MITOCHONDRIAL DNA PART B
2022, VOL. 7, NO. 10, 1876–1878
https://doi.org/10.1080/23802359.2022.2135404

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

OPEN ACCESS Check for updates

# Characterization of the complete chloroplast genome sequence of *Elaeagnus henryi* Warb. ex Diels (Elaeagnaceae)

Qinxiang Chang[a], Yan Li[a], Xiang Chen[b], Yan Yan[c] and Pengguo Xia[b]

[a]Department of Art Design, Taiyuan University, Taiyuan, China; [b]College of Life Sciences and Medicine, Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, Zhejiang Sci-Tech University, Hangzhou, China; [c]College of Life Science, Shaanxi Key Laboratory of Chinese Jujube, Yan'an University, Yan'an, China

**ABSTRACT**

*Elaeagnus henryi* Warb. ex Diels belongs to the Elaeagnaceae. Here, we reveal the complete chloroplast genome of *Elaeagnus henryi*. The complete chloroplast genome is 152,244 bp in length and contains a large single-copy (LSC) region of 82,235 bp, a small single-copy (SSC) region of 18,279 bp and a pair of inverted repeats (IRs) of 25,865 bp. There are 126 genes, including 81 protein-coding, 37 transfer RNA (tRNA), and eight ribosomal RNA (rRNA) genes. The total GC content of the chloroplast genome sequence is 37.1%. The maximum-likelihood phylogenetic analysis indicated that *E. henryi* was sister to *Elaeagnus pungens* (MW145133). The result may be because the species are advanced and developed from the same ancestor.

**ARTICLE HISTORY**
Received 15 May 2022
Accepted 9 October 2022

**KEYWORDS**
Chloroplast genome; Elaeagnaceae; *Elaeagnus henryi* Warb. ex Diels; phylogenetic analyses

*Elaeagnus henryi* Warb. ex Diels (*Elaeagnus henryi* Warb. ex Diels, Lecomte 1915) is an evergreen erect shrub with spiny, thorny leaf axils, and slightly curved. Leaves are leathery to thickly leathery, broadly elliptic, or obovate. The fruit is oblong, juicy, and red when ripe; the core is covered with silky cotton wool (Figure 1), distributed in Shaanxi, Hubei, Yunnan, Guangdong, and other places. Fruits are edible and stem bark can be used as paper or man-made fibers. The fruit stops dysentery, the leaf cures lung deficiency and shortness of breath, and cures vomiting blood or decocted water to wash scabies. However, current research on *E. henryi* is limited to its chemical composition, pharmacological effects, and cultivation strategies. The genetic background of *E. henryi* has been largely ignored. Here, we report and describe the complete chloroplast genome of *E. henryi* (GenBank accession number: MZ846204). This is the first report on the complete chloroplast genome of *E. henryi*, providing genomic and genetic resources for future molecular analyses.

Fresh leaves tissue of *E. henryi* was collected from Pingli County, Ankang City, Shanxi Province (32°18′34.23″ N, 109°19′7.2″ E, altitude 619 m). The voucher specimen was preserved at XBGH (The Herbarium of Xi'an Botanical Garden, http://www.xazwy.com) (voucher number: *Lulu Xun* et al. LB19896 and xunlulu@xab.ac.cn). Total genomic DNA was extracted using CTAB method (Doyle and Doyle 1987), and the cDNA library was prepared and sequenced with the Illumina Hiseq X-Ten platform (Illumina Inc., San Diego, CA).

**Figure 1.** The species reference image of *E. henryi*.

**CONTACT** Yan Yan sunnylikeme@163.com College of Life Science, Shaanxi Key Laboratory of Chinese Jujube, Yan'an University, Yan'an 716000, China; Pengguo Xia xpg_xpg@zstu.edu.cn College of Life Sciences and Medicine, Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, Zhejiang Sci-Tech University, Hangzhou 310018, China

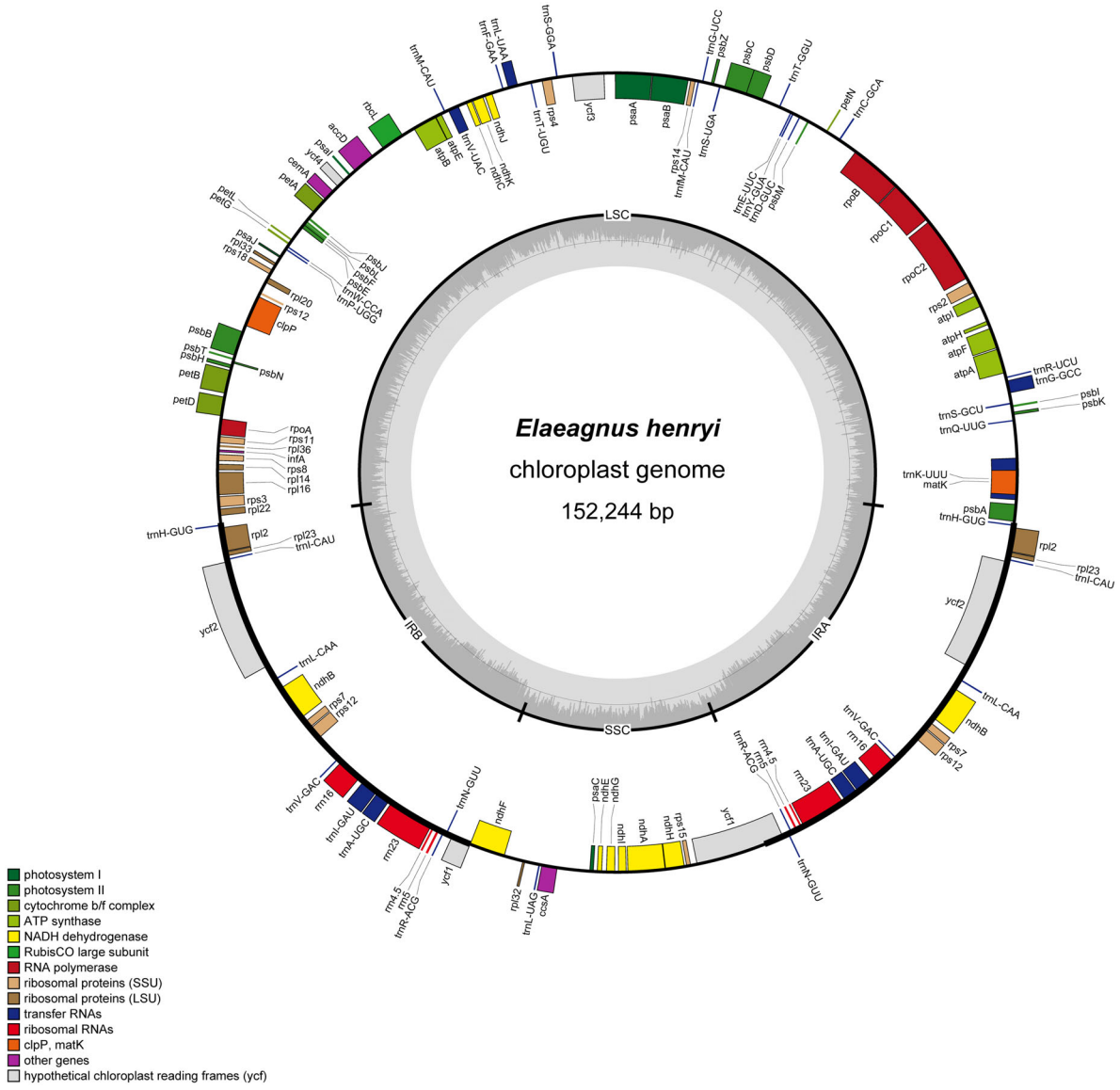


**Figure 2.** The genome map of *E. henryi*.

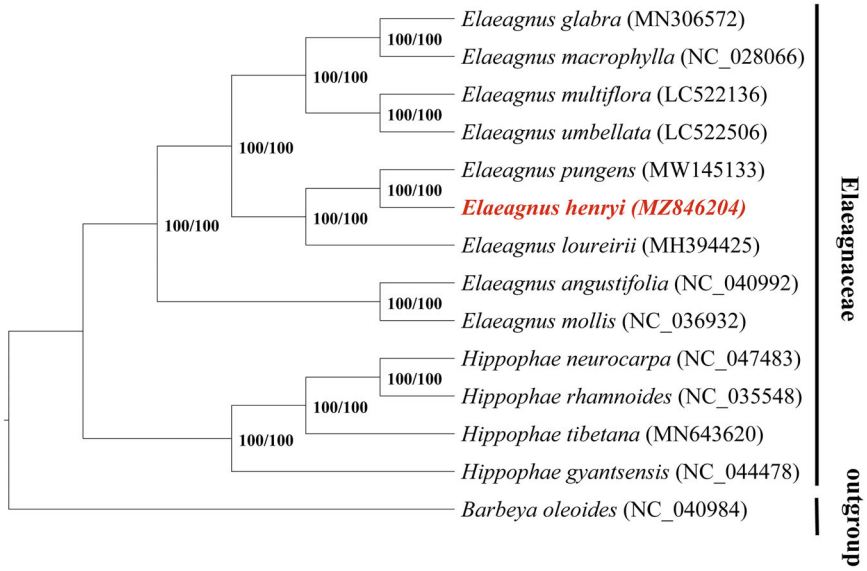


**Figure 3.** Molecular phylogeny of *E. henryi* and other related species based on the complete chloroplast genome. The complete chloroplast genome is downloaded from GenBank and the phylogenetic tree is constructed by the maximum-likelihood method with the best-selected K3Pu + F+R2 model and 1000 bootstrap replicates. Numbers above the branches represent bootstrap values from maximum-likelihood analyses, respectively.

The sequencing library was constructed by the Illumina Hiseq™ platform with an insert size of about 400 bp. The sequences were filtered following the protocol of Yao et al. (2016). A total of 3 Gb clean data were de novo assembled by SPAdesv.3.11.0 software (Bankevich et al. 2012). The extracted DNA was deposited at Key Laboratory of Plant Secondary Metabolism and Regulation of Zhejiang Province, Zhejiang Sci-Tech University (http://sky.zstu.edu.cn).

Then, the software NOVOPlasty v2.7.2 (Dierckxsens et al. 2017) was used to assemble the complete chloroplast genome of *E. henryi* with default settings. The sequence was annotated using Geneious Prime software, and the complete chloroplast genome annotation of *E. henryi* was thus obtained and submitted to GenBank (accession number MZ846204).

The complete chloroplast genome sequence of *E. henryi* (GenBank accession number MZ846204) was 152,244 bp, and the total GC content of the chloroplast genome sequence is 37.1%. The chloroplast genome consists of two reverse repeat regions (IR repeat) of 25,865 bp, a large single-copy (LSC) region of 82,235 bp, and a small single-copy (SSC) region of 18,279. We found that the complete chloroplast genome encoded 126 genes, including 81 protein-coding genes, 37 transfer RNA (tRNA) genes, and eight ribosomal RNA (rRNA) genes (Figure 2).

The evolutionary relationships of *E. henryi* and other 14 related species from Elaeagnaceae were analyzed using the whole chloroplast genome sequences. One species, *Barbeya oleoides* from Barbeyaceae (NC_040984) was selected as the outgroup according to the results of Choi et al. (2015). Sequence alignment was conducted using MAFFT version 7.0 (Katoh et al. 2019) and phylogenomic analysis was conducted using the maximum-likelihood (ML) methods with the IQTREE v1.6.7 (Nguyen et al. 2015) tools. The ML analyses were performed using K3Pu + F+R2 as the best-fit nucleotide substitution model and 1000 bootstrap replicates. The result of the analysis showed that the *E. henryi* has the closest relationship with *Elaeagnus pungens* (GenBank accession number MW145133). Furthermore, the phylogenetic tree also reflected the relationship among *E. henryi* and other species (Figure 3). The complete chloroplast genome sequence of *E. henryi* can provide necessary data for phylogenetic studies of Elaeagnaceae. It is hoped that this study will help resolve the intrageneric and interspecific phylogeny of Elaeagnaceae.

## Acknowledgements

This work was supported by Doctoral Support Project of Yan'an University (YDBK2019-64). The species was identified by Lulu Xun who was from Xi'an Botanical Garden.

## Ethical approval

Research and collection of plant material was conducted according to the guidelines provided by Xi'an Botanical Garden. Permission was granted by Hangzhou Academy of Agricultural Sciences to carry out research on the species.

## Author contributions

P. X.: conceived and designed this study. Y. L., X. C., and Q. C.: substantial contributions to the acquisition, analysis, and interpretation of data for the work. Y. Y. and P.X.: wrote the manuscript, drafting the work, and revising it critically for important intellectual content. All authors have read and agreed to the published version of the manuscript.

## Disclosure statement

The authors report no conflicts of interest.

## Funding

This work was supported by Doctoral Support Project of Yan'an University [YDBK2019-64].

## ORCID

Pengguo Xia http://orcid.org/0000-0003-3572-7616

## Data availability statement

The data that support the findings of this study are openly available in NCBI (https://www.ncbi.nlm.nih.gov) GenBank with the accession number (MZ846204). The associated BioProject, SRA, and BioSample numbers are PRJNA756420, SRR15533155, and SAMN20865498, respectively.

## References

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.

Choi KS, Son OG, Park SJ. 2015. The chloroplast genome of *Elaeagnus macrophylla* and trnH duplication event in Elaeagnaceae. PLOS One. 10(9):e0138727.

Dierckxsens N, Mardulyn P, Smits G. 2017. NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic Acids Res. 45(4):e18.

Doyle JJ, Doyle JL. 1987. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. Phytochem Bull. 19:11–15.

Katoh K, Rozewicki J, Yamada KD. 2019. Mafft online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform. 20(4):1160–1166.

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.

Yao X, Tan YH, Liu YY, Song Y, Yang JB, Corlett RT. 2016. Chloroplast genome structure in *Ilex* (Aquifoliaceae). Sci Rep. 6:28559.