Tropical Plants

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Camellia wuzhishanensis (Theaceae), a new decaploid species discovered in the tropical rainforest of Wuzhishan, Hainan, China

Authors

Chengzhi Xie[#], Shihui Zhang[#], Qingxia Wu, Mengyu Zhang, Sheng Luo, ..., Yongzhong Chen[*], Hanggui Lai[*], Haiyan Hu[*]

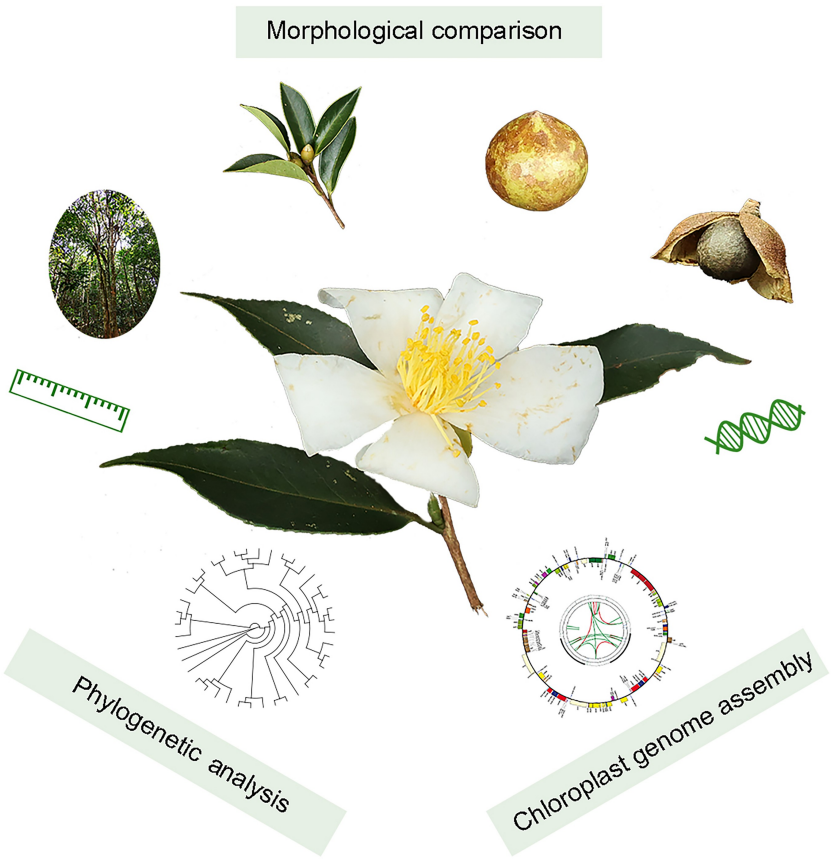
Correspondence

chenyongzhong06@163.com; laihanggui8938@163.com; huhaiyan@hainanu.edu.cn

In Brief

This study formally describes *Camellia wuzhishanensis* (Theaceae), a decaploid species endemic to the tropical rainforest of Wuzhishan, Hainan, China. Phylogenetic analysis of chloroplast genomes supports its placement within sect. *Paracamellia*, while morphological traits distinguish it from closely related species. Restricted to a single population and narrow distribution, it is assessed as Critically Endangered (CR) under IUCN criteria. Urgent targeted conservation efforts are required to safeguard this evolutionarily distinct and habitat-limited plant.

Graphical abstract



Highlights

- Discovery of *Camellia wuzhishanensis*: a critically endangered decaploid (2n = 10x = 150) species endemic to Hainan's tropical rainforests, distinguished by its exceptional height (12−18 m) and unique morphological traits.
- Molecular phylogenetic evidence: chloroplast genome analysis resolves its close relationship with *C. hainanica* and other sect. *Paracamellia* species, yet confirms genetic distinctiveness.
- Ecological adaptation: first report of a decaploid Oil-camellia thriving in high-elevation tropical rainforests, suggesting specialized survival strategies.
- Conservation urgency: classified as Critically Endangered (IUCN CR B2a,b(v)) with < 100 individuals in a 2 km^2 range, demanding immediate protective measures.

Citation: Xie C, Zhang S, Wu Q, Zhang M, Luo S, et al. 2025. *Camellia wuzhishanensis* (Theaceae), a new decaploid species discovered in the tropical rainforest of Wuzhishan, Hainan, China. *Tropical Plants* 4: e033 https://doi.org/10.48130/tp-0025-0024

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Camellia wuzhishanensis (Theaceae), a new decaploid species discovered in the tropical rainforest of Wuzhishan, Hainan, China

Chengzhi Xie[1,2#], Shihui Zhang[2#], Qingxia Wu[1,2], Mengyu Zhang[1,2], Sheng Luo[2], Jie Gao[2], Fei Chen[1,2], Yuanhao Ding[1,2], Jinping Liu[1,2], Dongyi Huang[1], Wenquan Wang[1,2], Yongzhong Chen[3,4,5,6*], Hanggui Lai[1,2*] and Haiyan Hu[1,2*]

[1] *College of Breeding and Multiplication (Sanya Institute of Breeding and Multiplication), Hainan University, Sanya 572025, Hainan, China*
[2] *College of Tropical Agriculture and Forestry, Hainan University, Haikou 570228, Hainan, China*
[3] *Research Institute of Youcha, Hunan Academy of Forestry, Changsha 410004, Hunan, China*
[4] *National Engineering Research Center of Youcha, Changsha 410004, Hunan, China*
[5] *Yuelushan Laboratory, Changsha 410012, Hunan, China*
[6] *State Key Laboratory of Utilization of Woody Oil Resource, Changsha 410004, Hunan, China*
[#] Authors contributed equally: Chengzhi Xie, Shihui Zhang
* Corresponding authors, E-mail: chenyongzhong06@163.com; laihanggui8938@163.com; huhaiyan@hainanu.edu.cn

Abstract

Camellia wuzhishanensis has been identified as a newly discovered decaploid species within the family Theaceae, endemic to the pristine tropical rainforests of Wuzhishan, Hainan, China. Detailed morphological examination reveals that *C. wuzhishanensis* is distinguished by its greater height, reaching up to 12–18 m, and shares a decaploid ploidy level with *C. hainanica*, another species native to Hainan Island. Unique traits such as branchlets, leaf size, flower size, stamens, and capsules further distinguish it from related species. Through phylogenetic analysis of complete chloroplast genome sequences, the study positions *C. wuzhishanensis* within the *Camellia* genus, showing close genetic relationships with *C. fluviatilis*, *C. zijinica*, *C. osmantha*, *C. furfuracea*, *C. drupifera*, and *C. hainanica*, while being more distantly related to *C. oleifera*. Integrating morphological and molecular evidence supports its classification as a new species within sect. *Paracamellia*. Given its limited range and potential threats, *C. wuzhishanensis* is classified as Critically Endangered (CR) according to IUCN Red List criteria, underscoring the need for conservation efforts.

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Introduction

Camellia Linnaeus[1] is the most species-rich genus in the Theaceae family and holds significant economic value among its 12 genera[2]. The genus is predominantly found in the tropical and subtropical regions of East Asia, with over 80% of its species located in China[2,3]. Within this genus, certain species possess high seed oil content and are collectively referred to as Oil-camellia, primarily including those from sect. *Paracamellia*, which Ming redefined by merging it with sect. *Oleifera* to create a new classification under the same name[4]. Among them, *C. oleifera* Abel[5], the most widely cultivated, is recognized as one of the world's four major woody oil-seed crops[6]. It holds tremendous potential for development and utilization, making it the main species for woody edible oils[6,7].

Hainan has a long history of Oil-camellia cultivation, with records dating back 500 years to the Ming Dynasty in the 'Zheng De Qiong Tai Zhi', where it is referred to as 'Shan You'[8]. Despite the economic significance of Oil-camellia, the classification research on these species in Hainan has encountered challenges. Due to the limitations of traditional classification methods, there are challenges in achieving clear identification and accurate distribution data. Some studies have classified the local Oil-camellia in Hainan as *C. drupifera* Loureiro[9], *C. oleifera*, or as geographical substitutes[4,10,11]. However, significant morphological, ecological, and economic differences raise questions about the accuracy of these classifications[10].

Recent studies have clarified the germplasm resources of Oil-camellia in Hainan. Xu et al. identified a new species, *C. hainanica* YL Zhao et ZG Xu, *sp. nov.*[12]. This discovery adds clarity to the taxonomy of Oil-camellia in the region. Furthermore, chromosomal ploidy plays a significant role in species differentiation within this genus. For instance, *C. fluviatilis* Handel-Mazzetti[13] and *C. crapnelliana* Tutcher[14] is diploid (2n = 2x = 30), while both *C. oleifera* and *C. osmantha* Ma et al.[15] are primarily hexaploid (2n = 6x = 90)[16]. The widely distributed *C. drupifera* in South China is octoploid (2n = 8x = 120), whereas the native *C. hainanica* found in Hainan is primarily decaploid (2n = 10x = 150)[17]. Ye et al. conducted a study examining a range of samples from Hainan, revealing that all 60 specimens assessed were either octoploid or decaploid, with decaploids accounting for 83.3% of the samples[18]. This suggests that decaploid *C. hainanica* is the dominant form among the large, ancient Oil-camellia trees in Hainan. Additionally, Zhang et al.[17] performed ploidy identification across 23 Oil-camellia populations in 16 cities and counties throughout Hainan, identifying 16 decaploid samples and seven octoploid samples. Notably, ancient Oil-camellia trees over 100 years old and wild populations in tropical rainforests were all categorized as decaploid.

In our further analysis of native Oil-camellia populations, we observed significant morphological differences between the wild decaploid population in Wuzhishan and *C. hainanica*. Characteristic features of this population indicate it belongs to *C.* sect. *Paracamellia*. Given that this population does not match any previously recorded species, we describe it here as a new species (Fig. 1). To evaluate its phylogenetic position, we conducted analyses based on chloroplast genomes. Additionally, we carefully compared the capsules of the two native decaploid Oil-camellia species from Hainan.

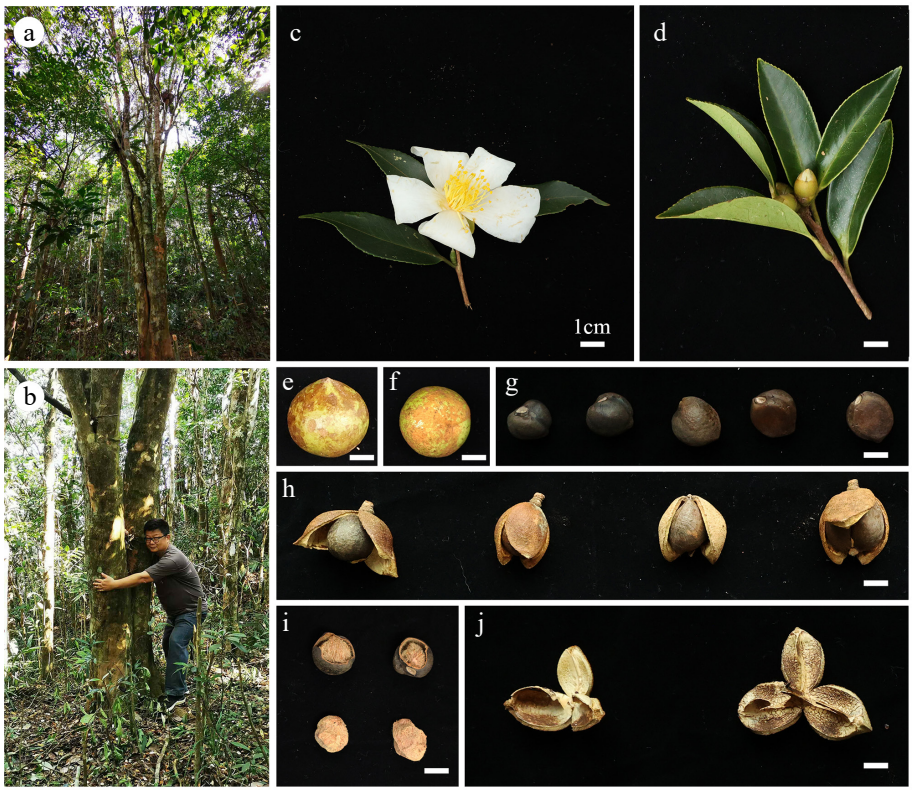

Fig. 1 *Camellia wuzhishanensis*. (a), (b) Habitat. (c) Flowering branch. (d) Terminal buds. (e) Side view of the capsule. (f) Front view of the capsule. (g) Seeds. (h) Dry capsules. (i) Interior of dry seeds. (j) Loculicidal pericarps.

Materials and methods

DNA extraction and sequencing

The seeds of the newly discovered species, *C. wuzhishanensis*, were collected from the primary tropical rainforest in Wuzhishan, Hainan Province, China.

Next-generation sequencing technology (high-throughput sequencing) was employed to extract the total genomic DNA from the plant materials, and the chloroplast genome was assembled using the GetOrganelle software[19]. Additionally, we utilized the online annotation tool CpGAVAS (http://47.96.249.172:16019/analyzer/annotate) to annotate genes within the chloroplast genome (Fig. 2)[20].

Phylogenetic analysis

To determine the phylogenetic position of the new species within the genus *Camellia*, we reconstructed a phylogenetic tree using maximum likelihood (ML) analysis based on the chloroplast genome. Apart from the new species, all other chloroplast genomes were downloaded from the NCBI database. In the phylogenetic tree, *Apterosperma oblata*, *Gordonia fruticosa*, and five closely related *Polyspora* species from the Theaceae family were used as outgroups[12]. Sequence alignment was performed using MAFFT version 7 with default settings (https://mafft.cbrc.jp/alignment/server/). The phylogenetic tree was constructed using MEGA11 software with the maximum likelihood method, selecting the best-fit model TVM + F + I + R5, and performing 1,000 bootstrap replicates[21]. The tree files were then visualized and annotated using iTOL (https://itol.embl.de/)[22]. Accession numbers for the sequences are provided in Fig. 3.

Morphological description

Morphological observations of the new species were based on live plants and dried specimens, all of which are designated as type specimens deposited at Shanghai Chenshan Herbarium (CSH). The length and width of all structures were measured with a caliper. Additionally, we compared the capsules and seeds of two native decaploid Oil-camellia species from Hainan: the new species and *C. hainanica*. High-resolution photographs of the live plants were provided by Hang-Gui Lai, Hai-Yan Hu, and Cheng-Zhi Xie. Conservation assessment was conducted following IUCN guidelines[23].

Results

Chloroplast genome of *C. wuzhishanensis*

The chloroplast genome of *C. wuzhishanensis* has a total length of 156,906 bp with a GC content of approximately 37.29%. The genome contains 87 protein-coding genes, 37 tRNA genes, and eight rRNA genes (Fig. 2).

Phylogenetic analysis

The maximum likelihood (ML) phylogenetic tree based on chloroplast genome sequences indicates that the new species *C. wuzhishanensis* belongs to the genus *Camellia*. It is closely related to showing close genetic relationships with *C. fluviatilis*, *C. zijinica*, *C. osmantha*, *C. furfuracea*, *C. drupifera*, and *C. hainanica*. However, it can be clearly distinguished from *C. hainanica*, which is widely distributed on Hainan Island (Fig. 3).

Taxonomy

Camellia wuzhishanensis* H.G.Lai, H.Y.Hu & C.Z.Xie, *sp. nov. (Figs 1 & 4).

Type: CHINA. Hainan Province: Wuzhishan, Hainan Tropical Rainforest National Park, Mao Rui Division, Core Area, in the tropical rainforest, elev. ca. 718 m, 20 October 2024, *CSH0217777* (holotype CSH!).

Diagnosis: Being close to *C. osmantha* in having similar shape and color of corollas and capsules. However, it mainly differs in the

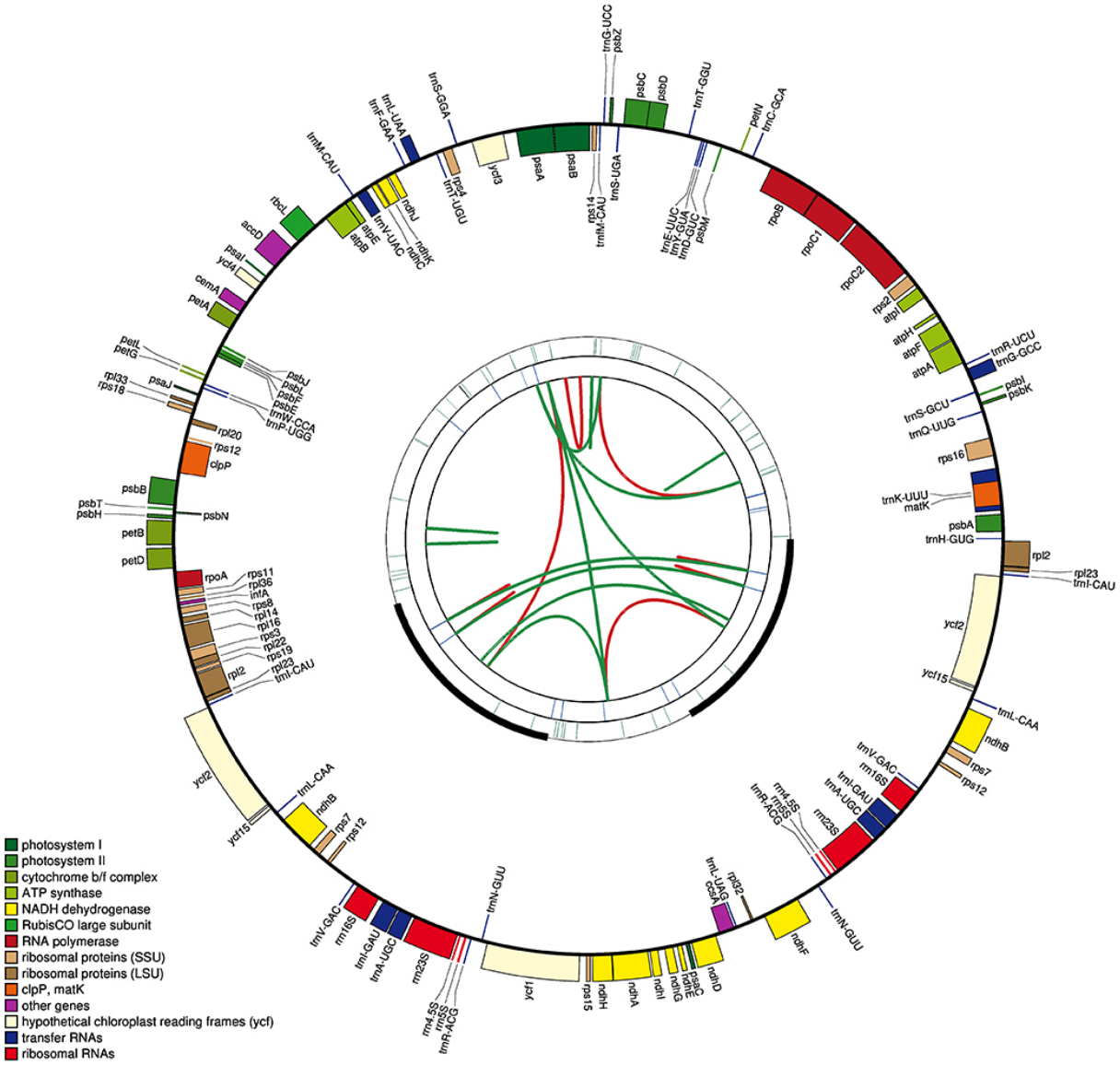

Fig. 2 Chloroplast genome of *Camellia wuzhishanensis*.

higher life form (tree, 12–18 m tall vs shrub, 3–4.5 m tall), different distributions within China (Hainan, Wuzhishan vs Guangxi), and higher ploidy level (10 vs 6) (Table 1).

Description: Trees 12–18 m tall, 58 cm dbh. Young branches reddish brown; current year branchlets puberulent, soon glabrescent. Petiole puberulent; leaf blade obovate or obovati-elliptic, 3.5–5.5 × 1.5–2.5 cm, leathery, abaxially pale green, adaxially dark green and shiny, both surfaces glabrous, midvein raised on both surfaces, secondary veins 6 or 7 on each side of midvein, secondary and reticulate veins abaxially obscure, base cuneate, margin serrulate, apex acute to acuminate and with an obtuse tip. Flowers axillary or subterminal, solitary, 3.5–4.5 cm in diam., subsessile. Bracteoles and sepals 8 or 9, caducous; outer 3 or 4 bracteoles and sepals semiorbicular; inner bracteoles and sepals ovate, outside apically pubescent, inside glabrous, margin ciliolate. Petals 5 or 6, white, almost distinct, obovate, or oblong-obovate, 1.5–2.5 × 0.9–2.2 cm, apex emarginate or 2-lobed. Stamens 0.8–1.4 cm, glabrous; outer filament whorl basally connate. Ovary globose, tomentose, 3-loculed; styles apically 3-lobed to 3-parted, base tomentose. Capsule globose to ovoid, 1.8–4 cm, 1- or 2-loculed with 1 seed per locule; pericarp splitting into three valves. Seeds brown, globose, ca. 1.8 cm in diam. 2n = 150.

Phenology: Flowering from October to December, fruiting from October to the following October.

Etymology: The specific epithet 'wuzhishanensis' means the species is collected from Wuzhishan of Hainan Island, China.

Vernacular name: '五指山油茶' (Chinese pinyin: wu zhi shan you cha).

Distribution, habitat, and conservation status: Only one population of *C. wuzhishanensis* has been found in its type locality with a distribution of about 2 km^2 and less than 100 individuals, at an elevation of ca. 718 m in the tropical rainforest. Therefore, this species is assessed to be Critically Endangered [CR, B2a, b(v)] according to the IUCN Standards and Petitions Committee (2022). Further field investigation is needed to confirm this assessment.

Additional specimens examined (paratype): CHINA. Hainan Province: Wuzhishan, Hainan Tropical Rainforest National Park, Mao Rui Division, Core Area, in the tropical rainforest, elev. ca. 718 m, 20 October 2024, *CSH0217778* (CSH!).

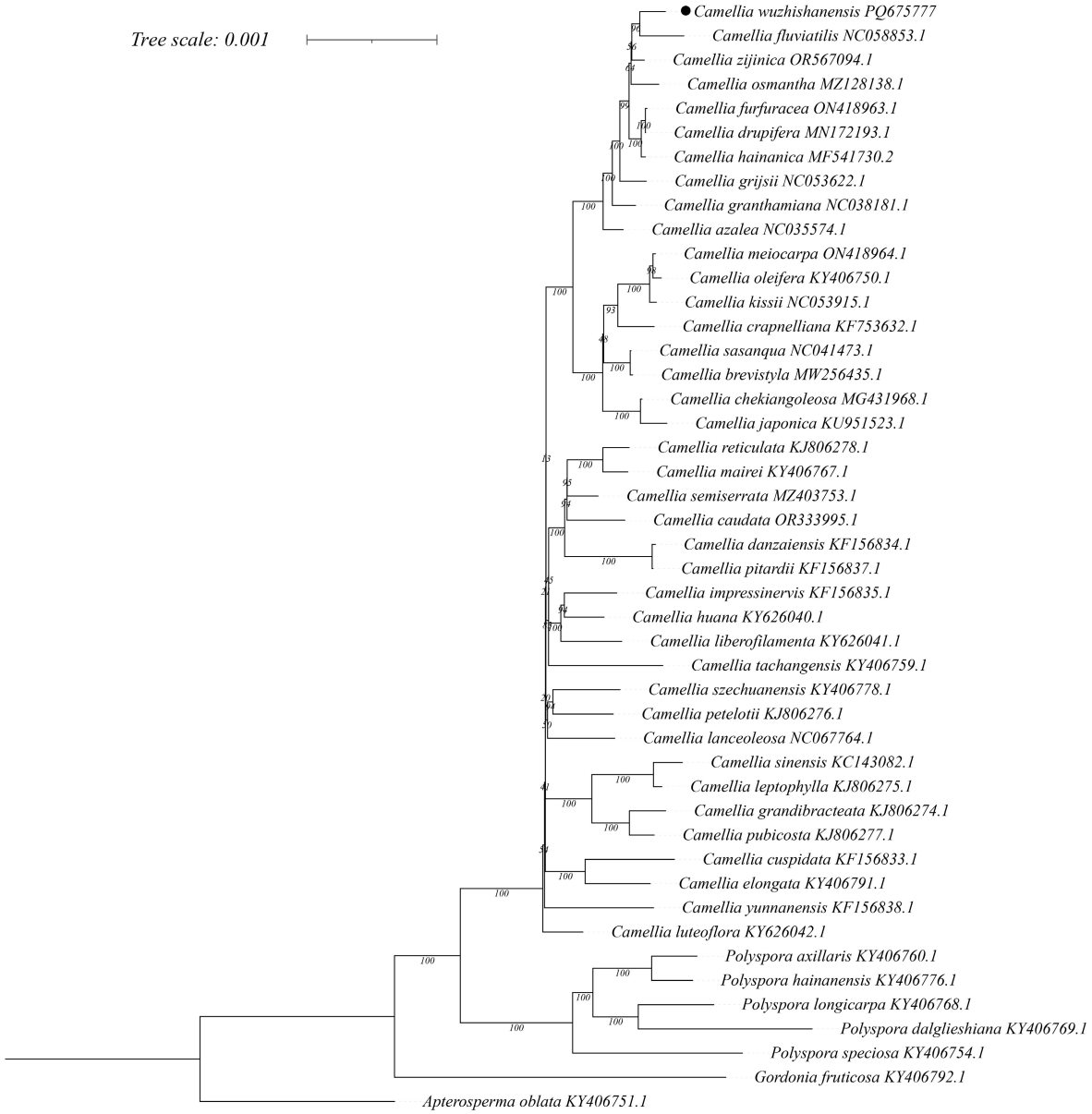

Fig. 3 Phylogenetic relationships of *Camellia wuzhishanensis* and related species inferred from maximum likelihood analysis based on complete chloroplast genome sequences.

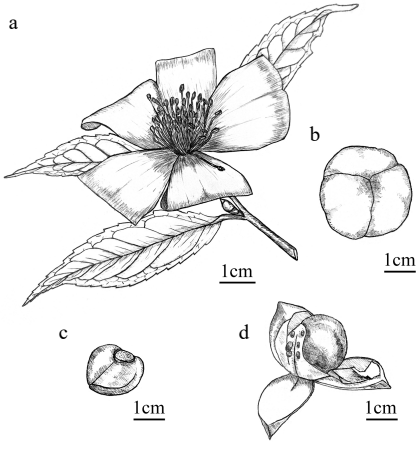

Fig. 4 *Camellia wuzhishanensis*. (a) Flowering branch. (b) Front view of the capsule. (c) Seed. (d) Loculicidal capsule. Illustration by Cheng-Zhi Xie.

Discussion

The biodiversity of *Camellia* in tropical Hainan reflects complex evolutionary adaptations. According to the Flora of China, Hainan hosts 12 native species spanning four sections: *Thea* (e.g., *C. sinensis* varieties), *Corallinae* (e.g., *C. amplexifolia*, *C. parviflora*), *Eriandria* (e.g., *C. caudata* var. *gracilis*), and *Paracamellia* (e.g., *C. drupifera*, *C. oleifera*, *C. kissii*). Nearly half of the species occur below 1,000 m, with only *C. caudata* var. *gracilis*, *C. furfuracea*, *C. kissii* and *C. sinensis* varieties overlapping the elevational range of *C. wuzhishanensis*. Historically, Hainan's Oil-camellias were broadly categorized as *C. drupifera* or *C. oleifera*[4,10,11], but recent studies have unveiled finer distinctions, including the recognition of *C. hainanica* and the novel species described here.

Previous literature recorded another variety of *C. caudata* distributed in Wuzhishan. We conducted comparative studies between these two sympatric *Camellia* species. Our integrated evidence—phylogenetic and morphological—definitively places *C. wuzhishanensis* within sect. *Paracamellia*. Chloroplast genome analysis

Table 1. A comparison among *C. wuzhishanensis* and similar species.

Characteristics	*C. wuzhishanensis*	*C. hainanica*	*C. drupifera*	*C. osmantha*	*C. fluviatilis*
Ploidy	10	10	8	6	2
Life form	Tree, 12–18 m tall	Shrub or small tree, 3–5 m tall	Shrub or small tree, 2–8 m tall	Shrub, 3–4.5 m tall	Shrub, 1.5–3.5 m tall
Branchlets	Reddish brown, young pubescent, old glabrous	Reddish brown, pubescent	Grayish brown, young pubescent, old glabrous	Grayish brown, young pubescent, old glabrous	Reddish brown, pubescent
Leaf shape	Obovate or obovati-elliptic	Elliptic or oblong-elliptic	Elliptic or oblong-elliptic	Obovate, obovati-elliptic or oblong	Lanceolate to narrowly lanceolate
Leaf size	3.5–5.5 × 1.5–2.5 cm	5–8 × 2–3 cm	5–10 × 2–5 cm	3.5–6 × 1.8–3.5 cm	5–8.5 × 1–2.2 cm
Flower size	3.5–4.5 cm in diam.	6–9.3 cm in diam.	6–10 cm in diam	2.5–3 cm in diam.	1.5–6 cm in diam.
Bracteoles and sepals	8–9	10–12 or more	9	10–12 or more	8–9
Petals	5–6, 1.5–2.5 × 0.9–2.2 cm	5–7, 3–4.5 × 1.5–3 cm	9, 4.5–6 × 3–4.5 cm	6–8, 1.2–2.2 × 0.9–1.5 cm	5–6, 0.8–3 × 0.4–2 cm
Stamens	0.8–1.4 cm, glabrous; outer filament whorl basally connate	1.2–1.5 cm, glabrous; outer filament whorl basally connate	1.2–1.7 cm, glabrous, outer filament whorl basally connate	0.5–1.1 cm, glabrous; outer filament whorl basally connate	0.5–0.7 cm, glabrous; outer filament whorl basally connate
Ovary	Tomentose, 3-loculed	Tomentose, 3-4-loculed	Tomentose, 3-5-locular	Tomentose, 3-loculed	Tomentose, 3-loculed
Styles	Apically 3-lobed to 3-parted, base tomentose	3-4, apically 3-4-parted or distinct nearly to base glabrous or base tomentose	Apically 3-lobed to 3-parted, glabrous or base tomentose	Apically 3-lobed to 3-parted, base tomentose	3, glabrous, distinct nearly to base
Capsules	1.8–4 cm in diam., pericarp brown, glossy	3–6 cm in diam., pericarp brown, rough	4–6 cm in diam., pericarp green, surface rough and brownish furfuraceous	1.8–2.3 cm in diam., pericarp brown, glossy	1.5–1.7 cm in diam., pericarp brown, glossy
Distribution within China	Hainan, Wuzhishan	Hainan	Guangxi, Guangdong, and Hainan	Guangxi	Guangdong, Guangxi, and Hainan

clusters it with *C. fluviatilis*, *C. hainanica*, and allied species, while revealing substantial divergence from *C. caudata* (sect. *Eriandria*) (Fig. 3). Morphologically, *C. wuzhishanensis* is distinguished by its arborescent habit (12–18 m tall), subsessile emarginate-petaled flowers, glabrous filaments, and 3-loculed globose-ovoid capsules—a suite of traits incongruent with any known variety of *C. caudata* or other Hainan *Camellia*. Its decaploid genome further corroborates its status as an independent evolutionary lineage endemic to Wuzhishan's montane rainforests.

Ecologically, *C. wuzhishanensis* and *C. hainanica* exemplify adaptive radiation within Hainan's Oil-camellias. Both decaploid species share a recent common ancestor yet occupy divergent niches: *C. wuzhishanensis* thrives > 780 m with smaller organs, suggesting specialization to stable high-elevation climates, whereas *C. hainanica* dominates lower elevations with larger capsules and higher seed yield (Fig. 5, Table 2). Economically, this divergence leads to complementary applications: the height and single-trunk growth of *C. wuzhishanensis* make it suitable for reforestation and urban landscaping, while its robust root system enables its use as an ideal rootstock for grafting other *Camellia* species introduced to the mountainous areas of Hainan. In contrast, *C. hainanica* remains crucial for traditional oil production. Future research should investigate the genomic basis of their polyploidy-mediated adaptation and resilience under climate change scenarios.

In conclusion, our study advances the taxonomic understanding of Hainan's *Camellia* diversity by integrating phylogenetic, morphological, and ecological evidence. While previous research has clarified the taxonomic status of *C. hainanica* within Hainan's Oil-camellias, our work further identifies *C. wuzhishanensis* as a distinct new species with unique evolutionary and ecological characteristics. The niche partitioning between *C. wuzhishanensis* and *C. hainanica* underscores their complementary economic potential—ranging from ecological restoration to high-value oil production. These findings not only expand the known diversity of Hainan's endemic

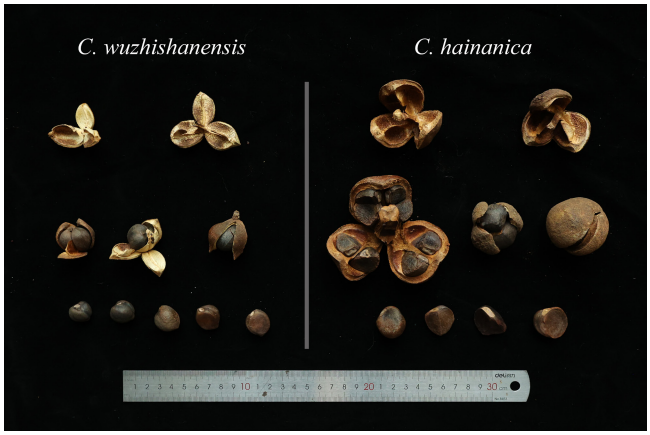

Fig. 5 Comparison of loculicidal pericarps, loculicidal capsules, and seeds between *C. wuzhishanensis* and *C. hainanica*.

Table 2. Comparison of capsules, seeds, pericarps, and pollens between *C. wuzhishanensis* and *C. hainanica*.

Parameter	*C. wuzhishanensis*	*C. hainanica*
Mean fresh capsules weight (g)	10.5	46.7
Fresh capsules weight range (g)	3.8–32.3	17.6–107.1
Mean fresh capsules diameter (cm)	2.6	4.4
Fresh capsules diameter range (cm)	1.8–4.0	3.3–5.9
Fresh pericarps thickness range (mm)	1.5–3.0	3.0–7.0
Mean dry capsules weight (g)	5.1	27.1
Dry capsules weight range (g)	2.5–14.8	11.9–66.5
Mean number of seeds per capsule	1.4	5.3
Number of seeds per capsule range	1–6	1–12
Mean dry pericarps weight (g)	2.6	13.2
Dry pericarps weight range (g)	1.0–6.9	5.4–37.9
Mean total seed weight per dry capsules (g)	2.5	13.9
Total seed weight per dry capsules range (g)	1.0–9.5	4.8–28.7
Mean individual dry seeds weight (g)	1.9	2.9
Individual dry seeds weight range (g)	0.8–3.3	1.2–6.3
Mean seed proportion of total dry capsules weight (%)	49.5	51.7
Seed proportion of total dry capsules weight range (%)	26.4–67.0	26.5–77.3
Mean pollen length (μm)	51.9	57.2
pollen length range (μm)	41.9–57.8	48.5–64.2

Camellia but also provide a foundation for their conservation and sustainable use in both natural and cultivated landscapes.

Author contributions

The authors confirm their contributions to the paper as follows: study conception and design, project supervision: Hu H, Lai H, Chen Y; draft manuscript preparation: Xie C, Hu H; genome analysis and annotation: Xie C; sample collection and experiments: Zhang S, Wu Q, Zhang M, Luo S, Gao J, Chen F, Ding Y, Liu J, Huang D, Wang W; data analysis: Xie C; manuscript revision: Xie C, Hu H. All authors reviewed the results and approved the final version of the manuscript.

Data availability

The chloroplast genome sequences of *Camellia wuzhishanensis* are deposited in GenBank of the National Center for Biotechnology Information (NCBI) repository, accession number PQ675777.

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Conflict of interest

The authors declare that they have no conflict of interest.

Dates

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