Complete mitochondrial genome sequence of *Acer miaotaiense* (Aceraceae)

Dan Liu**ab, Ping Ding**ab, Hai-Li Guoa, Ying Chenb, Kun Zhaoa, Hai-Ping Yanga, Ting Xuab, Li-Jiang Liuab,
Qi Jinga, Shang-Jun Hana, Bo-Qiang Tonga and Wen-Qing Lia

aShandong Provincial Center of Forest and Grass Germplasm Resources, Jinan, China; bShandong Forestry Protection and Development Service Center, Jinan, China; cLand Spatial Data and Remote Sensing Technology Institute of Shandong Province, Jinan, China

**ABSTRACT**

*Acer miaotaiense* P. C. Tsoong is a rare and endangered tree endemic to the Qinling Mountains of China and is listed as a national third-class protected plant. In this study, we sequenced the complete mitochondrial genome of *Acer miaotaiense* using the Illumina Novaseq 6000 and Nanopore platforms. The total mitochondrial genome length is 819,227 bp and has 69 genes, including 41 protein-coding, 25 tRNA, and 3 rRNA genes. The genome nucleotide composition was asymmetric, with an overall G + C content of 45.7%. Phylogenetic analysis indicated that *Acer miaotaiense* is closely related to the congeneric *Acer yangbiense*.

*Acer miaotaiense*, Aceraceae, is a deciduous tree named after its discovery location of Miaozi, Liuba County of Shanxi Province, by the Chinese botanist Zhong Buqiu in 1954, and is mainly distributed in the Shanxi and Gansu provinces of the central and western Qinling Mountains in China (IB-CAS 1989). Aceraceae has high utilization value, with its tough wood used in construction, and utensils manufacturing, its seeds for industrial oil, and its fruits, leaves and bark as raw materials of tannin extract (Zhou and Yao 2003). It has thus in recent years become the subject of biological, ecological, and genetic studies. Aceraceae has strict habitat requirements, and its natural populations currently exhibit dynamic characteristics of gradual decline (Meng et al. 2016). These populations’ genetic structures are characterized by low levels of genetic diversity associated with strong genetic differentiation, and of which genetic drift and inbreeding have been identified as the main influencing factors (Li et al. 2005). Understanding a species’ genetic structure and population genetic differentiation is essential prerequisites for formulating informed protection strategies.

Excellent germplasm resources are the basis for breeding and genetic improvements. Although the complete chloroplast genome of *A. miaotaiense* has been reported (Zhang et al. 2016), the species’ genetic information remains incomplete. The highly conserved nature and fast evolutionary rate of mitochondria make them an ideal tool for studying evolution and molecular ecology (Janouskovec et al. 2013). Therefore, in this study, we sequenced the complete *A. miaotaiense* mitochondrial genome, which will be helpful in exploring the species’ origin and evolution. This information will promote species molecular systematics and conservation genetics, and provide a reference for conducting theoretical studies.

The plant materials used in this study were collected from the Houzhenzi Ecological Experimental Forest Farm, Zhouzhi County, Xi’an City, Shaanxi Province (altitude:1,621 m, coordinates:33.856726°N, 107.789374°E), and subsequently submitted to the Acer gene bank (36.77°N, 117.471°E). A specimen was deposited at the herbarium of Shandong Provincial Center of Forest and Grass Germplasm Resources (Biao Han, hanbiao3361@shandong.cn) under barcode number SDF1003756. Total genomic DNA (saved in the DNA library of Shandong Provincial Center of Forest and Grass Germplasm Resources with the code mtq2016cp03) was extracted using a Plant DNA extraction Kit (TIANGEN, Beijing, China) according to the manufacturer’s instructions.

We used both Nanopore GridION sequencing (Oxford Nanopore Technology, Oxford Science Park) and Illumina Novaseq 6000 platforms to sequence and construct the library of raw sequence data (Nanopore raw data was 12.9 Gb, N50 is 8,784 bp and Illumina raw data was 10.46 Gb). After filtering, clean data were used to assemble de novo the mitochondrial genome using Canu 2.1 with default settings (Koren et al. 2017). We used Blastn and tRNA scan-SE 2.0 to annotate the protein coding, rRNA, and tRNA genes (Lowe and Eddy 1997). The annotated mitogenome was deposited in GenBank under the accession number MZ636518. The Blast Web server with ‘Align two or more sequences’ option was used to find conserved segments between multiple query sequences, and BMGE (Criscuolo and Gribaldo 2010).

**CONTACT** Bo-Qiang Tong tbi01001@shandong.cn; Wen-Qing Li liwenqing0666@shandong.cn Shandong Provincial Center of Forest and Grass Germplasm Resources, No. 2011, Gangjiu Road, Ganggou Street, Jinan, Shandong 250102, China

**ARTICLE HISTORY**

Received 31 October 2021 Accepted 12 July 2022

**KEYWORDS**

*Acer miaotaiense*; mitochondrial genome; phylogenetic relationship

**REFERENCES**

Janouskovec et al. 2013.
Zhang et al. 2016.
Zhou and Yao 2003.
Meng et al. 2016.
Li et al. 2005.
selected regions for the construction of the evolutionary tree (Bi et al. 2018). The model-finder was then used to chop the model WAG + I + G, and the Maximum Likelihood (ML) phylogenetic tree was constructed by RAxML v8.2.9 software with 1,000 bootstrap replicates (Stamatakis 2014).

The *A. miaotaiense* complete mitochondrial genome was assembled into a single circular-mapping molecule of 819,227 bp with a GC content of 45.7%. The overall A, C, G, and T contents were 27.2, 22.8, 22.9, and 27.1%, respectively. The mitogenome contained 69 genes, including 41 protein-coding genes, 25 tRNA genes, and three rRNA genes. Among the 41 protein-coding genes, seven contained introns—ccmFc and rps14 had a single intron, and nad1, nad2, nad4, nad5, and nad7 had four introns. Five genes (nad1, nad2, nad4, nad5, and nad7) were trans-spliced.

To determine the phylogenetic position of *A. miaotaiense*, phylogenetic analyses were conducted based on the mitogenome sequences of 14 species from GenBank using maximum likelihood (ML) methods, with *Brassica oleracea* as the outgroup. As expected, the phylogenetic results showed that *A. miaotaiense* was closely related to *Acer yangbiense*, and was clustered into a group with *Sapindus mukorossi* and *Xanthoceras sorbifolium*. This analysis also supported *Aceraceae* and *Sapindaceae* as sister taxa with a bootstrap probability of 100% (Figure 1), which was consistent with prior results based on morphology and other molecular methods (de Jong 1994; Gadek et al. 1996; Yang and Li 2010).

**Ethical approval statement**

The authors complied with the international Union for Conservation of Nature (IUCN) policies research involving species at risk of extinction (see Guidelines for appropriate uses of IUCN Red List data), the Convention on Biological Diversity and the Convention on Trade in Endangered Species of Wild Fauna and Flora. The research was approved by the Department of Wild Fauna and Flora Protection of China’s National Forestry and Grassland Administration, and the contract number is 2020070316.

**Author contributions**

Dan Liu (experimental design and thesis writing), Ping Ding (sequencing and conducting experiments), Hai-Li Guo (resource investigation, sampling and thesis writing), Ying Chen (data analysis), Kun Zhao (data analysis), Hai-Ping Yang (sampling and sequencing), Ting Xu (data analysis), Li-Jiang Liu (sampling), Qi Jing (data analysis), Shang-Jun Han (analysis), Bo-Qiang Tong (paper revision), and Wen-Qing Li (experimental design, paper revision); and that all authors agree to be accountable for all aspects of the work.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

The study was financially supported by Wild Plant Conservation and Management Project of ‘Preservation of Germplasm Resources of Chinese Endemic Species of Wild Plants under National Key Protection’ [2019073031] and Project of Shandong Natural Science Foundation Committee ‘Study on Fragmented Population Characteristics and Genetic Structure of Juglans mandshurica, a National Class II Endangered Plant, in Shandong Province’ [ZR2019MC055].

**ORCID**

Dan Liu \(\text{http://orcid.org/0000-0002-2198-3910}\)
Data availability statement

The genome sequence data are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov/] under the accession no. MZ636518. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA748856, SRR15304752, SRR15304753 and SAMN20353478 respectively.

References

Bi GQ, Mao YX, Xing QK, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110(1):18–22.

Criscuolo A, Gribaldo S. 2010. BMGE (Block Mapping and Gathering with Entropy): a new software for selection of phylogenetic informative regions from multiple sequence alignments. BMC Evol Biol. 10(1):210–221.

de Jong PC. 1994. Taxonomy and reproductive biology of maples-Maples of the World. In: van Gelderen DM, de Jong PC, Oterdoom HJ, editors. Portland: Timber Press; p. 69–103.

Gadek PA, Fernando ES, Quinn CJ, Hoot SB, Terrazas T, Sheahan MC, Chase MW. 1996. Sapindales: molecular delimitation and infraordinal groups. Am J Bot. 83(6):802–811.

IB-CAS. 1989. Rare and endangered plants in China. Shanghai: Shanghai Educational Publishing House.

Janouskovec J, Liu S-L, Martone PT, Carre W, Leblanc C, Collen J, Keeling PJ. 2013. Evolution of red algal plastid genomes: ancient architectures, introns, horizontal gene transfer, and taxonomic utility of plastid markers. PLoS One. 8(3):e59001.

Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. 2017. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res. 27(5):722–736.

Li S, Yan GQ, Zhao GF. 2005. Population genetic structure and genetic diversity of Acer miaotaiense. J Northwest University. 35(1):71–75.

Lowe TM, Eddy SR. 1997. tRNA scan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25(5):955–964.

Meng QF, Gao HL, Li HX, Xu HJ. 2016. Biological and ecological characteristics of rare and endangered species of Acer miaotaiense. Henan Science. 34(11):1830–1834.

Stamatakis A. 2014. RAxML Version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313.

Yang PM, Li JM. 2010. Research advances on taxonomic studies in aceraeae. J Henan Inst Sci Technol. 38(01):36–39.

Zhang Y, Li B, Chen H, Wang YC. 2016. Characterization of the complete chloroplast genome of Acer miaotaiense (Sapindales: Aceraceae), a rare and vulnerable tree species endemic to China. Conservation Genet Resour. 8(4):383–385.

Zhou TL, Yao DS. 2003. Precious tree species—Acer miaotaiense. Forestry of Gansu. 4(3):41.