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Camellia tuxingsunii (Theaceae), a New Species with Small Flowers of sect. *Camellia* from Central Yunnan, Southwest China

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Abstract

Camellia tuxingsunii (Theaceae), a new species of sect. *Camellia* from central Yunnan, Southwest China, is described and illustrated. The species is distinguished by its relatively small leaves, flowers and fruits, and may represent one of the smallest-flowered species currently known in sect. *Camellia*. It is currently known from dry open forests and thickets on mountain slopes at elevations of 1300–1400 m in Xinping County, on the margin of the Yuanjiang dry–hot valley. Maximum likelihood phylogenetic analysis based on complete plastid genome sequences reveals that sect. *Camellia* is not monophyletic. *C. tuxingsunii* falls within the southwestern Chinese clade of sect. *Camellia* and is most closely related to *C. mairei* and *C. omeiensis*. Morphologically, however, it most closely resembles *C. saluenensis*. Its ecology and potential threats are discussed. Following IUCN Red List categories and criteria, the species is preliminarily assessed as Data Deficient (DD), as comprehensive surveys across its potential distribution range have not yet been completed.

Keywords: *Camellia*; sect. *Camellia*; morphology; phylogeny; plastid genome

1. Introduction

Camellia is the most species-rich genus in the family Theaceae. It has over 400 published names, with 240 to 280 recognized species [1, 2]. It is mainly distributed in tropical and subtropical Asia, ranging from the eastern Himalayas eastward to the Korean Peninsula and Japan, southward to the Indochina Peninsula, and the Malay Archipelago [3-6]. China harbors the richest species diversity of *Camellia*, with more than 230 documented species, most of which are found in southwestern and southern China, especially in the provinces of Guangxi, Guangdong, Guizhou, Sichuan and Yunnan [7, 8]. Plants of the genus *Camellia* are shrubs or small trees. Their flowers have imbricate bracts and sepals, basally fused petals and numerous stamens arranged in 2–6 whorls; capsules dehisce from the apex; and seeds that are wingless, hemispherical or polygonal [9, 10]. *Camellia* species are of economic importance as sources of beverages, edible oils and ornamental plants, and also serve as valuable wild germplasm resources for the genetic improvement of tea plants and *C. oleifera* [11-20]. Additionally, camellias are well-known woody ornamentals in horticulture. Species such as *C. japonica*, *C. sasanqua* and *C. reticulata* have a long history

Academic Editor: Mario A. Pagnotta

Received: 16 September 2026
Revised: 9 November 2026
Accepted: 10 November 2026
Published: 12 November 2026

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of cultivation, and numerous cultivars with diverse flower colors, flower forms, flowering periods, and plant architectures have been developed through selective breeding and interspecific hybridization. To date, over 23,000 cultivars have been registered or published [3, 21].

Although *Camellia* is a relatively well-circumscribed natural group, its infrageneric classification has long been controversial, particularly regarding species delimitation, subgeneric and sectional division, and phylogenetic relationships [22]. Various authors have proposed competing infrageneric classifications for the genus *Camellia*, resulting in three markedly different systems put forward by Sealy [9], Zhang [23] and Ming [24], respectively. In 1958, Sealy [9] published a comprehensive worldwide revision of this genus, dividing 82 species into 12 sections and leaving 24 species unplaced due to a lack of clarity in their identities and positions, in his monograph *A Revision of the Genus Camellia.* Zhang [23] divided *Camellia* into four subgenera and 19 sections, and recognized a total of 196 species. Zhang and Ren [10] later updated this taxonomic treatment, retaining four subgenera while increasing the number of sections to 20. They recognized approximately 280 *Camellia* species worldwide, of which 238 occur in China. In contrast to the taxonomic treatment of Zhang and Ren, Ming [24, 25] followed a lumping approach to species delimitation. He recognized 119 species globally, and divided them into two subgenera and 14 sections. In *Flora of China*, Ming and Bartholomew [26] recognized 97 species from China, 76 of which are endemic. Recent molecular phylogenetic studies based on nuclear, transcriptome, and plastid genome data have demonstrated that several traditionally circumscribed subgenera and sections are non-monophyletic, rendering the current infrageneric classification inadequate to reflect the full evolutionary history of *Camellia* [27-29]. Moreover, with the continued deepening of field surveys and taxonomic research, numerous new species of *Camellia* continue to be discovered and formally described in recent years, which underscores that our understanding of the genus's species diversity remains incomplete [5, 30-34].

Camellia sect. *Camellia* is one of the most species-rich and horticulturally valuable groups within the genus [35], including iconic ornamental species such as *C. japonica* and *C. reticulata* [36, 37]. This section was first proposed by Zhang and has been widely recognized by subsequent taxonomists [23, 38]. Zhang and Ren subdivided it into two subsections and recognized a total of 57 species, of which 55 occur in China and two in Japan [10]. Ming acknowledged the section's delimitation but adopted a much broader species concept, accepting only 12 species [24, 25, 39]. However, molecular systematic studies have challenged the traditional classification of sect. *Camellia*: not only are species numbers and delimitation contentious, but the section also appears not to represent a natural evolutionary lineage [6, 16, 40-42]. Phylogenetic reconstructions based on ribosomal DNA, low-copy nuclear genes, transcriptome and plastid genome data have consistently failed to recover the monophyly of traditionally defined sect. *Camellia* [43-45].

During field surveys in southwestern China, we discovered an unusual plant of *Camellia* in Xinping County, central Yunnan Province. Morphologically, it can be readily assigned to sect. *Camellia*, but it does not match any currently recognized species. Its most distinctive trait is the markedly smaller flower length compared with those of most known species in this section. Following a comprehensive review of the *Camellia* taxonomic literature and detailed comparisons with protologues, type specimens and herbarium material of morphologically similar taxa, we confirmed that this entity represents a previously undescribed species. This study formally describes and names the new species, clarifies its diagnostic differences from close relatives, infers its systematic position via complete plastid genome phylogeny, and documents its distribution, habitat, population status and preliminary conservation assessment.

https://doi.org/10.3390/d18110699

2. Materials and Methods

2.1. Morphological Analyses

Morphological studies followed the standard protocols for plant taxonomic surveys and herbarium-based research [46]. Fresh materials were dissected and examined in the laboratory at Yunnan University. Only one population of the species has been discovered to date. Field observations were conducted on three separate occasions covering both flowering and fruiting periods, and three corresponding gatherings were used for quantitative character measurement and voucher specimen preservation. The characters examined included leaf shape and dimensions, petiole length, floral dimensions, petal and stamen numbers, fruit dimensions, seed morphology, and other diagnostic vegetative and reproductive structures. Specimens were examined under an Olympus SZX2 stereomicroscope (Tokyo, Japan), and dimensions were measured with rulers or vernier calipers. Comparative data for closely related species were obtained from the taxonomic literature [26, 47] and digitized specimens (over 300 sheets for *C. saluenensis*, over 200 sheets for *C. mairei* and *C. omeiensis*). Digital images were also examined through the Global Biodiversity Information Facility (https://www.gbif.org, accessed on 28 July 2026), Global Plants on JSTOR (https://plants.jstor.org, accessed on 2 August 2026), and the Chinese Virtual Herbarium (https://www.cvh.ac.cn/, accessed on 2 August 2026), together with physical specimens housed at CDBI, KUN, PE, PYU, and YUKU (herbarium acronyms follow [48]). Relevant taxonomic treatments were also extensively reviewed [9, 10, 24, 25].

2.2. Phylogenetic Study

The complete plastid genome sequences were used to assess the phylogenetic placement of the new species. Total genomic DNA was extracted from silica gel-dried leaves using a DNA-secure Plant Kit (Tiangen, Beijing, China). Sequencing was performed using a genome skimming approach [49, 50]. Library construction and paired-end sequencing were conducted by Novogene Bioinformatics Technology Co., Ltd. (Tianjin, China). Sequencing on an Illumina NovaSeq 6000 platform generated approximately 3 Gbp of raw data.

Low-quality reads were filtered using Fastp v0.23.4 [51]. The complete plastid genome was assembled using GetOrganelle v1.7.7.0 [52] and annotated using GeSeq [53], followed by manual verification in Geneious v2025.0.2 [54]. Reference sequences comprised *C. luteoflora* (NC_082978.1), *C. amplexicaulis* (NC_051559.1), *C. piquetiana* (NC_087752.1), *C. sinensis* (OL690371.1), *C. polyodonta* (OL742653.1), and *C. sinensis* var. *assamica* (OQ503532.1). The complete plastid genome sequence of *C. tuxingsunii* was deposited in GenBank under accession number PZ569105.1, and the voucher specimen, *H. C. Wang et al. XP30031*, is deposited at YUKU. It was collected from the same population as the holotype, *H. C. Wang et al. XP33210*, on a different date.

The phylogenetic dataset comprised 112 complete plastid genome sequences. One sequence, that of the new species, was newly sequenced in this study; the remaining 111 were downloaded from NCBI and represent 58 *Camellia* species and two outgroup species. Sampling covered 13 sections: sect. *Camellia*, sect. *Eriandria*, sect. *Theopsis*, sect. *Glaberrima*, sect. Thea, sect. *Chrysantha*, sect. *Tuberculata*, sect. *Longipedicellata*, sect. *Brachyandra*, sect. *Oleifera*, sect. *Furfuracea*, sect. *Paracamellia* and sect. *Luteoflora*. Following the phylogenetic study of *Camellia* by Zhao et al. [6], *Pyrenaria oblongicarpa* and *Polyspora penangensis* were selected as outgroups. The GenBank accession numbers for these species are provided in the Supplementary Files (Table S1).

Sequences were aligned using MAFFT v7.505 [55], with the "--auto" strategy and automatic sequence orientation adjustment "--adjustdirection", yielding an initial alignment of 159,212 bp. Poorly aligned positions were removed using trimAl v1.2rev57 with the "-

automated1" option [56]. This removed 4253 columns (2.67%), resulting in a final matrix of 112 sequences and 154,959 aligned sites. Both copies of the inverted repeat (IR) region were retained in the whole-plastome alignment. The final matrix contained only 0.04% gaps or ambiguous characters. Phylogenetic analyses were performed using maximum likelihood (ML). ModelFinder [57], implemented in IQ-TREE v2.2.0, selected TVM+F+I+I+R7 as the best-fit nucleotide substitution model according to the Bayesian information criterion (BIC). ML inference was conducted in IQ-TREE v2.2.0 [58] using the command iqtree2 -s concatenation.phy -m TESTNEW -alrt 1000 -bb 2000 -bcor 0.90 -nt AUTO. Branch support was evaluated using 2000 ultrafast bootstrap replicates (UFBoot) and 1000 replicates of the Shimodaira–Hasegawa approximate likelihood ratio test (SH-aLRT). The UFBoot convergence threshold was set to 0.90 using "-bcor 0.90". The reported final correlation coefficient for split occurrence frequencies was 0.999, exceeding the default threshold of 0.99. The resulting phylogenetic tree was visualized using TVBOT (https://www.chiplot.online/tvbot.html, accessed on 25 May 2026) [59].

3. Results

3.1. Characteristics of the Plastid Genome

The plastid genome of *C. tuxingsunii* is 157,162 bp in length, with a GC content of 37.3%. Its length is consistent with those reported for *Camellia* species [60, 61]. The genome has a typical circular quadripartite structure, consisting of a large single-copy (LSC) region of 86,451 bp, a small single-copy (SSC) region of 18,193 bp, and a pair of inverted repeat regions (IRa and IRb), each 26,259 bp in length (Figure 1). The GC contents of the LSC, SSC, and IR regions are 35.3%, 30.6%, and 42.9%, respectively. In total, 133 genes were annotated, including 88 protein-coding genes, 37 transfer RNA (tRNA) genes, and 8 ribosomal RNA (rRNA) genes.

3.2. Phylogenetic Analysis

The phylogenetic dataset comprised 112 complete plastid genome sequences, representing 58 *Camellia* species and two outgroup species. The final alignment was 154,959 bp in length and contained 1571 parsimony-informative sites and 2147 singleton sites. TVM+F+I+I+R7 was selected as the best-fit model based on the Bayesian Information Criterion (BIC). The relevant analysis files are provided in the Supplementary Files.

The ML analysis recovered seven major clades (clades I–VII) within *Camellia* (Figure 2), and all major nodes received moderate or higher bootstrap support (BS ≥ 80). Clade I (BS = 98) was sister to the remaining sampled *Camellia* species and consisted mainly of members of subg. *Thea*. Clade II (BS = 80), and clade IV (BS = 100) comprised members of subg. *Camellia*, whereas clade III (BS = 100) consisted of members of subg. *Metacamellia*. Clade V (BS = 97) mainly consisted of subg. *Thea* and a small number of species from subg. *Camellia*. Clade VI (BS = 100) was a sister group to clade VII (BS = 100), both consisting mainly of members of subg. *Thea*. Members of different subgenera and sections were distributed across multiple major clades in the phylogenetic tree, and some subgenera and sections defined by Zhang's [10] classification system were not recovered as monophyletic.

Sect. *Camellia* was not recovered as monophyletic in our plastid phylogenetic tree (Figure 2); instead, its members were resolved in clades IV and VII. Clade IV received maximum bootstrap support (BS = 100) and was further divided into two subclades (A and B). Subclade A consisted of members of sects. *Camellia*, *Paracamellia*, *Oleifera*, and *Furfuracea*, and was structured into two secondary lineages. The first lineage, highly supported (BS = 100), comprised *C. chekiangoleosa, C. japonica, C. edithae, C. subintegra, C. polyodonta, and C. uraku* from sect. *Camellia; C. kissii*, *C. confusa*, and *C. brevistyla* from sect.

Paracamellia; and *C. oleifera* and *C. meiocarpa* from sect. *Oleifera.* The second lineage consisted of *C. gigantocarpa* and *C. crapnelliana* from sect. *Furfuracea*. Subclade B is likewise resolved into two secondary lineages: one consisted exclusively of species from sect. *Camellia* and the other comprised taxa from sects. *Oleifera*, *Paracamellia*, and *Furfuracea*.

The well-supported clade VII (BS = 100) split into four subclades (C–F), recovering five sections. Subclade C (BS = 100) contained only *C. leptophylla* of sect. *Thea*. Subclade D was sister to the combined E + F clade (BS = 99). Subclade E included species from sects. *Eriandria* and *Theopsis*. Subclade F was composed entirely of sect. *Camellia* species, including the new species *C. tuxingsunii* sp. nov. Within this subclade, *C. tuxingsunii* was recovered as sister to a small lineage comprising *C. mairei* and *C. omeiensis*, with moderate bootstrap support (BS = 87).

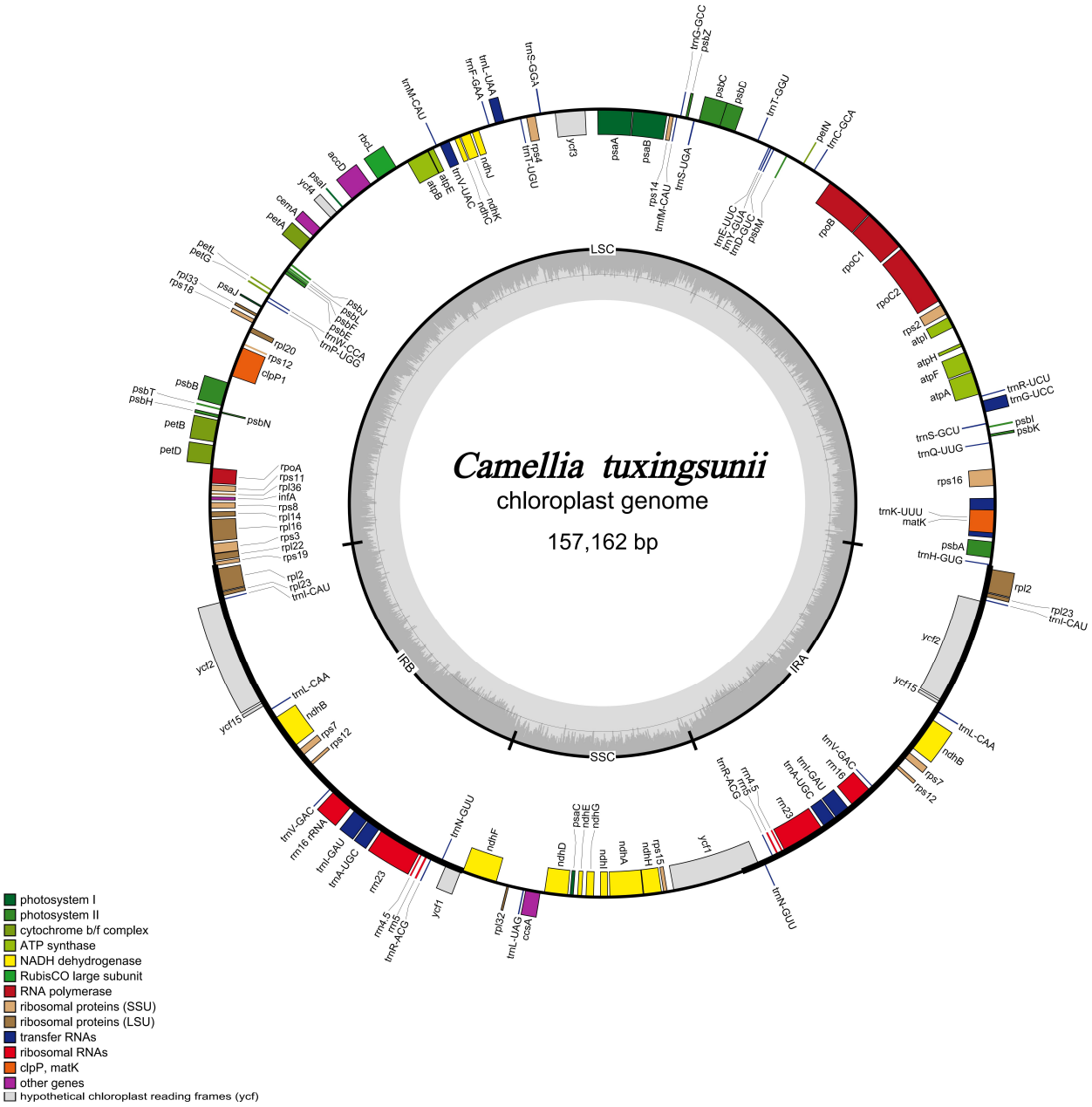


Figure 1. Plastid genome map of *Camellia tuxingsunii*. Genes outside the circle are transcribed counterclockwise, whereas those inside are transcribed clockwise. The dark gray and light gray regions of the inner circle indicate the GC and AT contents, respectively.

https://doi.org/10.3390/d18110699

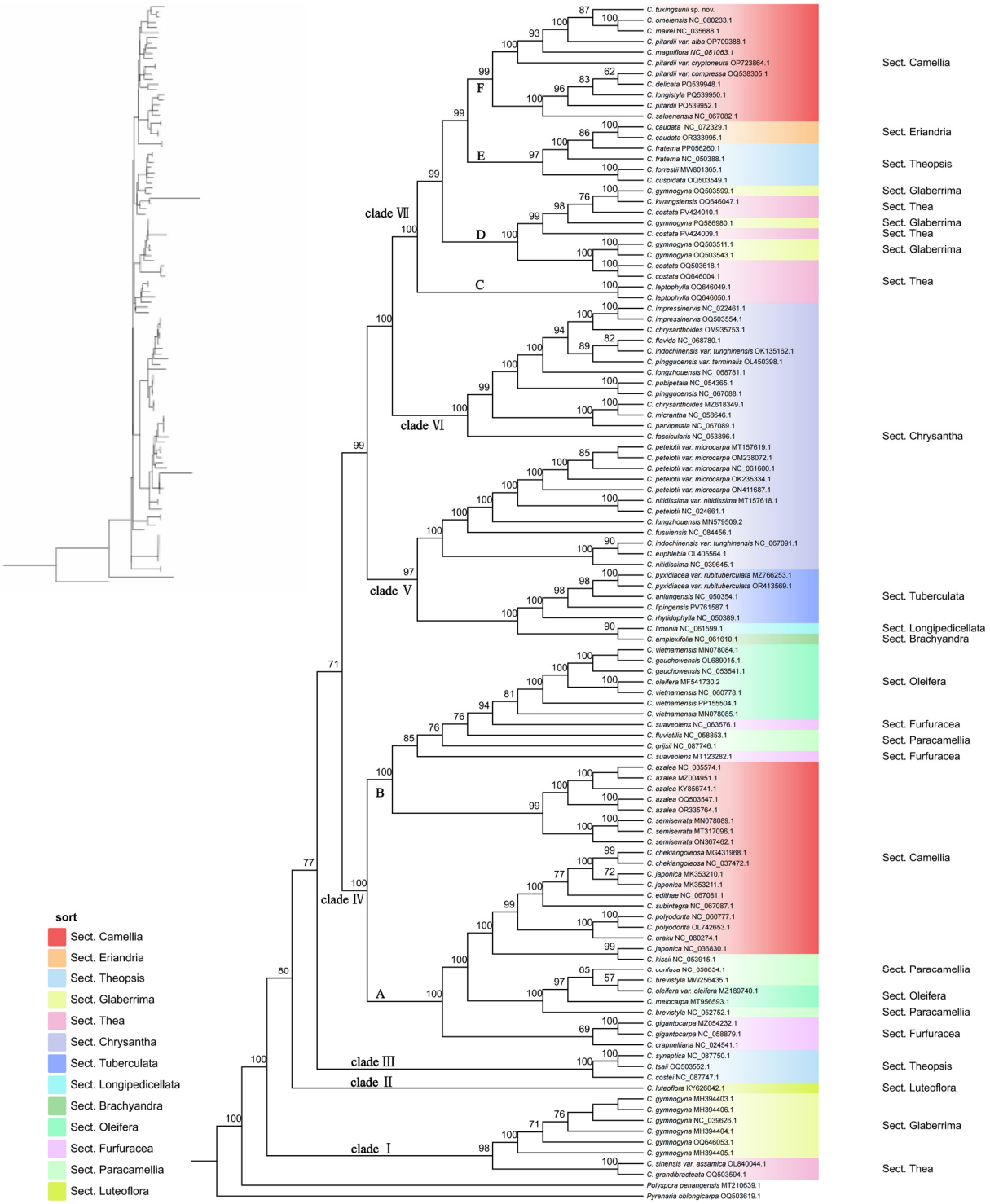


Figure 2. Maximum likelihood phylogeny of *Camellia* inferred from complete plastid genome sequences, showing the phylogenetic placement of *C. tuxingsunii*. Bootstrap support values are indicated above the branches. Sections are color-coded and labeled on the right. Sectional circumscriptions follow Zhang Hongda (1981) [23]. Numbers above the branches indicate ultrafast bootstrap (UFBoot) support values.

3.3. Taxonomy Treatment

Camellia tuxingsunii Huan C. Wang & Jiangquan Wang, sp. nov. (Figures 3 and 4).

Type: China. Yunnan Province: Yuxi City, Xinping County, Yangwu Town, Zhaomike Village, near the top of the mountain, alt. 1360 m, 23°56′45″ N, 102°07′46″ E, 8 March 2026, fl., *H. C. Wang et al. XP33210* (Holotype: YUKU02074892!; Isotypes: YUKU02074903!, YUKU02074904!).

Diagnosis: *Camellia tuxingsunii* Huan C. Wang & Jiangquan Wang is morphologically most similar to *C. saluenensis*, but clearly differs from the latter by young branches glabrous (vs. pubescent), thinly coriaceous leaf blade oblong to narrowly ovate (vs. coriaceous to thickly coriaceous, elliptic to lanceolate), apex acuminate, rarely acute (vs. usually acute, rarely acuminate), abaxial surface glabrous (vs. sparsely pilose with pubescent midrib), petiole glabrous (vs. pubescent), flowers red (vs. pink to white), and fruits broadly ellipsoid to ovoid (vs. depressed globose to subglobose), usually with length exceeding width (vs. usually shorter than or subequal to width), glabrous (vs. more or less pubescent) at maturity. It is also similar to *C. mairei* and *C. omeiensis* in floral shape and color, but differs markedly in its much smaller leaves and flowers and completely glabrous (vs. villous) staminal filaments.

Description: Shrubs 1–2 m tall. Stems erect, smooth, cylindrical, branched. Young branches usually glabrous; current year branchlets reddish-brown; year-old branchlets grayish-brown. Leaves simple, alternate, petiolate; petioles 4–6 mm glabrous; thinly coriaceous leaf blade oblong to narrowly ovate, 4–7 cm long, 1.5–2.0 cm wide, apex acuminate, rarely acute, base cuneate, margin crenulate, adaxially dark green, conspicuously glossy, abaxially pale green, both surfaces glabrous; midvein abaxially elevated and adaxially slightly impressed, secondary veins 7–8 on each side of midvein. Flowers axillary or subterminal, solitary, sessile, small. Bracteoles and sepals 9–11 imbricate, caducous after anthesis; outer bracteoles broadly triangular or semicircular, 3–6 mm long and 5–10 mm wide; inner bracteoles obovate, 6–10 mm long and 8–12 mm wide,margin ciliolate. Petals 6–8 obovate to broadly obovate, 2.5–3.0 cm long and 1.5–2.5 cm wide, basally connate for 5 mm; outer 1–2 petals apex rounded to obtuse; inner petals apex emarginate, margin ciliolate. Stamens numerous, 2.4–2.6 cm long, in 2 whorls; filaments 2.3–2.5 cm long, glabrous; outer filament whorl connate for basal 1/2; anthers ca. 1.2 mm, pale yellow, longitudinally cleft. Ovary white tomentose; styles basally connate, apically 3-parted, basally tomentose. Capsule broadly ellipsoid to ovoid, usually with length exceeding width, glabrescent at maturity, 2.5–2.9 cm in diam, 3-loculed, with 1 or 2 seeds per locule; pericarp yellowish green to pale yellowish brown, 2–3 mm thick, with brown spots on the surface. Seeds brown, semiglobose or wedge-shaped, smooth.

Distribution and Habitat: *Camellia tuxingsunii* is known only from its type locality in Xinping County, Yunnan Province, southwest China. It grows on dry mountain slopes in open forests or thickets at 1300–1400 m elevation under a subtropical monsoon climate, with associated species including *Quercus franchetii*, *Keteleeria evelyniana*, *Anneslea fragrans*, *Pinus yunnanensis*, *Terminalia franchetii* and *Campylotropis macrocarpa,* and others.

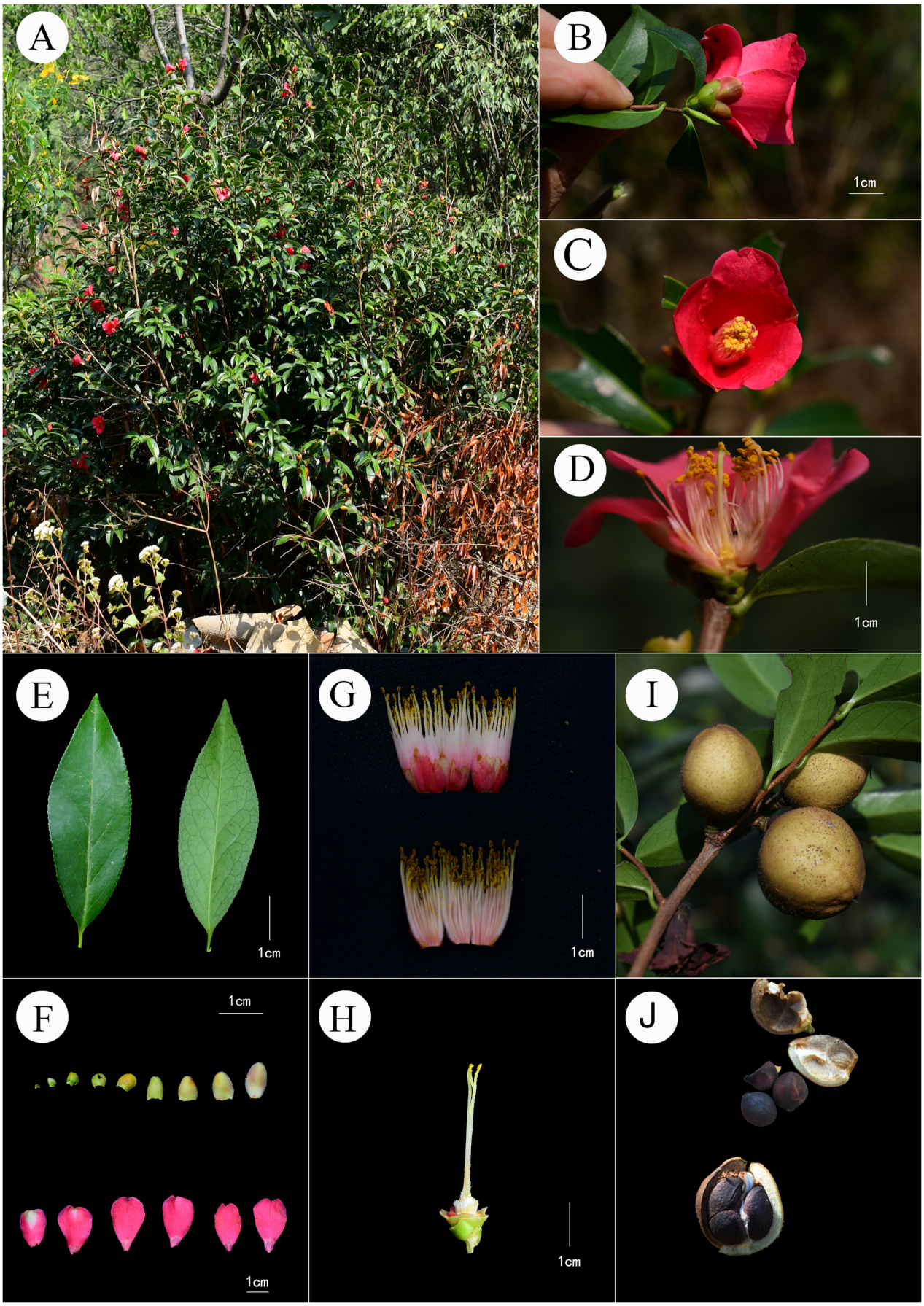


Figure 3. *Camellia tuxingsunii* sp. nov. (**A**) Habit. (**B**) Flower (side view). (**C**) Flower (front view). (**D**) Anatomy of a flower. (**E**) Adaxial and abaxial surfaces of leaves. (**F**) Petals and bracts. (**G**) Androecium. (**H**) Pistil. (**I**) Fruits. (**J**) Seeds.

https://doi.org/10.3390/d18110699



Figure 4. Holotype of *Camellia tuxingsunii* sp. nov. (YUKU-02074892).

Phenology: Flowering is from March to May, and fruiting is from September to October.

Etymology: The specific epithet *tuxingsunii* is derived from Tu Xingsun, a character from the classic Chinese mythological novel *Investiture of the Gods*. The figure is renowned for his short stature; the name is here used to allude to the notably small leaves and flowers of this new species, highlighting its most distinctive diagnostic trait.

Chinese name: Tǔ Xíng Sūn Hóng Shān Chá (土行孙红山茶).

Additional specimens examined (paratypes): China. Yunnan Province: Yuxi City, Xinping County, Zhaomike Village, 23°55′35.76″ N, 102°07′46″ E, 1380.30 m, 30 March 2025, fl., *H. C. Wang et al. XP30031* (YUKU02074883); the same locality, 21 September 2025, fr., *H. C. Wang et al. XP32426* (YUKU02074905).

3.4. A Key to Camellia tuxingsunii and Its Closely Related Species

1a Leaf blade secondary veins adaxially strongly impressed; filaments densely villous 2;
1b Leaf blade secondary veins adaxially visible or raised, rarely slightly impressed, sometimes obscure; filaments glabrous or subglabrous 4;
2a Leaf blade margin pectinately serrulate; bracteoles and sepals ca. 15, ± persistent in young fruit ..... *C. polyodonta*;
2b Leaf blade margin densely apiculately serrulate; bracteoles and sepals 8–10, caducous after anthesis 3;
3a Current year branchlets sparsely gray pubescent to subglabrous; year-old branchlets glabrous; filaments villous ..... *C. mairei* var. *mairei*;
3b Current year branchlets densely yellowish villous; year-old branchlets with persistent trichomes turning black at length; filaments slightly pilose or glabrous ..... *C. mairei* var. *velutina*;
4a Leaf blades small, usually less than 6 cm long; flowers relatively small, petals 2–4 cm long 5;
4b Leaf blades larger, usually more than 6 cm long; flowers larger, petals more than 4 cm long 6;
5a Young branches, petioles and midrib on abaxial leaf surface glabrous; leaf blades oblong to narrowly ovate, apex acuminate, rarely acute; flowers red; capsules broadly ellipsoid to ovoid, usually longer than wide, glabrous at maturity ..... *C. tuxingsunii*;
5b Young branches, petioles and midrib on abaxial leaf surface pubescent; leaf blades elliptic to lanceolate, apex usually acute, rarely acuminate; flowers pink to white; capsules depressed globose to subglobose, usually shorter than or subequal to wide, more or less pubescent at maturity ..... *C. saluenensis*;
6a Current year branchlets pubescent but glabrescent; leaf blade abaxially pubescent at least when young, apex acute to shortly acuminate with an obtuse tip; flowers usually red ..... *C. reticulata*;
6b Current year branchlets glabrous; leaf blade abaxially glabrous, apex acuminate to caudate; flowers usually pink to white, rarely red 7;
7a Leaf blades oblong-elliptic or oblong-oblanceolate, 6–10(–12) × 2.5–3.5(–4) cm, coriaceous to thinly coriaceous; flowers 5–6 cm in diam.; capsules 2.5–3.5 × 3–5 cm ..... *C. pitardii* var. *pitardii*;
7b Leaf blades elliptic, 9–14 × 4–6.4 cm, thickly coriaceous; flowers 8–10 cm in diam.; capsules 6–7 × ca. 8 cm ..... *C. pitardii* var. *compressa*.

4. Discussion

4.1. Non-Monophyly of sect. Camellia and Phylogenetic Position of Camellia tuxingsunii

Our plastid phylogeny supports that the traditionally circumscribed sect. *Camellia* is not monophyletic, with its members distributed across two distantly related clades (clades IV and VII) (Figure 2). This result is broadly congruent with previous phylogenetic studies based on nuclear ribosomal DNA, plastid markers and transcriptomic data, collectively indicating that the current morphology-based sectional delimitation does not reflect natural evolutionary relationships within *Camellia* [6, 16, 42, 45, 62].

Within clade IV, species of sect. *Camellia* are further split into two well-supported subclades, both of which are nested among species from sects. *Oleifera*, *Paracamellia*, and *Furfuracea*. A similar topological pattern was reported by Pang et al. [63], who also recovered multiple independent lineages of sect. *Camellia* within the subg. *Camellia* clade. The close phylogenetic affinity between sect. *Camellia* and the oil-tea clade (sects. *Oleifera* and *Paracamellia*) has been noted in several earlier studies [16, 45]. Given the well-documented effects of cytoplasmic inheritance, hybridization, introgression and incomplete lineage sorting on plastid tree topology in *Camellia* [29, 63], a robust infrageneric revision will require expanded taxon sampling and evidence from low-copy nuclear genes or whole-genome data.

In contrast to the East and South China distribution of sect. *Camellia* members in clade IV, the species in subclade F (clade VII) are concentrated in southwestern China, mainly on the Yunnan–Guizhou Plateau and adjacent regions, corresponding largely to subsect. *Reticulatae* sensu Zhang [10]. Subclade F is sister to subclade E, which comprises species from sects. *Eriandria* and *Theopsis*, with strong nodal support (BS = 99). A close relationship between sects. *Eriandria* and *Theopsis* has been consistently recovered in previous studies [42, 44, 62, 64], and our results further support their shared ancestry with the southwestern lineage of sect. *Camellia.*

In the plastid phylogenetic tree, *Camellia tuxingsunii* is nested within subclade F of clade VII, forming a moderately supported sister relationship (BS = 87) with the small clade comprising *C. mairei* and *C. omeiensis*. Subclade F consists exclusively of species from the traditional sect. *Camellia*, all endemic to the Yunnan–Guizhou Plateau and adjacent southwestern China, corresponding to subsect. *Reticulatae* sensu Zhang [10]. Morphologically, the new species possesses all diagnostic morphological traits of the section: solitary sessile subterminal flowers, undifferentiated caducous bracteoles and sepals, basally connate petals, outer staminal filaments fused into a tube, 3-loculed tomentose ovary, and basally connate 3-lobed styles. Its occurrence in central Yunnan also lies within the section's main diversity center [39]. Collectively, phylogenetic, morphological and biogeographic data are consistent with the assignment of this species to sect. *Camellia*; we retain this placement in accordance with the prevailing morphology-based classification.

4.2. Morphological Distinctiveness of Camellia tuxingsunii

Flower size and color are taxonomically diagnostic traits for sectional delimitation in *Camellia* [3]. Species of sects. *Theopsis* and *Eriandria* usually have small, mostly white flowers, with petal lengths of 1.5–2.0 cm and 1–2 cm, respectively [65, 66]. By contrast, members of sect. *Camellia* are typically characterized by large, predominantly red or pink flowers, with petals commonly 3–6 cm long and 2.5–4.5 cm wide [3]. Although *C. tuxingsunii* has the characteristic floral structure of sect. *Camellia*, its flowers are substantially smaller than those of most congeners in the section, with petals only 2.5–3.0 cm long. Among previously known species of sect. *Camellia*, *C. saluenensis* is regarded as having relatively small flowers [3, 25]. However, our field observations confirm that both the petal dimensions and overall flower diameter of *C. saluenensis* exceed those of *C. tuxingsunii*. *C. tuxingsunii* thus may represent one of the smallest-flowered species in sect. *Camellia* known to date.

Within sect. *Camellia*, *C. tuxingsunii* is morphologically most similar to *C. saluenensis*, as the two species share relatively small leaves and flowers, and both occur in southwestern China [10, 25]. *C. saluenensis* is a relatively widespread species with marked intraspecific morphological variation across its distributional range. Nevertheless, the two species are clearly distinguishable by a suite of diagnostic characters. Flower color is one of the most consistent diagnostic differences between the two. Our field observations and examination of herbarium material indicate that *C. saluenensis* has pink to white flowers (Figure 5), whereas *C. tuxingsunii* has red flowers (Figure 3). Additionally, *C. saluenensis* has pubescent young branches and petioles, and coriaceous to thickly coriaceous, elliptic to lanceolate leaf blades with a usually acute, rarely acuminate apex and a sparsely pilose abaxial surface with a pubescent midrib, whereas *C. tuxingsunii* has glabrous young branches and petioles, and thinly coriaceous, oblong to narrowly ovate leaves with an acuminate, rarely acute apex and a glabrous abaxial surface. Capsules of *C. saluenensis* are depressed globose to subglobose, usually shorter than or subequal to wide, and more or less pubescent at maturity, whereas those of *C. tuxingsunii* are broadly ellipsoid to ovoid, typically longer than wide, and glabrous at maturity. Geographically, *C. saluenensis* ranges mainly across western and northern Yunnan, southwestern Sichuan and northeastern Guizhou at elevations generally above 1600 m [10, 26], whereas *C. tuxingsunii* is currently known only from the Honghe (Yuanjiang) River valley in central Yunnan at around 1300–1400 m elevation. Furthermore, the two species are not recovered as closely related lineages in our plastid genome phylogenetic tree (Figure 2).

Our plastid phylogenetic analysis indicates that *C. tuxingsunii* is most closely allied to the lineage containing *C. mairei* and *C. omeiensis*, a relationship also supported by overall similarity in floral shape and color. Zhang (1981) recognized *C. mairei* and *C. omeiensis* as two distinct species [23], whereas Ming (2000) and Ming & Bartholomew (2007) treated them as conspecific [25, 26]. In view of their pronounced morphological similarity, largely overlapping distribution ranges and close phylogenetic affinity recovered in our plastid tree, we here follow the taxonomic treatment of Ming (2000) [25] and Ming & Bartholomew (2007) [25]. Nevertheless, *C. tuxingsunii* can be readily separated from *C. mairei* by a suite of stable diagnostic characters. In growth form, *C. mairei* is a large shrub or small tree, whereas *C. tuxingsunii* is a shrub usually no more than 2 m tall. *C. mairei* has larger leaf blades 6–15 cm long and 2.5–6.0 cm wide, with a caudate to long-acuminate apex and a pubescent midvein on the abaxial surface, whereas *C. tuxingsunii* has smaller leaves, 4–7 cm long and 1.5–2.0 cm wide, with an acuminate, rarely acute apex and a glabrous abaxial surface. *C. mairei* has larger flowers with outer petals 3.0–3.5 cm long and inner petals 4–5 cm long and has villous filaments, whereas *C. tuxingsunii* has smaller flowers with petals 2.5–3.0 cm long and glabrous filaments. Capsules of *C. mairei* are depressed globose to globose, relatively large, with a pericarp up to 1 cm thick, whereas those of *C. tuxingsunii* are broadly ellipsoid to ovoid and smaller, with a thin pericarp 2–3 mm thick. Geographically, *C. mairei* is found in western Sichuan and northeastern Yunnan, with no distributional overlap with *C. tuxingsunii* [3, 10, 26]. A morphological comparison of *C. tuxingsunii* with similar species is given in Table 1.



Figure 5. *Camellia saluenensis* and its floral color variation ((**A**–**D**) from Xiangyun, Yunnan; (**E**,**F**) from Luquan, Yunnan; (**G**) from Kunming, Yunnan). (**A**) Habit. (**B**,**C**) Flower, pink. (**D**) Flower bud. (**E**,**F**) Flower, pink to white. (**G**) Flower, white.

Table 1. Morphological comparison of *Camellia tuxingsunii* with the closely related species and similar species.

Character	***C. tuxingsunii***	***C. mairei* (*C. omeiensis*)**	***C. saluenensis***
Habit	shrubs, 1–2 m tall	shrubs or trees, 2–8 m tall	shrubs, 3–4.5 m tall
Young branches	glabrous	pubescent becoming glabrescent	pubescent
Current year branchlets	glabrous	gray pubescent or yellowish villous	glabrous
Leaf shape	blade oblong to narrowly ovate	elliptic, oblong-elliptic, or oblong-lanceolate	elliptic to lanceolate
Leaf size (cm)	4–7 cm long, 1.5–2.0 cm wide	6–15 cm long, 2.5–6.0 cm wide	3.8–6.3 cm long, 2–3 cm wide
Leaf apex	acuminate, rarely acute	caudate to long-acuminate	usually acute, rarely acuminate
Leaf base	cuneate	cuneate	attenuate
Indumentum of leaf	adaxial glabrous, abaxial glabrous	adaxial glabrous, pubescent midvein on the abaxial surface	abaxial sparsely pilose with pubescent midrib
Leaf margin	crenulate	densely apiculate–serrulate	serrulate
Petiole	0.5 cm, glabrous	1.0 cm, pubescent	0.5 cm, pubescent
Flower	dark red	dark red	pink to white

Bracteoles and sepals	9–11, margin ciliolate	8–10, both surfaces grayish yellow velutinous or inside glabrous	8, outside usually glabrous or rarely puberulent, margin ciliolate
Petals	6–8, margin ciliolate	outer 2–4 both surfaces white farinose-velutinous, inner glabrous	5, outer 1–2 pubescent
Petal size (cm)	2.5–3.0 cm long, 1.5–2.5 cm wide	outer 3.0–3.5 cm long, inner 4–5 cm long	2.5–3.8 cm long, 1.5–3.0 cm wide
Stamens	2.4–2.6 cm long, glabrous	3 cm long, pubescent	1.5–2.5 cm long, glabrous
Indumentum of ovary	white tomentose	yellow tomentose	white tomentose

Note: Data for *C. tuxingsunii* are from measurements of wild and herbarium material. Data for *C. mairei* and *C. saluenensis* are based on published accounts [9, 23, 25, 26, 47], field observations and herbarium specimens.

4.3. Ecology and Conservation of Camellia tuxingsunii

C. tuxingsunii is currently known only from dry mountain slopes in Xinping County, central Yunnan, on the edge of the Yuanjiang dry–hot valley at elevations of 1300–1400 m (Figure 6). The region has a subtropical monsoon climate with a pronounced foehn effect, characterized by distinct wet and dry seasons; rainfall is concentrated in the summer months, and the winter–spring period is marked by pronounced seasonal drought [67-69]. The Yuanjiang dry–hot valley is widely recognized as a center of plant endemism in southwestern China [70], and numerous narrowly endemic species have been described from the area in recent decades, including *Lysimachia ailaoshanensis*, *Tsaiodendron dioicum*, *Trigonostemon tuberculatus*, *Breynia hiemalis*, *Xantolis weimingii*, and *Cathetus yuanjiangensis* [71-76]. *Camellia tuxingsunii* grows in open forests and thickets, associated with *Quercus franchetii*, *Anneslea fragrans*, *Pinus yunnanensis, Terminalia franchetii and Campylotropis macrocarpa.* Compared with most other species in subclade F, which typically inhabit humid montane forests at 1200–2000 m [3, 77], *C. tuxingsunii* occurs in a markedly more seasonally dry habitat.

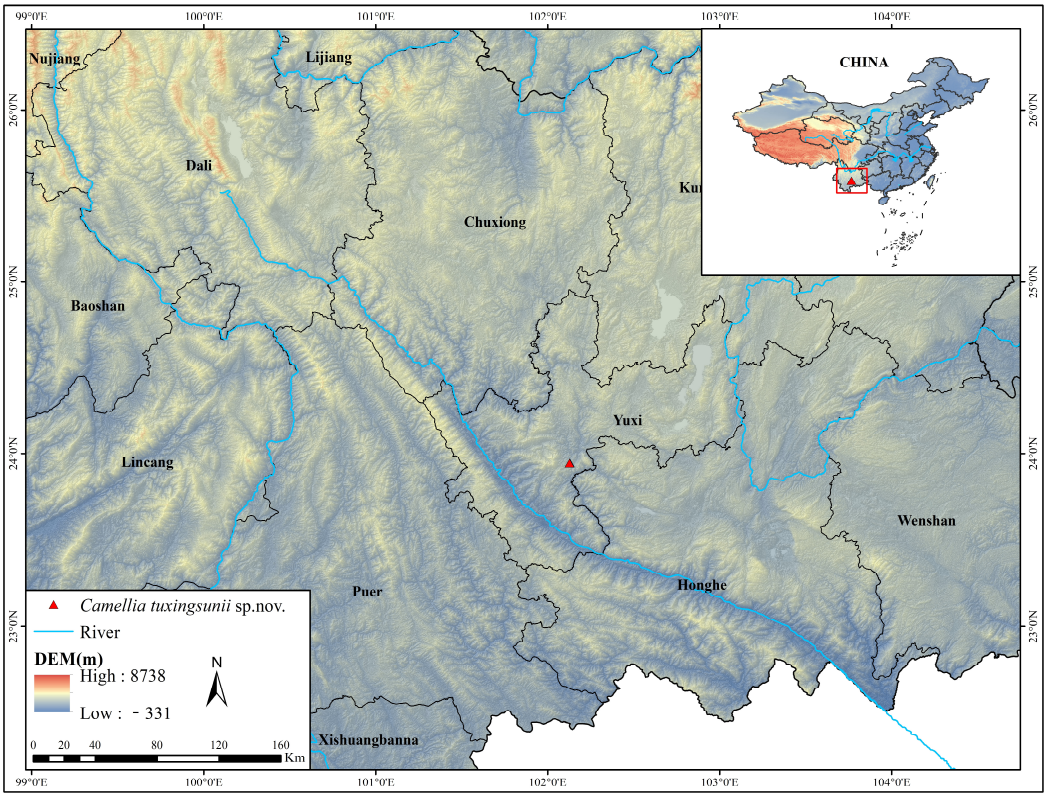


Figure 6. Geographical distribution of *Camellia tuxingsunii* sp. nov. (red triangle).

Targeted field surveys in the vicinity of the type locality have recorded only one population of *C. tuxingsunii*, with approximately 15–20 mature individuals observed. No additional populations have been found in adjacent areas, but comprehensive surveys across all similar dry-valley habitats in the region have not been conducted. The only known population is located outside formal protected areas, close to rural roads and farmland. It is therefore potentially vulnerable to habitat disturbance from road maintenance, agricultural expansion and other human activities. Wild *Camellia* species with ornamental traits may also be at risk of unregulated collection [78, 79], though no such activity has been documented for this species to date. Following the Guidelines for Using the IUCN Red List Categories and Criteria (version 16) [80], we preliminarily assessed this species as Data Deficient (DD). This assessment is based on the insufficiency of current data to reliably estimate the total population size, full extent of occurrence (EOO) and area of occupancy (AOO) across its potential range. Further intensive field surveys are required to establish the full extent of occurrence, area of occupancy, total number of mature individuals and actual threat levels, upon which a more robust conservation assessment can be based.

Supplementary Materials: The following supporting information can be downloaded at https://www.mdpi.com/article/10.3390/d18110699/s1: Table S1: GenBank accession numbers of the complete chloroplast genome sequences used in this study; Data S1: Plastid_treefile; Data S2: Plastid_alignment_mafft; Data S3: Plastid_alignment_mafft_trimAl.

Author Contributions: Conceptualization, J.-Q.W., T.-T.W. and H.-C.W.; methodology, J.-Q.W.; investigation, J.-Q.W., T.-T.W., J.-Y.W. and H.-C.W.; resources, H.-C.W.; data curation, J.-Q.W., T.-T.W. and J.-Y.W.; writing—original draft preparation, J.-Q.W. and T.-T.W.; writing—review and editing, T.-T.W. and H.-C.W.; visualization, J.-Q.W. and T.-T.W.; supervision, H.-C.W.; funding acquisition, H.-C.W. J.-Q.W. and T.-T.W. contributed equally to this work. All authors have read and agreed to the published version of the manuscript.

Funding: This work was supported by the Yunnan Provincial Wildlife Conservation Project (2025GS205Z-01) and the National Natural Science Foundation of China (31960040).

Institutional Review Board Statement: Not applicable.

Data Availability Statement: The processed sequence alignment, trimmed alignment, and inferred phylogenetic tree from this study are available in the Supplementary Files.

Acknowledgments: We are grateful to Tao Chen for assistance in preparing the distribution map.

Conflicts of Interest: The authors declare no conflicts of interest.

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https://doi.org/10.3390/d18110699