

Complete chloroplast genome of *Lycium ferocissimum* (Solanaceae), a species native to South Africa

Zhao Li^a, Xinyi Zhang^a, Qingde Zhang^a and Gulbar Yisilam^b

^aKey Laboratory of Plant Stress Biology, School of Life Sciences, Henan University, Kaifeng, China; ^bXinjiang Key Laboratory of Special Species Conservation and Regulatory Biology, Key Laboratory of Plant Stress Biology in Arid Land, College of Life Science, Xinjiang Normal University, Urumqi, China

ABSTRACT

Lycium ferocissimum, known as African boxthorn or boxthorn, is a shrub in the Solanaceae family. In this study, we characterized the complete chloroplast (cp) genome sequence of *L. ferocissimum* using genome skimming data. It had a circular mapping molecular with the length of 155,894 bp, with a large single-copy region (LSC, 86,536 bp) and a small single-copy region (SSC, 18,406 bp) separated by a pair of inverted repeats (IRs, 25,476 bp). The cp genome encodes 113 unique genes, consisting of 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes, with 20 duplicated genes in the IR regions. The phylogenetic analysis indicated that *L. ferocissimum* is sister to the other three *Lycium* species.

ARTICLE HISTORY

Received 26 December 2019
Accepted 7 January 2020

KEYWORDS

Lycium ferocissimum;
chloroplast genome;
phylogeny inference

Solanaceae are a monophyletic group containing approximately 100 genera and 2500 species (D'Arcy 1991; Olmstead and Bohs 2007). Species of this family occur on all temperate and tropical continents, and many of which are the world's most important agricultural species, including potatoes, tomatoes, eggplants, tobacco and chili peppers (Olmstead et al. 2008). However, the phylogeny of Solanaceae has remained obscure due to sparse taxonomic sampling and the limited resolving power of the DNA regions studied. *Lycium ferocissimum* Miers, known as African boxthorn or boxthorn, is a shrub in the Solanaceae family. The species is native to Cape Province and Orange Free State in South Africa and has become naturalized in Australia and New Zealand (Roy et al. 2004). In this study, we reported and characterized the complete cp genome of *L. ferocissimum* using genome skimming data. The genome sequence was registered into GenBank with the accession number MN866909.

One *L. ferocissimum* individual was collected from Cape Town (South Africa; 18°26'57.66"E, 30°36'00.34"S) and a voucher specimen (*Pan Li LP174773*) was deposited at the Herbarium of Zhejiang University (HZU). Genomic DNA was extracted from silica-dried leaf tissue using Plant DNAzol Reagent (LifeFeng, Shanghai). The cp genome was reconstructed based on the paired-end library (≤ 800 bp) data which sequenced on an Illumina HiSeq X10 at Beijing Genomics Institute (BGI, Wuhan, China) with *Lycium ruthenicum* (GenBank accession number: MG29825; Yisilam et al. 2018) as a reference. We annotated the cp genome implemented in Geneious R11 (Biomatters, Auckland, New Zealand) according to descriptions of previous studies (Liu et al. 2017, 2018). Phylogenetic tree for 19 complete cp

genome sequences of Solanaceae was inferred using the maximum likelihood (ML) method implemented in RAXML-HPC v8.1.11 on the CIPRES cluster (Miller et al. 2010) with *Cressa cretica* and *Ipomoea purpurea* as outgroups.



The cp genome of *L. ferocissimum* was 155,894 bp long comprising a pair of inverted repeat regions (IRs with 25,476 bp) divided by two single-copy regions (LSC with 86,536 bp and SSC with 18,406 bp). The cp genome encoded a total of 133 genes, of which 113 were unique and 20 were duplicated in the IR regions. The 113 unique genes consisted of 79 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. The overall GC content of the total length, LSC, SSC, and IR regions is 37.9%, 35.9%, 32.3% and 43.2%, respectively. Maximum likelihood (ML) analyses showed that a good resolution of the species of Solanaceae with strong support for all the nodes. The phylogenetic tree revealed that the four *Lycium* species formed one clade with full support, and *L. ferocissimum* is sister to the rest species within the genus (Figure 1).

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

This work was supported by the Key Scientific Research Projects of Colleges and Universities in Henan Province in 2019 [Grant No. 19A180001].

CONTACT Qingde Zhang  qdzhang@henu.edu.cn  Key laboratory of Plant Stress Biology, School of Life Sciences, Henan University, Kaifeng, 475001, China

© 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

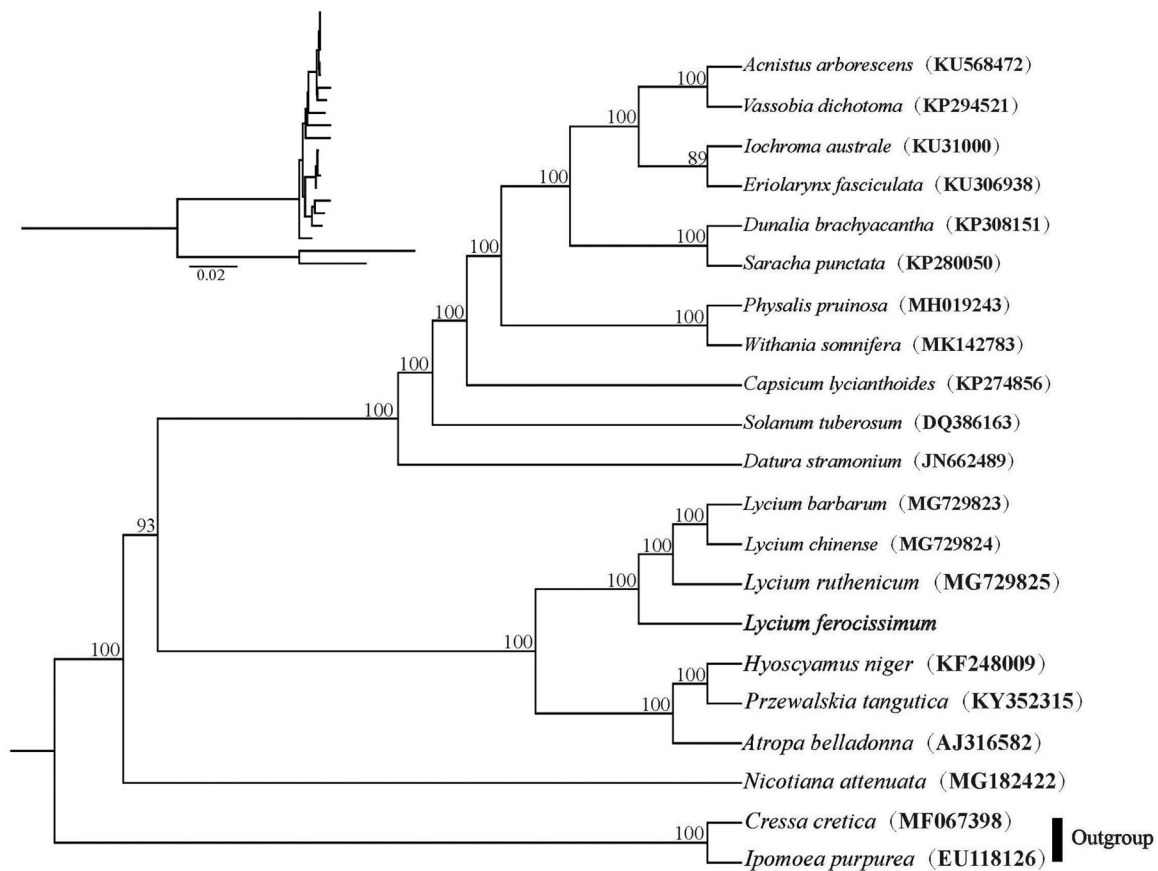


Figure 1. Phylogenetic relationships of Solanaceae inferred based on whole chloroplast genome sequences. Relative branch lengths are indicated at the top-left corner. Numbers above the branches represent bootstrap values from maximum-likelihood analyses.

References

- D'Arcy WG. 1991. The Solanaceae since 1976, with a review of its biogeography. In: Hawkes JG, Lester RN, Nee M, Estrada N, editors. Solanaceae III: taxonomy, chemistry and evolution. Kew: Royal Botanical Gardens; p. 75–138.
- Liu LX, Li R, James RP, Worth J, Li X, Li P, Cameron KM, Fu CX. 2017. The complete chloroplast genome of Chinese bayberry (*Morella rubra*, Myricaceae): implications for understanding the evolution of Fagales. *Front Plant Sci.* 8:968.
- Liu LX, Li P, Zhang HW, Worth J. 2018. Whole chloroplast genome sequences of the Japanese hemlocks, *Tsuga diversifolia* and *T. sieboldii*, and development of chloroplast microsatellite markers applicable to East Asian *Tsuga*. *J Forest Res.* 23(5):318–323.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. *IEEE Gateway Computing Environments Workshop (GCE)*; Deember 23; New Orleans (LA): IEEE; p. 1–8.
- Olmstead RG, Bohs L. 2007. A summary of molecular systematic research in Solanaceae: 1982–2006. VI International Solanaceae Conference: Genomics Meets Biodiversity; Madison (WI); p. 255–268.
- Olmstead RG, Bohs L, Migid HA, Santiago-Valentin E, Garcia VF, Collier SM. 2008. A molecular phylogeny of the Solanaceae. *Taxon.* 57(4): 1159–1181.
- Roy B, Popay I, Champion P, James T, Rahman A. 2004. An illustrated guide to common weeds of New Zealand. 2nd edition. Lincoln (New Zealand): New Zealand Plant Protection Society; p. 314. pp.
- Yisilam G, Mamut R, Li J, Li P, Fu CX. 2018. Characterization of the complete chloroplast genome of *Lycium ruthenicum* (Solanaceae). *Mitochondrial DNA Part B.* 3(1):361–362.