Characterization of the complete chloroplast genome of endangered Cycads Zamia fischeri Miq. ex Lem

Jin-Yan Lei, D. D. Hinsinger, Guo-Feng Jiang

MITOCHONDRIAL DNA PART B
2018, VOL. 3, NO. 2, 1059–1061
https://doi.org/10.1080/23802359.2018.1508387

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

Characterization of the complete chloroplast genome of endangered Cycads *Zamia fischeri* Miq. ex Lem

Jin-Yan Lei[a], Damien Daniel Hinsinger[a] and Guo-Feng Jiang[a,b]

[a]Plant Ecophysiology & Evolution Group, Guangxi Key Laboratory of Forest Ecology and Conservation, College of Forestry, Guangxi University, Nanning, Guangxi, PR China; [b]State Key Laboratory for Conservation and Utilization of Subtropical Agro-bioresources, Guangxi University, Nanning, Guangxi, PR China

ABSTRACT

The whole chloroplast (cp) genome sequence of *Zamia fischeri* has been characterized. The cp genome length was 164,767 bp in length, with a GC content of 39.7%, containing a large single copy (LSC) of 90,226 bp, a small single copy (SSC) of 23,223 bp, and a pair of inverted repeats (IRs) of 25,659 bp. The genome contained 127 genes, including 88 protein-coding genes, 31 tRNA genes, and 8 rRNA genes. A phylogenetic analysis based on complete chloroplast genomes in Cycads indicates that *Z. fischeri* clustered with another *Zamia* (*Z. furfuracea)*. This complete chloroplast sequence offers a promising tool for further species identification, population genetic conservation, and evolutionary studies of Zamiaceae, as well as for Cycadales.

ARTICLE HISTORY
Received 17 July 2018
Accepted 29 July 2018

KEYWORDS
Zamia fischeri; chloroplast; evolution; Cycads

Cycads are iconic relict species (Brenner et al. 2003), despite a recent diversification (Nagalingum et al. 2011; Xiao and Möller 2015; Jiang et al. 2016). With a total of 10 accepted genera and 351 accepted species in three families (Cycadaceae, Strangeriaceae, and Zamiaceae), Cycads are found in most of the tropical and subtropical regions (Calonje et al. 2013–2018). In the family Zamiaceae, *Zamia* consists of 77 species, most being endangered at different levels (Vovides and Chemnick 2010; Calonje et al. 2013–2018). *Zamia fischeri* Miq. is endemic to Mexico (San Luis Potosí, Querétaro, and Tamaulipas states) and is found from arid areas and open habitats to rainforests. It is listed as an endangered species due to severe natural habitat destruction (Vovides and Chemnick 2010). Therefore, a coordinated effort is urgently required to ensure its conservation, either *in situ* or *ex situ*.

Plastomes (cpDNA) used in conservation studies have been demonstrated to provide useful and abundant information on genetic diversity and evolution in many taxa (Ye et al. 2014; Gao and Gao 2017), and showed especially high-resolution phylogenetic tree in Cycads (Jiang et al. 2016). In this study, we assembled and characterized the plastome sequence of *Z. fischeri* based on Illumina pair-end data, and built a phylogenetic tree using plastomes available in Cycads.

Leaves from an individual *Z. fischeri* were collected in Xishuangbanna Tropical Botanical Garden (Menglun, PR China, 21°55′N,101°15′E). Total genomic DNA was extracted as previously described (Jiang et al. 2016; Xu et al. 2017). Library construction and sequencing were processed by Novogene (Beijing, PR China) using an Illumina HiSeq X Ten system (Illumina, San Diego, CA), according to the manufacturer instructions. We performed a *de novo* assembly as described previously (Hinsinger and Strijk 2017; Jiang et al. 2016). Genome annotation was performed using CpGAVAS (Liu et al. 2012).

We reconstructed the 164,767 bp long chloroplast of *Z. fischeri* (GenBank accession number MH311043). It contained a LSC, SSC, and a pair of inverted repeats (IRa and IRb) of 90,226, 23,223, and 25,659 bp, respectively (Figure 1). We identified 127 genes, including 88 protein-coding genes, 31 tRNA genes, and 8 ribosomal RNA genes. Of these genes, 13 genes were duplicated in the IR regions, including 4 protein-coding genes (*ndhB, ycf2, rps7, rps12*), 5 tRNA genes (*trnH-GTG, trnL-CAA, trnN-GTT, trnR-ACG*, trnV-GAC), and 4 rRNA genes (*4.5S, 5S, 16S, 23S*). Five genes (*ndhA, ndhB, rpl2, rpoC1, rps12*) contained one intron while two genes contained two introns (*clpP, ycf3*). The overall GC content of the plastome of *Z. fischeri* was 39.7%, while the GC content in LSC, SSC, IRa, and IRb regions were 38.8%, 36.9%, 42.4%, respectively.

Fourteen plastomes of cycads were retrieved from GenBank (accessed 2018/05/15), plus *Ginkgo biloba* as an outgroup (Figure 1), and aligned with MAFFT (Katoh and Standley 2013). We built a maximum likelihood (ML, TPM1uf + I + G model, 1000 bootstraps) tree using PHYML v3.3 (Guindon et al. 2009). All but one nodes were highly supported (BP ≥94%), with the two *Zamia* clustering together. The results of this phylogenetic analysis are highly consistent with a previous plastome-based study (Jiang et al.

CONTACT Guo-Feng Jiang gfjiang@gxu.edu.cn Plant Ecophysiology & Evolution Group, Guangxi Key Laboratory of Forest Ecology and Conservation, College of Forestry, Guangxi University, DaXueDongLu 100, Nanning, Guangxi 530005, PR China

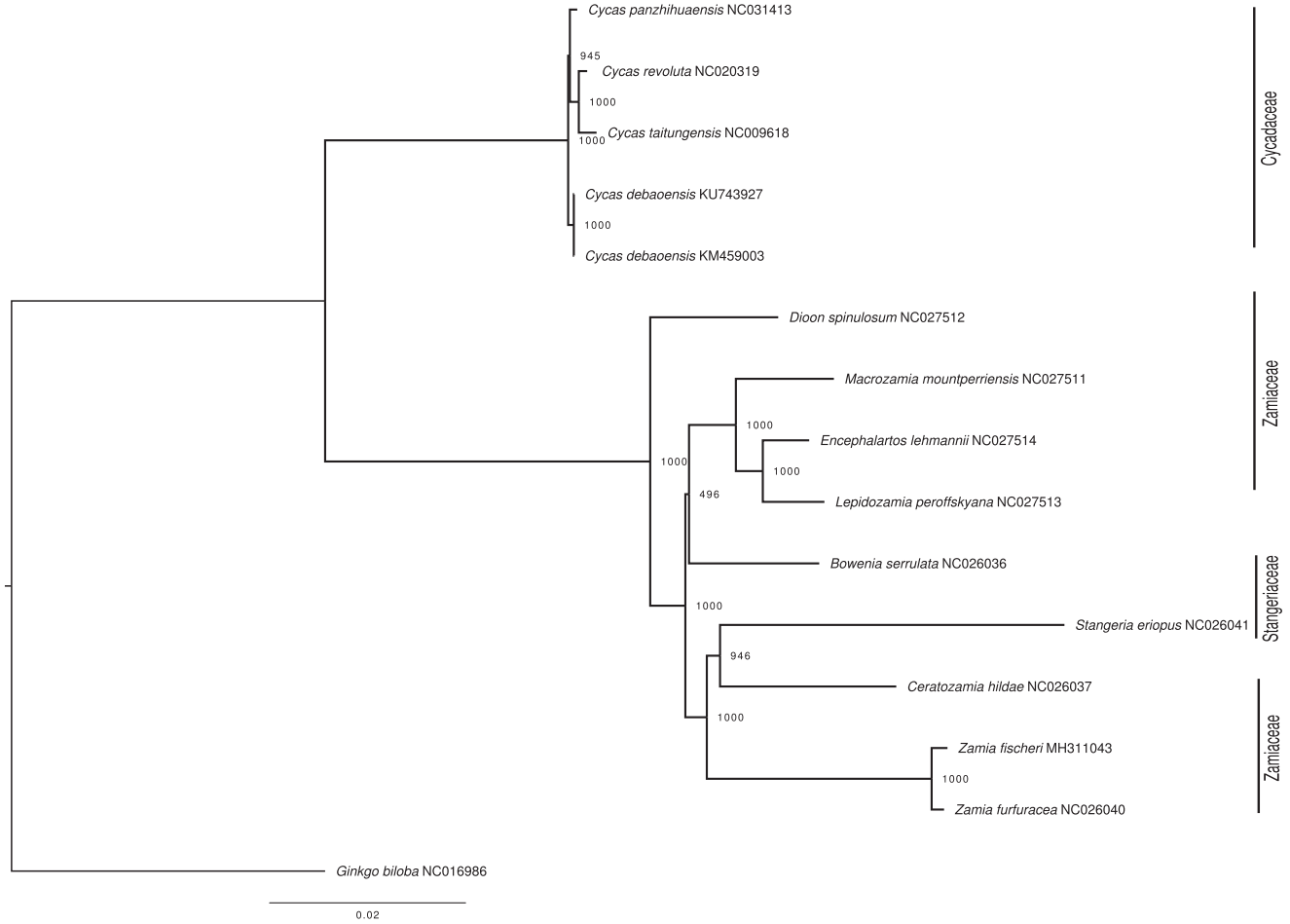

Figure 1. ML phylogenetic tree of the 14 available chloroplasts of Cycadales retrieved from GenBank, plus the plastome of *Ginkgo biloba* as outgroup. Bootstraps values (1000 replicates) are shown at the nodes. Scale in substitution per site.

2016). The plastome of *Z. fischeri* provides a useful bio-resource that will help to assess population diversity and demography for conservation purposes, and will also benefit to further genetic studies in Zamiaceae.

Acknowledgements

We would like to acknowledge the technical staff of the Xishuangbanna Tropical Botanical Garden (X.T.B.G., Chinese Academy of Sciences) for their assistance in collecting the specimen of *Z. fischeri*.

Disclosure statement

The authors report no conflicts of interest.

Funding

This work was supported by grants from the Natural Science Foundation of Guangxi Province of China [2014GXNSFBA118075 and 2015GXNSFAA139085] to G-F Jiang, China Postdoctoral Science Foundation Grants [No. 2015M582481 and 2016T90822] to Damien D. Hinsinger.

ORCID

Damien Daniel Hinsinger http://orcid.org/0000-0001-7459-7610
Guo-Feng Jiang http://orcid.org/0000-0002-3221-8608

References

Brenner ED, Stevenson DW, Twigg RW. 2003. Cycads: evolutionary innovations and the role of plant-derived neurotoxins. Trends Plant Sci. 8:446–452.

Calonje M, Stevenson DW, Stanberg L. 2013–2018. The world list of Cycads. [accessed 2018 July 16]. doi: http://cycadlist.org/.

Guindon S, Delsuc F, Dufayard J-F, Gascuel O. 2009. Estimating maximum likelihood phylogenies with PhyML. Methods Mol Biol. 537:113–137.

Gao CW, Gao LZ. 2017. The complete chloroplast genome sequence of semi-wild soybean, *Glycine gracilis* (Fabales: Fabaceae). Conservation Genet Resour. 9:343–343.

Hinsinger DD, Strijk JS. 2017. Toward phylogenomics of Lauraceae: the complete chloroplast genome sequence of *Litsea glutinosa* (Lauraceae), an invasive tree species on Indian and Pacific Ocean islands. Plant Gene. 9:71–79.

Jiang GF, Hinsinger DD, Strijk JS. 2016. Comparison of intraspecific, interspecific and intergeneric chloroplast diversity in Cycads. Sci Rep. 6:31473

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30:772–780.

Liu C, Shi L, Zhu Y, Chen H, Zhang J, Lin X, Guan X. 2012. CpGAVAS, an integrated web server for the annotation, visualization, analysis, and GenBank submission of completely sequenced chloroplast genome sequences. BMC Genomics. 13:715–721.

Nagalingum NS, Marshall CR, Quental TB, Rai HS, Little DP, Mathews S. 2011. Recent synchronous radiation of a living fossil. Science. 334:796–799.

Vovides A, Chemnick J. 2010. *Zamia fischeri*. The IUCN Red List of Threatened Species 2010. e.T42134A10662840. http://www.iucnredlist.org/details/full/42134/0 [accessed 2018 Jul 16].

Xiao LQ, Möller M. 2015. Nuclear ribosomal ITS functional paralogs resolve the phylogenetic relationships of a late-miocene radiation cycad Cycas (Cycadaceae). PLoS One. 10:e0117971

Xu LM, Hinsinger DD, Jiang GF. 2017. The complete mitochondrial genome of the *Agrocybe aegerita*, an edible mushroom. Mitochondrial DNA Part B. 2:791–792.

Ye C-Y, Lin Z, Li G, Wang Y-Y, Qiu J, Fu F, Zhang H, Chen L, Ye S, Song W, et al. 2014. *Echinochloa* chloroplast genomes: insights into the evolution and taxonomic identification of two weedy species. PLoS One. 9:e113657.