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Research Article

Sinosasa damingshanensis (Poaceae, Bambusoideae), a new combination supported by morphological and molecular evidence

Yi-Ting Zhang[1], Shu-Yan Lin[1], Zheng-Yang Niu[2], Wei-Xin Jiang[3], Nian-He Xia[2], Yu-Long Ding[1]

1 *College of Life Sciences, Nanjing Forestry University, Nanjing 210037, China*
2 *Key Laboratory of Plant Resources Conservation and Sustainable Utilization, Guangdong Provincial Key Laboratory of Digital Botanical Garden, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China*
3 *Guangxi Key Laboratory of Forest Ecology and Conservation, Key Laboratory of National Forestry and Grassland Administration on Cultivation of Fast-Growing Timber in Central South China, College of Forestry, Guangxi University, Nanning 530004, China*

Corresponding authors: Nian-He Xia (nhxia@scbg.ac.cn); Yu-Long Ding (ylding@vip.163.com)

Abstract

Morphological characteristics and phylogenetic analyses clearly revealed that *Chimonobambusa damingshanensis* should be a member of the genus *Sinosasa*, rather than *Chimonobambusa*, and is a distinct species close to *Sinosasa huapingensis* and *S. mingyueshanensis*. Morphologically, it differs from all the other known *Sinosasa* species by internodes initially with white pubescent, culm leaf auricles absent and triangularly subulate sheath blades, characteristics that are unusual in this genus. And this morphological distinction warrants recognition of *Ch. damingshanensis* as a new combination of *Sinosasa*.

Key words: Arundinarieae, new combination, phylogeny, taxonomy

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Introduction

Sinosasa L.C.Chia ex N.H.Xia, Q.M.Qin & Y.H.Tong (Poaceae, Bambusoideae), was first recognized as a genus of the temperate woody bamboo (i.e. Arundinarieae) by Q. M. Qin et al. (2021), and segregated from the genus *Sasa* Makino and Shibata (1901). It is characterized by racemose synflorescences, 3 stamens, 2 stigmas per floret, branches solitary and supranodal ridge strongly raised (Qin et al. 2021). So far, 8 species endemic to subtropical areas of China (Qin et al. 2021; Li et al. 2023), were included in the genus.

Chimonobambusa damingshanensis Hsueh & W. P. Zhang (1988) was described based on the only collection *C. J. Hsueh 8605* from Daming Mountain, Nanning, Guangxi Province, China. It is widely accepted in the flora accounts and monographs (Ohrnb 1990; Zhu et al. 1994; Hsueh and Wang 1996; Li and Stapleton 2006; Yi et al. 2008; Yi et al. 2009; Maria et al. 2018). In the protologue, it is described as "Rhizoma ampnipodiale; culmi graciles, erecti, caespitosi…; nodis culmorum plane protuberantibus, nodis vaginarum…basi 1-2 nodis radicibus aeriis…; Rami 1-3… Rami florum foliati; Ramuli florum basi 4-5-bracteati…". All the important characters provided by the authors fit well with the circumscription of *Chimonobambusa*. After careful examination of the types

(SWFC), we realized that the racemose synflorescence with real spikelets were misinterpreted as pseudospikelets and then the species *Ch. damingshanensis* is definitely not a member of the genus *Chimonobambusa*. In order to clarify the identity, we launched a special expedition to the type locality of the species, i.e. Daming Mountain, Nanning City, Guangxi Province of China, where only one bamboo with leptomorph rhizome, culm nodes prominent, culm sheath blades extremely small and foliage leaves with very long ligule, was found and it matches the protologue of *Ch. damingshanensis* very well. It is easily recognized as a member of *Sinosasa* rather than *Chimonobambusa* from branch compliment 1 per node, very prominent culm nodes and long ligule of foliage leaves. So, after comprehensive study, including morphological investigation, phenological observation, and phylogenetic reconstruction, *Chimonobambusa damingshanensis* was herein formally treated as a member of the genus *Sinosasa*, rather than *Chimonobambusa*.

Materials and methods

The specimens of *Chimonobambusa damingshanensis* were obtained from field trips in 25 December of 2024. Its type specimen, *C. J. Hsueh 8605*, deposited in the Herbarium of Southwest Forestry University (SWFC), was examined. Some detailed characters, e.g. sheath ligule, were observed with hand lens and stereomicroscope (Leica S6D).

A total of 24 species representing 10 genera of the tribe Arundinarieae (Bambusoideae) were utilized to reconstruct a phylogeny based on complete chloroplast (cp) genome, among which *Bambusa sinospinosa* McClure and *B. emeiensis* L. C. Chia & H. L. Fung were set as the outgroup taxa. All these sequences were previously published in GenBank. Accession numbers and voucher information are listed in Table 1.

By using the Plant Genomic DNA Kit (TSINGKE), total genomic DNA of *Ch. damingshanensis* was extracted from young and healthy leaves, and then sent to Novogene for DNA sequencing under the Illumina NovaSeq 6000 platform. A total of 40 G genome skimming data was used to assemble the complete chloroplast genome by GetOrganelle v 1.7.4 (Jin et al. 2018) using *Amborella trichopoda* Baill. (accession number: NC_005086) and *Chimonobambusa luzhiensis* (J. R. Xue & T. P. Yi) T. H. Wen & Ohrnb. (accession number: NC_062708) set as the reference, with k-mer values of 21, 45, 65, 85, 105, 125 bp. The Bandage software (Wick et al. 2015) was employed to graphically visualize the assembled chloroplast. The complete chloroplast (cp) genome was annotated, and manually corrected in Geneious v9.1.4 (Kearse et al. 2012).

The matrix of all the whole chloroplast genomes was aligned in MAFFT v. 7.490 (Katoh and Standley 2013). Phylogenetic trees were constructed by using Maximum Likelihood (ML) and Bayesian Inference (BI). ML analysis was generated by IQ-TREE v.1.6.8 (Nguyen et al. 2015). BI analysis was generated by using MrBayes v 3.2.6 under the Akaike information criterion (AIC) (Ronquist et al. 2012). The best substitution model of TPM1uf was defined by jModeltest2 2.1.6 (Darriba et al. 2012).

Posterior Probability (PP) was obtained from Metropolis-coupled Markov Chain Monte Carlo (mcmc nruns = 2; ngen = 10,000,000; printfreq = 1,000; samplefreq = 1,000; nchains = 4; 25% burn-in).

Table 1. List of 24 bamboo taxa sampled in the present study with related voucher and GenBank accession information.

Taxon	Voucher information	Accession number
Ingroup		
Acidosasa purpurea (Hsueh & T.P. Yi) Keng f.	Zhang08023 (KUN)	HQ337793
Ampelocalamus actinotrichus (Merr. & Chun) S.L. Chen, T.H. Wen & G.Y. Sheng	MPF10003 (KUN)	MF066245
Chimonobambusa angustifolia C.D. Chu & C.S. Chao	Wu20210053 (YAFG)	OK040768
Chimonobambusa damingshanensis Hsueh & W. P. Zhang	WM241225 (NF)	PV021571
Chimonobambusa hejiangensis C.D. Chu & C.S. Chao	GACP (NMGU)	MT884004
Chimonobambusa purpurea Hsueh & T.P. Yi	LW20200602-01 (CAAF)	MW030500
Chimonobambusa quadrangularis (Fenzi) Makino	CIMPC-RFM-20210302 (CMPC)	MW928533
Chimonobambusa sangzhiensis (B.M. Yang) N.H. Xia & Z.Y. Niu	NZY109 (IBSC)	OM867788
Chimonobambusa tumidissinoda Ohrnb.	MPF10083 (KUN)	MF066244
Chimonobambusa utilis (Keng) Keng f.	Not provided by the author	OK040769
Hsuehochloa calcareus (C.D. Chu & C.S. Chao) D.Z. Li & Y.X. Zhang	MPF10050 (KUN)	KJ496369
Indocalamus sinicus (Hance) Nakai	ZMY037 (KUN)	MF066250
Indosasa crassiflora McClure	BH58 (IBSC)	OK558536
Indosasa shibataeoides McClure	MPF10028 (KUN)	MF066251
Oligostachyum shiuyingianum (L.C. Chia & But) G.H. Ye & Z.P. Wang	DZL09122 (KUN)	JX513423
Pleioblastus amarus (Keng) Keng f.	Zhang Yu-QuC373 (SANU)	MH988736
Pleioblastus maculatus (McClure) C.D.Chu & C.S.Chao	MPF10161 (KUN)	JX513424
Sasa veitchii Rehder	LC1325 (ISC)	KU569975
Sinosasa fanjingshanensis N.H. Xia, Q.M.Qin & J.B. Ni	BH124 (IBSC)	OP850348
Sinosasa gracilis B.M.Yang	LX153 (IBSC)	OP973764
Sinosasa guangxiensis (C.D.Chu & C.S.Chao) N.H. Xia, Q.M. Qin & X.R. Zheng	CZY173 (IBSC)	OP850352
Sinosasa longiligulata (McClure) N.H. Xia, Q.M. Qin & J.B. Ni	CZY163 (IBSC)	OP850351
Outgroup		
Bambusa emeiensis L.C. Chia & H.L. Fung	Zhang08019 (KUN)	HQ337797
Bambusa sinospinosa McClure	Li043 (KUN)	MK679807

Results

The chloroplast genome size of *Chimonobambusa damingshanensis* is 139,964 bp and those of all the samples ranged from 139,394 bp (*Bambusa multiplex* L. C. Chia & H. L. Fung) to 140,013 bp (*Sinosasa gracilis*) with an alignment of 159,910 bp. The phylogenetic tree topology generated by ML and BI analyses was somewhat congruent, differing only in the support values of the nodes, so only the ML tree was shown with nodal support values from both methods labelled (Fig. 1). As shown in the majority-rule consensus tree, *Chimonobambusa damingshanensis* is distantly related to other *Chimonobambusa* species, but forms a monophyletic clade with four *Sinosasa* species with nodal support (BS = 77% and PP = 1.00).

Morphologically, *Chimonobambusa damingshanensis* resembles *Sinosasa huapingensis* N.H.Xia, Q.M. Qin & Y.H. Tong and *Sinosasa mingyueshanensis* N.H.Xia, Q.M.Qin & X.R. Zheng in having branches solitary, culm leaf auricles absent, foliage leaf auricles and oral setae present (Figs 2, 3). However, it can be easily distinguished from the latter two species by the morphological characters (Table 2).

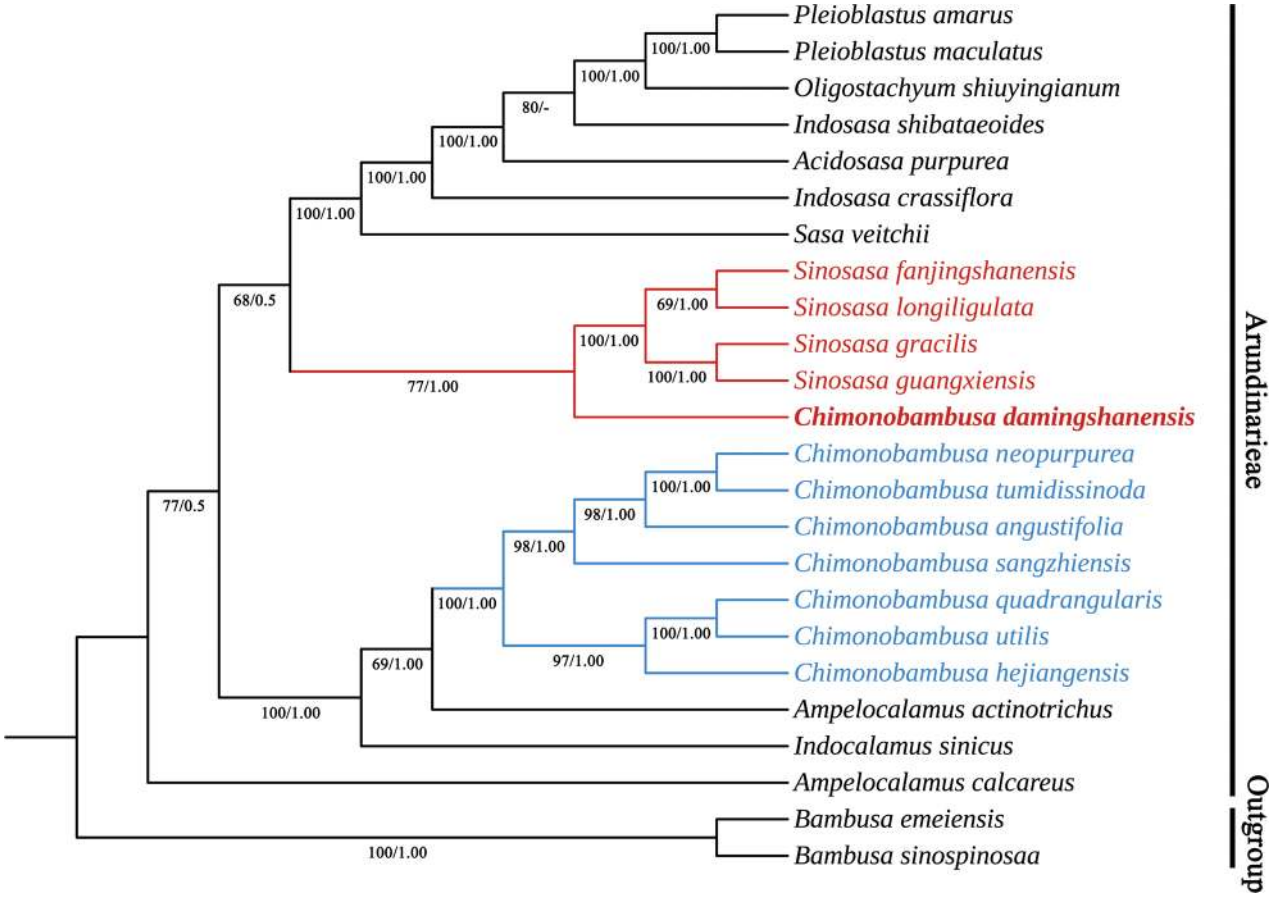


Figure 1. Phylogenetic relationships among *Chimonobambusa damingshanensis* and other 21species of Arundinarieae, based on plastid genome dataset with Maximum Likelihood and Bayesian analysis. Numbers above branches indicate maximum likelihood bootstrap support (BS) and posterior probabilities (PP), respectively.

Table 2. Morphological comparison of *Chimonobambusa damingshanensis* and two related species.

Morphology	*Ch. damingshanensis*	*S. huapingensis*	*S. mingyueshanensis*
Young culm internodes	white pubescent gradually glabrous	sparsely brown hirsute gradually deciduous	upper part initially densely brown strigose, gradually glabrescent
Sheath blades	Triangularly subulate	Lanceolate	Lanceolate
Foliage leaf sheaths	Glabrous	Puberulent	Glabrous
Oral setae	4–8, 2.5–6 mm	2–4, 2–6 mm	4–6, 10–20 mm
Number of leaves on ultimate branch	5–10	8–17	6–7
Number of secondary veins of blades	3–4 (6) pairs	5–7 pairs	6–7 pairs
blades both surfaces	glabrous	adaxially glabrous, abaxially puberulent	glabrous

Discussion

Our phylogenetic analysis demonstrated that *Sinosasa* is monophyletic (Fig. 1), consistent with the previous studies (Zeng et al. 2010; Guo et al. 2021). *Chimonobambusa damingshanensis* are described in the protologue as having 2 stigmas, and are observed in the type specimens as having true spikelets and 3 stamens. Molecular evidence from the plastid and morphological evidence

further confirmed that *Chimonobambusa damingshanensis* should be a member of *Sinosasa* rather than *Chimonobambusa*, and thus a new combination in *Sinosasa* is proposed.

Taxonomic treatment

***Sinosasa damingshanensis* (Hsueh & W.P.Zhang) N.H.Xia & Y.L.Ding, comb. nov.**
urn:lsid:ipni.org:names:77359971-1
Figs 2–4

Basionym. *Chimonobambusa damingshanensis* Hsueh & W. P. Zhang, Bamb. Res. 7(3): 5. (1988).

Lectotype (here designated). China • Guangxi, Nanning, Wuming, Daming Mountain, 12 Nov. 1986, *C. J. Hsueh 8605 fl.* (Lectotype: SWFC!).

Revised description. Shrubby bamboos. Rhizomes leptomorph, rhizome internodes cylindrical, 2.45–4.75 cm long, nearly solid; nodes prominent, 2–4 roots at each node; rhizome bud ovate, ca. 4 mm high. Culms 1.5–2 m tall, 5–8 mm in diam; internodes terete, 5.4–13 cm long, initially with white pubescent gradually glabrous; supranodal ridge conspicuous, intranodes glabrous, 3–4 mm tall, infranodal region with a creamy-yellow and sericeous ring; branches solitary at each branching node. Culm bud solitary, triangular-ovate, sunken into supranodal ridge. Culm leaf sheaths persistent or tardily deciduous, papery, shorter than or as long as internode, abaxially glabrous or sparsely strigose, 6.8–13.3 cm high; sheath scar flat or slightly prominent; auricles and oral setae absent; blades erect, triangularly subulate, 1.6–4.5 mm high, glabrous. Foliage leaves 5–10 per ultimate branch; foliage leaf sheaths glabrous, purple or purple-green; auricles linear, 1–2 mm wide; oral setae erect or curled, 4–8, pale yellow, 2.5–6 mm long, easily deciduous when old; ligules developed, (3.3) 6–10 (–16) mm high, papery. Blades lanceolate, papery, 12.5–31.7 × 1.0–4.9 cm, both surfaces glabrous, margins serrulate along both sides, secondary veins 3–4 (6) pairs, significantly elevated on the lower leaf surface. The unit of the inflorescence raceme-like; lemma papery, ovate-lanceolate, ca. 10 mm long, glabrous; palea shorter than lemma, 6–7 mm long, 2-keeled; 2 stigmas, 3 stamens; ovary ellipsoid; style short. Fruit unknown.

Notes. *Chimonobambusa damingshanensis* Hsueh & W. P. Zhang was originally described based on *C.J. Hsueh 8605* which contains multiple specimens. According to the ICN (Turland et al. 2018) Art. 8.1, "The type (holotype, lectotype, or neotype) of a name of a species or infraspecific taxon is either a single specimen conserved in one herbarium or other collection or institution, or a published or unpublished illustration", *C.J. Hsueh 8605 fl.* (SWFC, floriferous specimen) is designated here as the lectotype of *Ch. damingshanensis*. It has flower specimens and is more complete.

Phenology. New shoots produced during April to May.

Chinese name. 大明山华赤竹(Chinese pronunciation: dà míng shān huá chì zhú).

Distribution and habitat. Broad-leaved forests; It is endemic to Daming Mountain in Wuming District, Guangxi, China.

Additional specimen examined. *Sinosasa damingshanensis*: China • Guangxi: Nanning, Wuming, Daming Mountain, 23°29'43.9"N, 108°26'14.0"E, alt. 1224–1445 m a.s.l., 25 December 2024, *Y. L. Ding & Y. T. Zhang WM241225* (NF!).



Figure 2. *Chimonobambusa damingshanensis* Hsueh & W. P. Zhang. **A**–**D** *C.J. Hsueh 8605* (SWFC!). Photo by Yi-Ting Zhang.

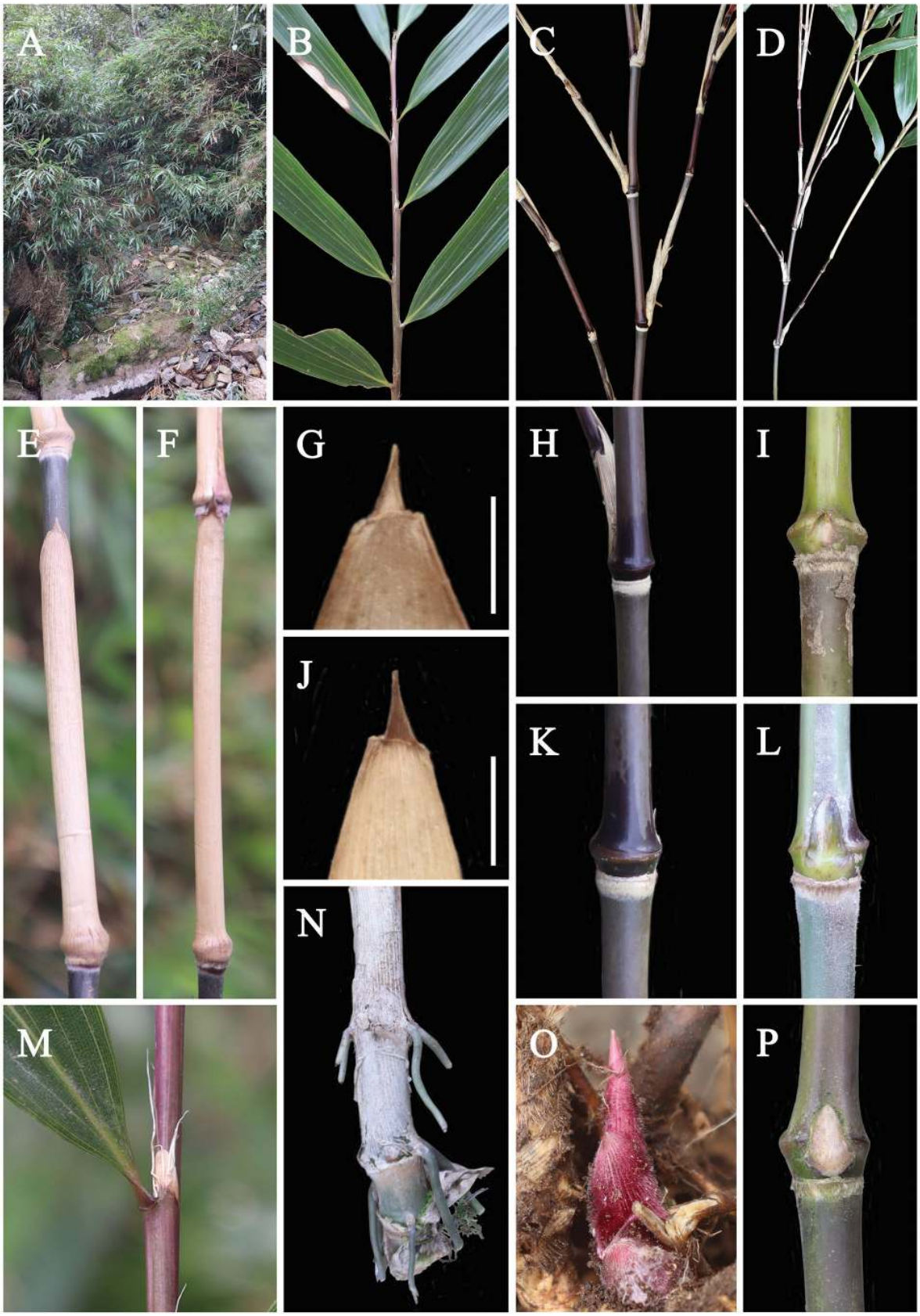


Figure 3. *Sinosasa damingshanensis* **A** habitat and plants **B** foliage leaf branches **C** solitary branch **D** leafy branchlet and culm **E, F** culm and culm sheath **G** adaxial view of sheath blade **H** branch complements with a solitary primary axis **I, L, P** culm bud **J** abaxial view of sheath blade **K** culm node **M** leaf sheath, ligule and oral setae **N** basal culm nodes with root thorns (uncommon) **O** development of bamboo shoot under the ground. Scale bars: 1 cm (**G, J**).

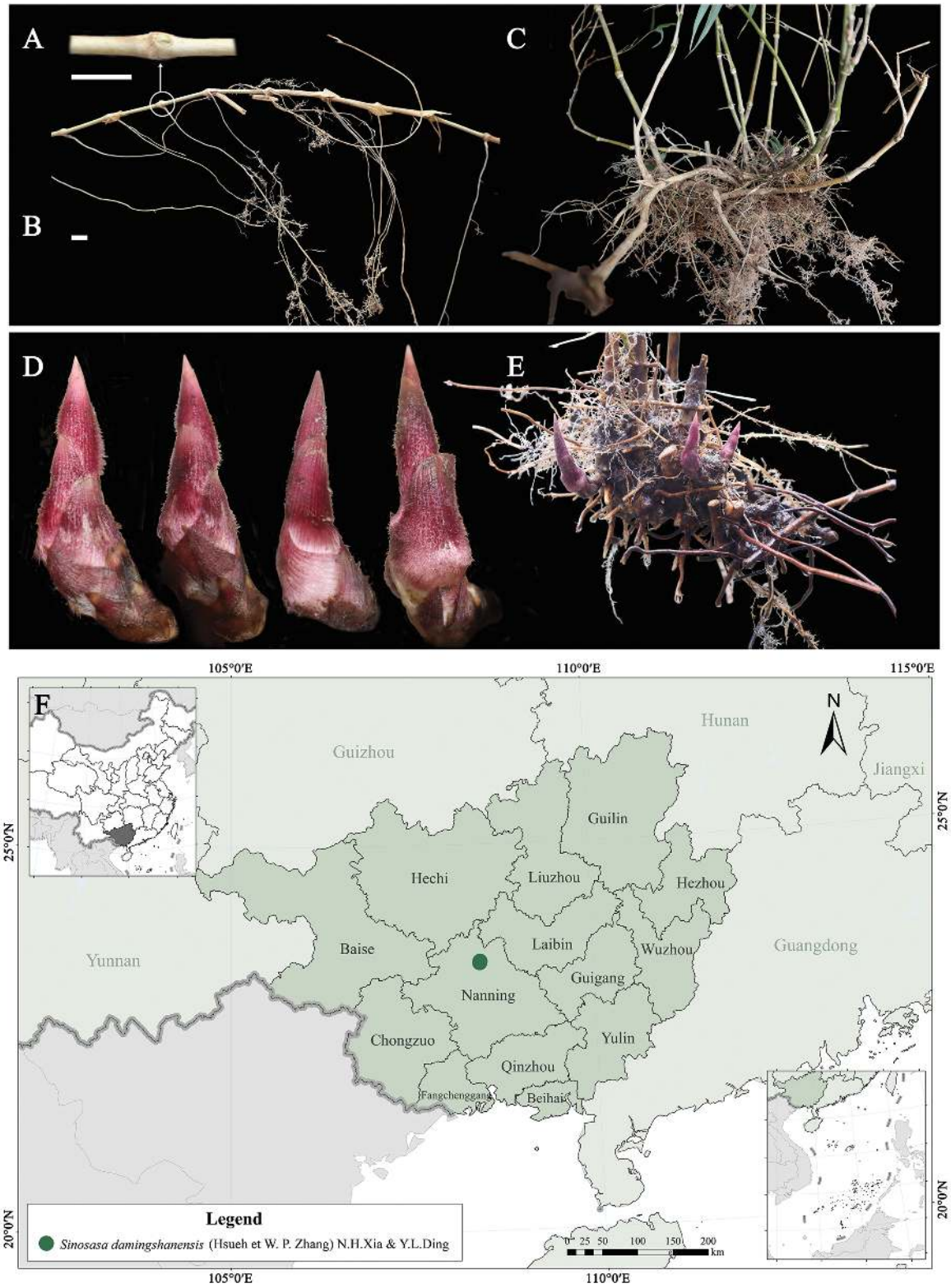


Figure 4. *Sinosasa damingshanensis* **A** rhizome bud **B, C, E** rhizome **D** development of bamboo shoot under the ground **F** distribution map of *Sinosasa damingshanensis* in Nanning, Guangxi, China. Scale bars: 1 cm (**A, B**).

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Yu-Long Ding, Nian-He Xia, Shu-Yan Lin, Wei-Xin Jiang, and Yi-Ting Zhang conducted fieldwork and specimen identification. Yi-Ting Zhang and Zheng-Yang Niu performed the molecular analyses and phylogenetic reconstruction. Both authors contributed equally to writing the manuscript.

Author ORCIDs

Yi-Ting Zhang https://orcid.org/0000-0002-7068-9830
Shu-Yan Lin https://orcid.org/0000-0001-6326-2516
Zheng-Yang Niu https://orcid.org/0000-0003-0281-1504
Wei-Xin Jiang https://orcid.org/0000-0001-6447-8087
Nian-He Xia https://orcid.org/0000-0001-9852-7393

Data availability

All of the data that support the findings of this study are available in the main text. The newly generated sequences were deposited in the GenBank database (accession numbers PV021571).

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