.12 with the parameter (-bb 1000) (Nguyen et al. 2015). All the Ananas species formed a monophyly. The A. comosus var. erectifolius was a basal species in the Ananas genus (Figure 1). In conclusion, the characterized cp genome sequence of A. comosus var. erectifolius provides a useful genetic resource for future phylogenetic identification and analysis of important agronomic and economic traits.

Disclosure statement
No potential conflict of interest was reported by the authors.

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Ethics statement
Ananas comosus var. erectifolius (L.B. Smith) Coppens & Leal is a cultivated plant species, and is not listed in the appendices I, II and III of the Convention on the Trade in Endangered Species of Wild Fauna and Flora, that has been valid from 22 June 2021 (https://cites.org/eng/app/appendices.php). No approvals were required for this study, which complied with all relevant regulations.

Authors’ contributions
CYL and YHH conceived and designed the experiments. WZ analyzed and interpreted the data performed the experiments. CYL wrote the paper. All authors have read and approved the manuscript for publication, and all authors agreed to be accountable for all aspects of the work.
Data availability statement

The genome sequence data that support the findings of this study are openably available in GenBank of NCBI at (https://www.ncbi.nlm.nih.gov/nuccore/MZ457322) under the accession no. MZ457322. The associated BioProject, SRA, and BioSample numbers are PRJNA742473, SRR14998994, and SAMN19955712 respectively.

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