MITOCHONDRIAL DNA PART B: RESOURCES
2024, VOL. 9, NO. 10, 1322–1326
https://doi.org/10.1080/23802359.2024.2410441

Taylor & Francis
Taylor & Francis Group

PLASTOME REPORT

OPEN ACCESS Check for updates

The complete chloroplast genome of *Buxus sinica* var. *parvifolia* (Buxaceae) and its phylogenetic analysis

Yue Yin, Tao Xiao and Yonghong Zhang

School of Life Sciences, Yunnan Normal University, Kunming, China

ABSTRACT
Buxus sinica var. *parvifolia* is a shrub or small arbor of the Buxaceae family, rich in various medicinal alkaloids and of great horticultural value. In this study, we sequenced, assembled, and annotated the complete chloroplast genome of *B. sinica* var. *parvifolia* for the first time. The length of the chloroplast genome is 158,995 bp with 38.1% overall GC content. It includes a large single-copy (LSC) region of 88,140 bp, a small single-copy (SSC) region of 17,761 bp, and two inverted repeat regions of 26,547 bp. Additionally, 132 functional genes in the genome are identified, including 87 protein-coding genes, eight ribosomal RNA genes, and 37 transfer RNA genes. Phylogenetic analysis showed that *B. sinica* var. *parvifolia* is closely related to *Buxus microphylla*. The complete chloroplast genome sequence of *B. sinica* var. *parvifolia* and its phylogenetic analysis provides useful genomic information for the further study of *B. sinica* var. *parvifolia* and other *Buxus* species.

ARTICLE HISTORY
Received 3 July 2024
Accepted 24 September 2024

KEYWORDS
Buxus sinica var. *parvifolia*; chloroplast genome; phylogenetic analysis

Introduction

Buxus sinica var. *parvifolia* M. Cheng is a perennial medicinal shrub or small arbor belonging to the genus *Buxus* in the Buxaceae, which occurs naturally in cliff habitats in semi-tropics alpine areas of China, at altitudes between 1200 and 3000 m above sea level (Cheng 1979; Min and Brückner 2008). Chemical compositional analyses have shown that *B. sinica* var. *parvifolia* contains more than 200 alkaloids (Lv et al. 2013) including cyclovirobuxine D (CVB-D) (Bai and Pang 2021). Modern pharmacological studies have shown that these alkaloids exhibit good anti-arrhythmic, anti-myocardial ischemic, and cardiotonic effects in animals and clinical trials (An and He 2015; Wang, Zhang, et al. 2022), and inhibit the proliferation of non-small cell lung cancer A549 (Ming et al. 2024). As an important horticultural plant, *B. sinica* var. *parvifolia* is hardy, drought-tolerant (Li et al. 2023; Jiang et al. 2024), and has strong particulate matter adsorption properties (Huang et al. 2023).

Since its narrow distribution and the large number of excavations for bonsai cultivation, the wild resources are on the verge of extinction. It has been listed as a second-grade protected plant in Anhui Province, China (Huang et al. 2005). In addition, the taxonomic status and phylogenetic relationships of *B. sinica* var. *parvifolia* in the genus *Buxus* have yet remained controversial. It was first published as a variety of *B. sinica* (Cheng 1979), while it was regarded as a synonym of *B. rugulosa* or a distinctive species with closer relationship to *B. henryi*, subsequently (Lin 2004; Wang et al. 2012). Currently, although few molecular studies involving RAPD, ISSR markers, and ITS sequences have been conducted, the intrageneric relationships and species discrimination of *B. sinica* var. *parvifolia* were still uncertain (Huang et al. 2008; Jiang et al. 2008; Wang et al. 2012).

The chloroplast genome, with its small size, highly conserved structure, and uniparental inheritance, can provide well solution for species discrimination and delimitation in taxonomically difficult taxa, as far as to inferring phylogenetics of angiosperms (Dodsworth 2015; Nguyen et al. 2024). Therefore, this study reports the complete chloroplast genome sequence of *B. sinica* var. *parvifolia* and further explores the phylogenetic relationships among the genus *Buxus*, which will contribute to future studies on species identification, phylogenetic evolution, and species conservation of *B. sinica* var. *parvifolia*.

Materials and methods

Fresh leaves of *B. sinica* var. *parvifolia* (Figure 1) were collected from Chenggong County, Kunming (24°52′0.995″N, 102°51′16.668″E), Yunnan Province, China. The voucher specimen (LMF09) has been deposited in the Herbarium of Yunnan Normal University (YNUB, website: https://life.ynnu.edu.cn/, Contact: Jian-Lin Hang, Email: hjlynub@163.com).

The genomic DNA from fresh samples was extracted using a modified CTAB (cetyltrimethylammonium bromide) method (Allen et al. 2006) and the constructed library was sequenced

CONTACT Yonghong Zhang daphnecn@aliyun.com School of Life Sciences, Yunnan Normal University, Kunming 650500, China
Supplemental data for this article can be accessed online at https://doi.org/10.1080/23802359.2024.2410441.

Figure 1. Plant morphological characteristics of *B. sinica* var. *parvifolia*. Yue Yin took these photos in Chenggong County, Kunming, Yunnan Province, China. (A) The leaves of this species are small, broadly elliptic, or broadly ovate. (B) The capsules of this species are glabrous.

using the Illumina HiSeq 2500-PE150 platform (Illumina, San Diego, CA). All raw reads were filtered to obtain clean reads with default parameters using NGS QC Toolkit v2.3.3 (Patel and Jain 2012). These trimmed reads were assembled by GetOrganelle software (Jin et al. 2020). Geneious v2022.2.2 (Kearse et al. 2012) was used for annotation based on the *B. microphylla* (GenBank accession number: NC_009599) chloroplast genome (Li, Li, et al. 2021) and then manually corrected. The circular genome map was generated using CPGAVAS2 (Shi et al. 2019, http://47.96.249.172:16019/analyzer/annotate). The schematic map of the trans-splicing and cis-splicing genes was generated using the CPGView software (Liu et al. 2023, http://www.1kmpg.cn/cpgview/). The assembly was further evaluated using Trim Galore 0.6.4 and Samtools (Li et al. 2009), respectively. The assembled chloroplast genome sequence was submitted to the GenBank (accession number: OQ236088) of the National Center for Biotechnology Information (NCBI). For phylogenetic analysis, the complete chloroplast genome sequences of 25 reported species were downloaded from NCBI (*Paeonia*: four species, *Dillenia*: two species, *Liquidambar*: two species, *Exbucklandia*: two species, *Loropetalum*: two species, *Altingia*: two species, *Pachysandra*: two species, and one species was selected from *Daphniphyllum*, *Cercidiphyllum*, *Hamamelis*, *Tetracera*, *Semiliquidambar*, *Tetracentron*, *Trochodendron*, and *Buxus*, respectively). The outgroup was *Meliosma oldhamii*. Sequences were aligned by MAFFT (Katoh and Toh 2010). The best nucleotide substitution model GTR + G + I was calculated by MEGA X (Kumar et al. 2018). Maximum-likelihood (ML) analysis was performed with RAxML v8.0 (Stamatakis 2014) using default parameters and 1000 bootstrap replicates.

Results

The complete chloroplast genome sequence of *B. sinica* var. *parvifolia* is 158,995 bp in length, containing a large single-copy (LSC) region of 88,140 bp, a small single-copy (SSC) region of 17,761 bp, and a pair of inverted repeat regions (IRa and IRb) of 26,547 bp (Figure 2). We annotated 132 genes, including 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes. The average coverage depth (1859.6×) of the *B. sinica* var. *parvifolia* chloroplast genome is shown in Figure S1. The base compositions of the chloroplast genome were uneven (A: 30.6%, T: 31.4%, G: 18.7%, C: 19.4%). The overall GC content of the chloroplast genome was 38.1%, and 43% for the IRs, which was higher than that in LSC and SSC regions (32.2%, and 36.3%, respectively). The GC content in the rRNA (55.4%) was higher than that in the tRNA (53.3%). In total, 19 genes replicate in the IR region, repeating inversely with each other, including eight protein-coding genes (*rpl*2, *rpl*23, *ycf*2, *ndh*B, *rps*7, *rps*12, *ycf*15, and *ycf*1), seven transfer RNA genes (*trn*I-CAU, *trn*L-CAA, *trn*V-GAC, *trn*I-GAU, *trn*A-UGC, *trn*R-ACG, and *trn*N-GUU), and four ribosomal RNA genes (*rrn*16S, *rrn*23S, *rrn*4.5S, and *rrn*5S). The *rps*12 is a trans-splicing gene (Figure S2) and 13 genes including *rps*16, *atp*F, *rpo*C1, *ycf*3, *clp*P, *pet*B, *pet*D, *rpl*16, *rpl*2, *ndh*B, *ndh*A, *ndh*B, and *rpl*2 are cis-splicing genes (Figure S3).

To understand the phylogenetic position of *B. sinica* var. *parvifolia*, we selected 25 reported chloroplast genomes, using *Meliosma oldhamii* as an outgroup. Our result indicated that *B. sinica* var. *parvifolia* was closely related to *B. microphylla* with 100% bootstrap support and was clustered with the clade of two *Pachysandra* species (BS = 100%) (Figure 3).

Discussion and conclusions

In this study, the chloroplast genome of *B. sinica* var. *parvifolia* is sequenced, assembled, and annotated for the first time. The chloroplast genome structures of *B. sinica* var. *parvifolia* contain one LSC region, one SSC region, and two IR regions, which is consistent with the basic quadripartite structure characteristics of angiosperm chloroplast genomes (Hansen et al. 2007). Meanwhile, it has a length of 158,995 bp, with 132 genes, which is not significantly different from the size reported in previous studies of *B. microphylla* (NC_009599, 159,010 bp with 139 genes, Hansen et al. 2007), indicating a close genetic relationship in the structural characteristics of the chloroplast genome.

B. sinica var. *parvifolia*, along with five other varieties, forms a subordinate taxonomic group of *B. sinica* (Min and Brückner 2008). Due to their similarity in leaf shape and capsule characteristics, it is difficult to identify their lineage relationship solely based on morphological features (Lin 2004). In

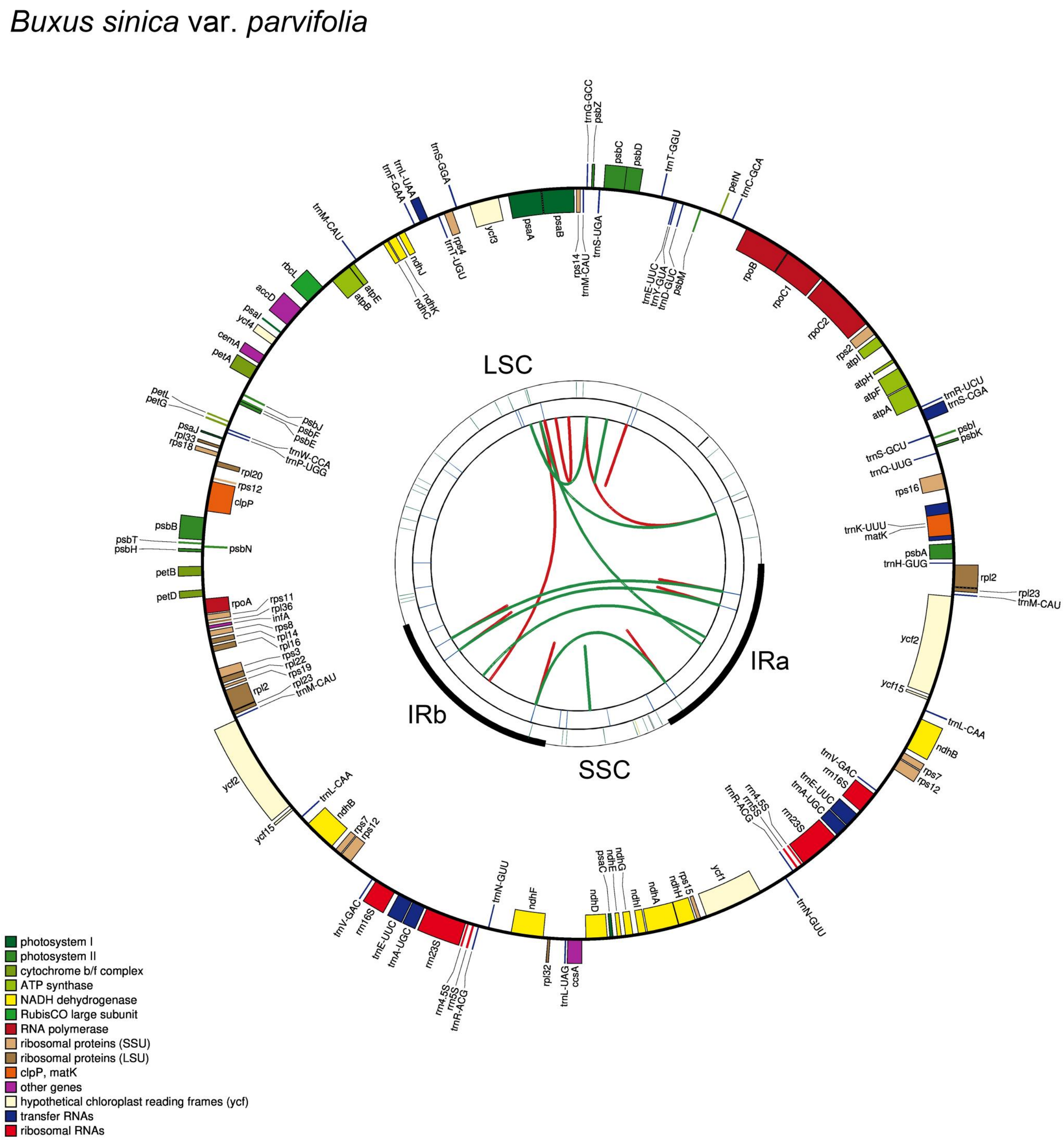

Figure 2. Gene map of the *B. sinica* var. *parvifolia* chloroplast genome. The map contains four rings. From the center going outward, the first circle shows the forward and reverse repeats connected with red and green arcs, respectively. The next circle shows the tandem repeats marked with short bars. The third circle shows the microsatellite sequences identified using MISA. The fourth circle shows the gene structure on the plastome. The genes were colored based on their functional categories.

this study, the results of phylogenetic analysis show that there is a sister relationship between *B. sinica* var. *parvifolia* and *B. microphylla*. In previous study, Wang et al. (2012) proposed that *B. sinica* var. *parvifolia* should be a sister species instead of a variant of *B. sinica*, with closer genetic relationship to *B. henryi*, utilizing ITS sequences. However, in both studies, it was inadequate with only one variant, *B. sinica* var. *parvifolia*, to explore the intraspecific phylogenetic relationship. Therefore, to better understand the intrageneric and intraspecific phylogenetic relationships within the genus, it is necessary to further increase the samples of the chloroplast genome of *Buxus* in the future for in-depth research.

This study has contributed to the enlargement of the chloroplast genome database for *Buxus* and has provided valuable insights into the evolutionary relationships among various *Buxus* species.

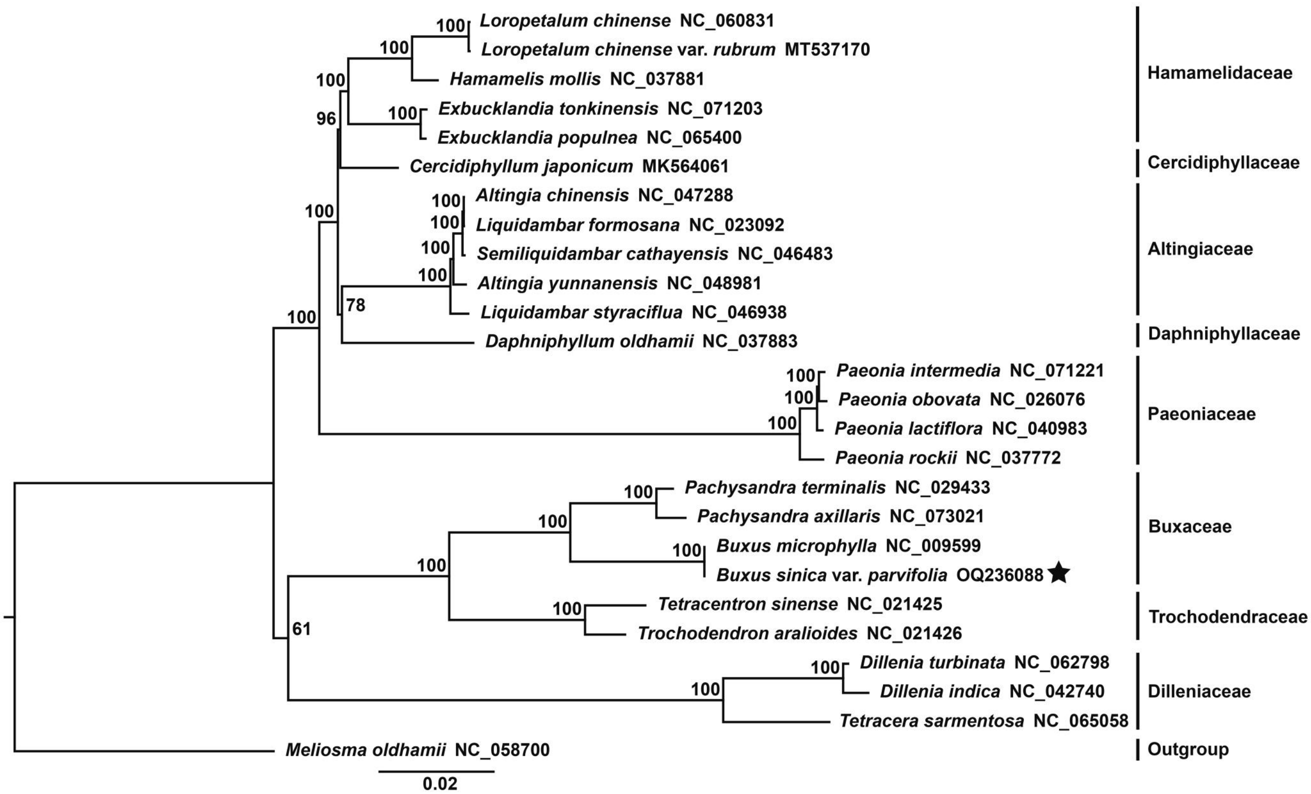

Figure 3. The phylogenetic position for *B. sinica* var. *parvifolia* according to the ML phylogenetic tree constructed based on 26 chloroplast genomes with *Meliosma oldhamii* as outgroup. The numbers above the nodes indicate the bootstrap values from 1000 replicates analysis. The scale bar in the lower left corner of the figure represents the evolutionary distance, with a unit length of 0.02. The following sequences were used: *Altingia chinensis* NC_047288, *Altingia yunnanensis* NC_048981 (Qiu et al. 2020), *Buxus microphylla* NC_009599 (Hansen et al. 2007), *Buxus sinica* var. *parvifolia* OQ236088 (this study), *Cercidiphyllum japonicum* MK564061 (Zhu et al. 2019), *Daphniphyllum oldhamii* NC_037883 (Dong et al. 2013), *Dillenia indica* NC_042740 (Tan et al. 2019), *Dillenia turbinate* NC_062798 (Li, Xie, et al. 2021), *Exbucklandia populnea* NC_065400, *Exbucklandia tonkinensis* NC_071203, *Hamamelis mollis* NC_037881 (Dong et al. 2018), *Liquidambar formosana* NC_023092 (Dong et al. 2013), *Liquidambar styraciflua* NC_046938, *Loropetalum chinense* NC_060831 (Wang, Chen, et al. 2022), *Loropetalum chinense* var. *rubrum* MT537170, *Meliosma oldhamii* NC_058700, *Pachysandra axillaris* NC_073021, *Pachysandra terminalis* NC_029433 (Sun et al. 2016), *Paeonia intermedia* NC_071221, *Paeonia lactiflora* NC_040983 (Samigullin et al. 2018), *Paeonia obovate* NC_026076, *Paeonia rockii* NC_037772 (Bai et al. 2018), *Semiliquidambar cathayensis* NC_046483 (Tang et al. 2020), *Tetracentron sinense* NC_021425 (Sun et al. 2013), *Tetracera sarmentosa* NC_065058, and *Trochodendron aralioides* NC_021426 (Sun et al. 2013).

Author contributions

Yonghong Zhang designed the research and revised the manuscript. Yue Yin analyzed data and prepared a preliminary manuscript. Tao Xiao analyzed the data and revised the manuscript. All authors read and approved the final manuscript, and agreed to be accountable for all aspects of the work.

Ethical approval

This research does not involve ethical issues. *Buxus sinica* var. *parvifolia* does not belong to the China Species Red List. The collection of plant material was carried out according to guidelines provided by the authors' institution (Yunnan Normal University) and national regulations.

Disclosure statement

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

Funding

This study is supported by the National Natural Science Foundation of China [31760048].

ORCID

Yonghong Zhang http://orcid.org/0000-0001-6583-3255

Data availability statement

The data that support the findings of this study are openly available in GenBank of NCBI (https://www.ncbi.nlm.nih.gov/) with accession number OQ236088. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA945587, SRR23884465, and SAMN33789276, respectively.

References

Allen GC, Flores-Vergara MA, Krasynanski S, Kumar S, Thompson WF. 2006. A modified protocol for rapid DNA isolation from plant tissues using cetyltrimethylammonium bromide. Nat Protoc. 1(5):2320–2325. doi:10.1038/nprot.2006.384.

An Y, He QY. 2015. The pharmacological action and clinical application of the components of Xinnaoning capsule. Beijing Med J. 37(1):103–104.

Bai GQ, Guo HW, Zhao N, Li SF, Zhang Y. 2018. The complete chloroplast genome of *Paeonia rockii* (Paeoniaceae), an endangered endemic species to China. Conserv Genet Resour. 10(3):453–456. doi:10.1007/s12686-017-0847-5.

Bai YE, Pang Y. 2021. Review of the research on *Buxus sinica*. J Inn Mong Agric Univ (Nat Sci Ed). 42(1):114–120.

Cheng M. 1979. New taxa of Buxaceae from China with discussions on some species. J Syst Evol. 17(3):97–103.

Dodsworth S. 2015. Genome skimming for next-generation biodiversity analysis. Trends Plant Sci. 20(9):525–527. doi:10.1016/j.tplants.2015.06.012.

Dong WP, Xu C, Cheng T, Lin K, Zhou SL. 2013. Sequencing angiosperm plastid genomes made easy: a complete set of universal primers and a case study on the phylogeny of Saxifragales. Genome Biol Evol. 5(5): 989–997. doi:10.1093/gbe/evt063.

Dong WP, Xu C, Ping W, Cheng T, Yu J, Zhou SL, Hong DY. 2018. Resolving the systematic positions of enigmatic taxa: manipulating the chloroplast genome data of Saxifragales. Mol Phylogenet Evol. 126:321–330. doi:10.1016/j.ympev.2018.04.033.

Hansen DR, Dastidar SG, Cai ZQ, Penaflor C, Kuehl JV, Boore JL, Jansen RK. 2007. Phylogenetic and evolutionary implications of complete chloroplast genome sequences of four early-diverging angiosperms: *Buxus* (Buxaceae), *Chloranthus* (Chloranthaceae), *Dioscorea* (Dioscoreaceae), and *Illicium* (Schisandraceae). Mol Phylogenet Evol. 45(2):547–563. doi:10.1016/j.ympev.2007.06.004.

Huang R, Tian Q, Zhang Y, Chen Z, Wu YH, Li ZZ, Wen ZB. 2023. Differences in particulate matter retention and leaf microstructures of 10 plants in different urban environments in Lanzhou City. Environ Sci Pollut Res Int. 30(47):103652–103673. doi:10.1007/s11356-023-29607-1.

Huang Y, Zhai JR, Ji KS. 2005. A morphologic analysis on clonal germplasm resources of *Buxus sinica* var. *parvifolia*. J For Eng. 116(3):43–45.

Huang Y, Ji KS, Jiang ZH, Tang GG. 2008. Genetic structure of *Buxus sinica* var. *parvifolia*, a rare and endangered plant. Sci Hortic. 116(3):324–329. doi:10.1016/j.scienta.2008.01.001.

Jiang CB, Zhang JP, Peng XZ, Li JK, Yang X. 2024. Simulation of pollutant deep transport characteristics in a partially infiltrated bioretention system. J Water Process Eng. 58(1):104928. doi:10.1016/j.jwpe.2024.104928.

Jiang ZH, Ji KS, Huang Y. 2008. Analysis of genetic diversity of two populations of *Buxus sinica* var. *parvifolia* by RAPD. J Nanjing For Univ. 32(1):11–14.

Jin JJ, Yu WB, Yang JB, Song Y, dePamphilis CW, Yi TS, Li DZ. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):241. doi:10.1186/s13059-020-02154-5.

Katoh K, Toh H. 2010. Parallelization of the MAFFT multiple sequence alignment program. Bioinformatics. 26(15):1899–1900. doi:10.1093/bioinformatics/btq224.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649. doi:10.1093/bioinformatics/bts199.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35(6):1547–1549. doi:10.1093/molbev/msy096.

Li DM, Li J, Wang DR, Xu YC, Zhu GF. 2021. Molecular evolution of chloroplast genomes in subfamily Zingiberoideae (Zingiberaceae). BMC Plant Biol. 21(1):558. doi:10.1186/s12870-021-03315-9.

Li F, Xie XN, Huang R, Tian EW, Li C, Chao Z. 2021. Chloroplast genome sequencing based on genome skimming for identification of Eriobotryae folium. BMC Biotechnol. 21(1):69.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup. 2009. The Sequence Alignment/Map format and SAMtools. Bioinformatics. 25(16):2078–2079. doi:10.1093/bioinformatics/btp352.

Li YW, Shao XN, Yu JL, Zhou CL, Li HF. 2023. Morphological characteristics and water harvesting function of six urban shrub species: implications on sustainable greenspaces in a semi-humid region. Urban Ecosyst. 26(4):1155–1168. doi:10.1007/s11252-023-01373-5.

Lin Q. 2004. A new synonym of *Buxus rugulosa* Hatusima. Bull Bot Res. 24(4):402–403.

Liu SY, Ni Y, Li JL, Zhang XY, Yang HY, Chen HM, Liu C. 2023. CPGView: a package for visualizing detailed chloroplast genome structures. Mol Ecol Resour. 23(3):694–704. doi:10.1111/1755-0998.13729.

Lv X, Yu X, Guo Q, Ma YQ. 2013. Progress on study of *Buxus* alkaloids. Chin J Exp Tradit Med Formulae. 27(1):72–76.

Min TL, Brückner P. 2008. Buxaceae. In: Wu ZY, Raven PH, Hong DY, editors. Flora of China. Vol. 11. Beijing (China)/St. Louis (MI): Science Press/Missouri Botanical Garden Press; p. 321–332.

Ming Y, Zhao S, Zhao YM, Xu XY. 2024. The chemical components in the leaves of *Buxus microphylla* on the proliferation of non-small cell lung cancer A549 research on inhibitory effects. J Yichun Univ. 46(3):20–23.

Nguyen HD, Vu MT, Do HDK. 2024. Characterization of the complete chloroplast genome of *Helicteres hirsuta* Lour. 1790 (Helicteriodeae: Malvaceae). Mol Ecol Resour. 9(5):568–573.

Patel RK, Jain M. 2012. NGS QC toolkit: a toolkit for quality control of next generation sequencing data. PLoS One. 7(2):e30619. doi:10.1371/journal.pone.0030619.

Qiu Q, Yang DJ, Xu LH, Xu YM, Wang Y. 2020. The complete chloroplast genome sequence of *Altingia yunnanensis*. Mitochondrial DNA B Resour. 5(1):1050–1051. doi:10.1080/23802359.2020.1721369.

Samigullin TH, Logacheva MD, Degtjareva GV, Efimov SV, Terentieva EI, Vallejo-Roman CM. 2018. Complete plastome sequence of *Paeonia lactiflora* Pall. (Paeoniaceae: Saxifragales). Mitochondrial DNA B Resour. 3(2):1110–1111. doi:10.1080/23802359.2018.1501311.

Shi LC, Chen HM, Jiang M, Wang LQ, Wu X, Huang LF, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. Nucleic Acids Res. 47(W1):W65–W73. doi:10.1093/nar/gkz345.

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313. doi:10.1093/bioinformatics/btu033.

Sun YX, Moore MJ, Meng AP, Soltis PS, Soltis DE, Li JQ, Wang HC. 2013. Complete plastid genome sequencing of Trochodendraceae reveals a significant expansion of the inverted repeat and suggests a Paleogene divergence between the two extant species. PLoS One. 8(4):e60429. doi:10.1371/journal.pone.0060429.

Sun YX, Moore MJ, Zhang SJ, Soltis PS, Soltis DE, Zhao TT, Meng AP, Li XD, Li JQ, Wang HC. 2016. Phylogenomic and structural analyses of 18 complete plastomes across nearly all families of early-diverging eudicots, including an angiosperm-wide analysis of IR gene content evolution. Mol Phylogenet Evol. 96:93–101. doi:10.1016/j.ympev.2015.12.006.

Tan XH, Wang JH, Zhao KK, Zhu ZX, Wang HF. 2019. Complete plastome sequence of *Dillenia indica* Linn. (Dilleniaceae): an endangered (EN) species in South China. Mitochondrial DNA B Resour. 4(1):55–56. doi:10.1080/23802359.2018.1536454.

Tang XH, Fan HH, Zhang J, Huang Y. 2020. The complete chloroplast genome of *Semiliquidambar cathayensis* H. T. Chang 'T5' (Hamamelidaceae). Mitochondrial DNA B Resour. 5(2):1267–1268. doi:10.1080/23802359.2020.1730264.

Wang NJ, Chen SF, Xie L, Wang L, Feng YY, Lv T, Fang YM, Ding H. 2022. The complete chloroplast genomes of three Hamamelidaceae species: comparative and phylogenetic analyses. Ecol Evol. 12(2):e8637. doi:10.1002/ece3.8637.

Wang R, Zhang Y, Muhammad I, Tian Y, Fu DL, Yu HJ, Xiao X, Yan SK, Jin HZ. 2022. Chemical constituents and cardioprotective effects of *Buxus sinica* var. *parvifolia* M. Cheng. Chem Reagents. 44(8):1111–1117.

Wang XF, Liu NN, Ji KS. 2012. Molecular evolutionary characteristics of the plant ITS sequences in *Buxus* genus. Tree Genet Mol Breed. 2(2):8–14. doi:10.5376/tgmb.2012.02.0002.

Zhu SS, Yin PP, Yap ZY, Qiu YX. 2019. Chloroplast genomes of two extant species of tertiary relict *Cercidiphyllum* (Cercidiphyllaceae): comparative genomic and phylogenetic analyses. Mitochondrial DNA B Resour. 4(1):1551–1552. doi:10.1080/23802359.2019.1602011.