The complete chloroplast genome of *Hylotelephium erythrostictum* (Miq.) H. Ohba (Crassulaceae)

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*ABSTRACT*

The species *Hylotelephium erythrostictum* is well known as an ornamental plant in China. Here, we report the complete chloroplast genome (cp) of *H. erythrostictum* using the next-generation sequencing. It shows a total length of 151,707 bp with typical quadripartite structure. The genome is composed of the large single copy region (LSC) of 83,070 bp, the small single copy region (SSC) of 17,018 bp, and two separated inverted regions (IRs) of 25,793 bp, respectively. It contains 134 genes, including 80 protein-coding genes (PCGs), 8 rRNA genes, and 37 tRNA genes. The overall GC content of the cp genome is 37.7%. Maximum likelihood (ML) tree based on ten complete chloroplast genomes of Crassulaceae and one outgroup species suggested a monophyly formed by *H. erythrostictum* together with *Hylotelephium ewersii*, which demonstrate a comparably closer phylogenetic relationship. The complete chloroplast genome of this *H. erythrostictum* provides valuable information and further phylogenetic reconstruction of the Crassulaceae family.
content of the cp genome is 37.7%. The whole cp genome of *H. erythrostictum* contains 134 genes with 80 PCGs, 37 tRNA genes, and 8 rRNA genes. Among these genes, 60 PCGs and 22 tRNA genes are located in the LSC region, while 12 PCGs and one tRNA gene occur in the SSC region. All these eight rRNA genes are duplicated in the IR regions. IR regions contain six PCGs and seven tRNA genes, if counting only once. Among the annotated genes, a total of 15 genes contain one intron, which are *trn*K-*UUU*, *trn*L-*UAA*, *rps*16, *trn*V-*UAC*, *ndh*F, *trn*G-*GCC*, *trn*I-*GAU*, *trn*A-*UGC*, *atp*F, *ndh*A, *rpo*C1, *pet*D, *pet*B, and *rpl*16, while three genes including *clp*P, *ycf*3, and *rps*12 possess two introns. The numbers and genes that contain one or two introns are exactly the same as *Sedum tricarpum*, which is largely due to the low variation based on cpDNA genome and the relatively close phylogenetic relationship between *H. erythrostictum* and *Sedum tricarpum* in the Crassulaceae family. A well supported phylogenetic tree is reconstructed, suggesting a monophyly formed by *H. erythrostictum* together with *H. ewersii* (Figure 1). The two species demonstrate a comparably closer phylogenetic relationship with the clade consisting of *Graptopetalum amethystinum*, *Sedum lineare*, *Rosularia alpestris*, and *Aeonium arboreum*.

**Funding**

This research was supported by the National Natural Science Foundation of China [82174272, 31470312], the Research Project of Zhejiang Chinese Medical University [2020ZG33].

**Data availability statement**

The complete chloroplast genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) under the accession no. MZ519882. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA749471, SRR15239599, and SAMN20371389, respectively.

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