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# ***Goodyera medogensis* (Orchidaceae) a new species from Tibet, China**

 **Tong Yi-Hua, Mei Sun, Bing-Mou Wang, Huaizhen Tian**

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# *Goodyera medogensis* (Orchidaceae), a new species from Tibet, China

Yi-Hua Tong<sup>1,2,#</sup>, Mei Sun<sup>3,#</sup>, Bing-Mou Wang<sup>4</sup>, Huai-Zhen Tian<sup>3</sup>

**1** Key Laboratory of Plant Resources Conservation and Sustainable Utilization & Key Laboratory of Digital Botanical Garden of Guangdong Province, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, 510650, China **2** Center of Conservation Biology, Core Botanical Gardens, Chinese Academy of Sciences, Guangzhou, 510650, China **3** School of Life Sciences, East China Normal University, Shanghai 200241, China **4** Panyu Central Hospital, Guangzhou, 511402, China

# Yi-Hua Tong and Mei Sun contributed equally to this work.  
Corresponding author: Huai-Zhen Tian (thz0102@126.com)

## Abstract

A new species of *Goodyera* (Orchidaceae) from Tibet, China, *G. medogensis*, is described and illustrated here. This new species is most morphologically similar to *G. hemsleyana*, but differs by the thick grid lines of reticulations with blurred margin on adaxial surface of leaf blades, inflorescence with more flowers, petals obliquely obovate-rhombic, labellum yellow or yellowish, without lamella on blade, and floral bracts, sepals and ovary with non-glandular trichomes. Molecular phylogenetic study also supports that *G. medogensis* is a new species and belongs to *G.* subsection *Reticulum*.

## Key words

Jewel orchid, morphology, new species, phylogeny

## Introduction

The genus *Goodyera* R. Br. (Orchidaceae), known as jewel orchids, consists of about 100 species distributed in South Africa, Madagascar, Asia, Southwest Pacific islands, Northeast Australia, Europe, and North America (Chen et al. 2009). This genus belongs to the subtribe Goodyerinae of the tribe Cranichideae in the subfamily Orchidoideae (Pridgeon et al. 2003). *Goodyera* is characterized by elongate creeping rhizome, cymbiform lip with a concave-saccate hypochile, sectile pollinia and one stigma.

There are approximately 34 species of *Goodyera* in China, out of which 15 are endemic (Chen et al. 2009; Jin and Yang 2015; Zhou et al. 2016; Wang et al. 2020; Zhou et al. 2020). During a botanical survey in Medog County, Tibet Autonomous Region in January 2021, a few living plants of an unknown jewel orchid with reticulated leaves was collected and cultivated in Kunming Botanical Garden. It blooms vigorously with many beautiful flowers in August. We also found flowering individuals in the field at the same time. It is similar to *G. hemsleyana* King & Pantl. However, it has greenish flowers with yellow lips, while *G. hemsleyana* has pink flowers with white lips. Besides, the reticulations on leaf blades of the two species are also different.

Based on detailed examination of the morphological characters of our materials and its

similar species, and molecular phylogenetic evidence, we concluded that this species is new to science. It is described and illustrated here as *G. medogensis* H. Z. Tian, Y. H. Tong & B. M. Wang.

### Materials and methods

Voucher specimens of *G. medogensis* were collected from Medog County and preserved at the herbarium of South China Botanical Garden, Chinese Academy of Sciences (IBSC) and East China Normal University (HSNU). Fresh leaves used for molecular analyses were preserved in silica gel. Descriptions were based on living materials. Measurements were performed with a ruler, and small plant parts were observed and measured under a stereo microscope (Mshot-MZ101).

To study the phylogenetic position of the new species within the genus *Goodyera*, three DNA fragments, viz. internal transcribed spacer (ITS) and two plastid DNA regions (*matK* and *trnL-F*), were selected for building the phylogenetic tree based on previous studies (Hu et al. 2016; Zhou et al. 2020). In total, 32 species represented by 76 samples of *Goodyera* were analyzed with one sample of *Pachyplectron arifolium* Schltr. as the outgroup. All sequences were downloaded from GenBank except for the new species. Species names and GenBank accession numbers are provided in supplementary materials Table S1.

Total genomic DNA of the new species was extracted from silica gel-dried leaves using a modified CTAB method (Doyle and Doyle 1987). Polymerase Chain Reaction (PCR) amplification was carried out on TAKARA TP600 thermocycler (TAKARA BIO INC, Japan) using 25 µl reactions containing 12.5 µl 2× Taq PCR Master Mix (HuaGene, China), 8.5 µl ddH<sub>2</sub>O, 1.5 µl of each primer (10 µM) and 1 µl target DNA template. Detailed information of primers of relevant DNA fragments used in PCR amplification and sequencing, as well as the procedures of PCR, can be found in Table S2. The resulting amplicons were visualized by horizontal agarose gel electrophoresis (1%), colored with GoldView I (Solarbio, China). Clearly distinguishable bands were recorded, and then the corresponding PCR products were sequenced by Shanghai HuaGene Biotech Co., Ltd (Shanghai, China).

Sequences were firstly assembled and edited with Seqman (DNA STAR package, Madison, WI, USA) and then adjusted manually. Phylogenetic analysis was conducted using phylosuite ver. 1.2.2 (Zhang et al. 2020). Sequences were aligned with MAFFT (Katoh and Standley 2013). Ambiguously aligned fragments were removed using Gblocks (Talavera and Castresana 2007) with all parameters at their default settings. After that, we replace the "-" at both ends of the sequence with "?" instead to represent missing data using MEGA version X 10.1.6 (Kumar et al. 2018). Next, *matK* and *trnL-F* were concatenated as well as ITS, *matK* and *trnL-F* respectively to two datasets. Thus, three datasets were constructed in total: the cpDNA dataset (including *matK* and *trnL-F*), the nrDNA dataset (including ITS) and the nr+cpDNA dataset (ITS, *matK* and *trnL-F*). The three datasets were analyzed by using Bayesian inference (BI) and maximum likelihood (ML) methods respectively. Best-fit evolutionary model for Mrbayes and IQ-TREE were selected under the Bayesian Information Criterion (BIC) using ModelFinder (Kalyaanamoorthy et al., 2017). The best-fit models for the Maximum likelihood (ML) analysis are K80+R2 (ITS) and K3Pu+F+R2 (cpDNA,

nr+cpDNA), and for Bayesian inference (BI) they are K2P+G4 (ITS) and GTR+F+G4 (cpDNA, nr+cpDNA).

Based on these models, the Maximum Likelihood (ML) analysis was performed with IQ-TREE (Nguyen et al. 2015) for 10000 ultrafast (Minh et al., 2013) bootstraps, and Bayesian Inference (BI) phylogenies were inferred using MrBayes 3.2.6 (Ronquist et al. 2012). BI analysis consisted of two simultaneous runs and four simultaneous Markov Chain Monte Carlo (MCMC) chains, and ran for 3000000 generations with chain sampling every 1000 generations. The average deviation of split frequencies fell below 0.01, and initial 25% of sampled data were discarded as burn-in. The phylogenetic trees were visualized and modified in FigTree version 1.4.3 (Rambaut and Drummond 2016).

## Results

Our ML and BI phylogenetic trees constructed by the three datasets showed that our four samples of *G. medogensis* cluster into one separate subclade (Figures 1a, 1b, 2), which locates in the clade of *Goodyera* subsection *Reticulum* S. W. Chung & C. H. Ou (Hu et al., 2016) consisting of other seven species, viz. *G. biflora* (Lindl.) Hook. f., *G. hachijoensis* Yatabe, *G. hemsleyana* King & Pantling, *G. hispida* Lindl., *G. pusilla* Bl., *G. vittata* Benth. ex Hook. and *G. yamiana* Fukuy., which have relatively obvious reticulations on the leaves and lip sac with hairs inside. Thus, the results of phylogenetic analyses supported that *G. medogensis* is a new species belonging to the subsection *Reticulum*., and it has close relationship with *G. biflora*, *G. hemsleyana* and *G. vittata*.

## Taxonomic treatment

*Goodyera medogensis* H. Z. Tian, Y. H. Tong & B. M. Wang, sp. nov.

Figure 3

**Type.** China. Tibet Autonomous Region: Medog County, Renqingbeng Temple, under evergreen broad-leaved forest, cultivated in Kunming Botanical Garden, 3 August 2021 (fl.), B. M. Wang TYH-2523 (holotype: IBSC, isotype: HSNU).

**Diagnosis.** Similar to *G. hemsleyana*, but distinguished by the grid lines of reticulations on adaxial surface of leaf blades thick with blurred margin (vs. thin with clear margin), inflorescence with more flowers ((6–)12–15 vs. 4–10), petals obliquely obovate-rhombic (vs. obliquely ovate-oblong), labellum yellow or yellowish (vs. white, with light greenish to pinkish tinge at apex) without lamella on blade (vs. with a low bi-lamellate callus), and floral bracts, sepals as well as ovary with non-glandular trichomes (vs. glandular).

**Description.** Terrestrial herb, 12–25 cm tall. Rhizome 4–6 cm long, 1.5–3 mm in diam., greenish, rooting at nodes. Roots fleshy, 0.7–7 cm long, yellowish brown, with minute root hairs. Stem erect, terete, 4–9 cm long, 2.7–4.0 mm in diam., pale green, glabrous, with few sheaths at base formed by withered bases of petioles. Leaves 3–7; petiole 1.1–1.6 cm long, sheathing at base; lamina ovate, 1.9–4.2 × 1.5–2.6 cm, obtuse at base, acute at apex, adaxially green to bluish green with greenish-white reticulations, grid lines thick, margin blurred, transverse ones 5–7, abaxially pale

green, 5–7-veined. Inflorescence a terminal raceme, laxly (6–)12–15-flowered, spirally arranged, pubescent; peduncle 4.0–6.5 cm long, pubescent, with 2–3 sheathing bracts; sheathing bracts 1.5–1.9 × 0.6–0.8 cm, oblong-lanceolate, acute at apex, pale green, clasping, more or less pubescent, especially on the margin, 3–5-veined; rachis 3.5–7 cm long, pubescent. Floral bracts ovate-lanceolate, 1.4–1.7 × 0.5–0.6 cm, acuminate to acute at apex, pale green, longer than ovary, sometimes shortly ciliate at margins, pubescent abaxially, trichomes multicellular, up to 0.8 mm, glabrous adaxially, 3-veined. Flowers resupinate, opening weakly, 8–10 mm long. Sepals 1-veined, acute at apex, olive greenish, with reddish or brownish tinge when old, with dense clavate trichomes outside, trichomes up to 0.5 mm long; dorsal sepal ovate-lanceolate, 8–9 × 2–3 mm, forming hood with petals; lateral sepals ovate-lanceolate, 8–9 × 3.5–4 mm. Petals obliquely obovate-rhombic, 8.0–8.5 × 3.0–3.5 mm, acuminate to acute at apex, white, with reddish or brownish tinge at central part, glabrous, 1-veined. Labellum oblong-ovate, 6–7 mm long, yellow or yellowish; sac ca. 1.5–2.5 × 2.5–3.5 mm, with glandular hairs inside; blade oblong to oblong-lanceolate, entire, 5.0–6.5 × 2.0–3.0 mm, margins slightly undulate, obtuse to subacute at apex. Column ca. 1 mm long; rostellum 3.5–4.0 mm long, bifid, acuminate at apex. Stigma suborbicular, ca. 1 × 1 mm, entire. Anther cap yellowish brown, ovate, ca. 2.5 × 1.5 mm. Pollinarium 3–3.5 mm long; pollinia 2, oblong-obclavate, 0.8–1 mm long, dull yellowish white, sectile, bifid; caudicles 1.5–1.7 mm long; viscidium narrowly ovate-oblong, 2–3 × ca. 0.5 mm, acute at apex, membranous. Ovary terete, including pedicel 6.0–7.5 × ca. 2.0 mm, pale green, twisted, pubescent.

**Etymology.** The species epithet is named after the type locality, Medog County.

**Vernacular name.** 墨脱斑叶兰 (Chinese pinyin: mò tuō bān yè lán).

**Distribution and habitat.** This species is currently known only from Medog County, Tibet, China. It grows under evergreen broad-leaved forests at elevations of 1600–2300 m.

**Conservation status.** During our three surveys in January, June and August 2021, *Goodyera medogensis* was found in the forests of Medog Town and Beibeng Township of Medog County with about more than 200 individuals. However, since the population assessment of this species in the whole Medog County has not been made, conservation status of this new species is best classified as ‘Data Deficient’ (DD) (IUCN Standards and Petitions Committee 2019).

**Phenology.** Flowering in July–August.

**Additional specimens examined (paratypes).** CHINA. Tibet Autonomous Region, Medog County, Bari village, elev. 1750 m, 23 June 2021, cultivated in East China Normal University, 10 August 2021 (fl.), *J. Huang & M. Sun 21062310* (HSNU); *ibid.*, Medog village, 19 August 2021, *H. Z. Tian et al. 21081914* (HSNU); *ibid.*, Gelin village, 21 August 2021, *H. Z. Tian et al. 21082102* (HSNU).

## Discussion

According to Hu et al. (2016), sect. *Reticulum* is one of the four sections of *Goodyera*, and can be further divided into two subsections, viz., *G.* subsect. *Reticulum* S. W. Chung & C. H. Ou and *G.* subsect. *Foliosum* S. W. Chung & C. H. Ou. Most species of sect. *Reticulum* have reticulated venation on leaves and not opened lateral sepals. According to phylogenetic trees based on the three datasets in this study, although the sister group matter is still unclear for the conflicting results showed by nrDNA and cpDNA, position of the new species that belongs to subsect. *Reticulum* is confirmed. It is closer to *G. hemsleyana*, which is supported by the morphological and phylogenetic evidences.

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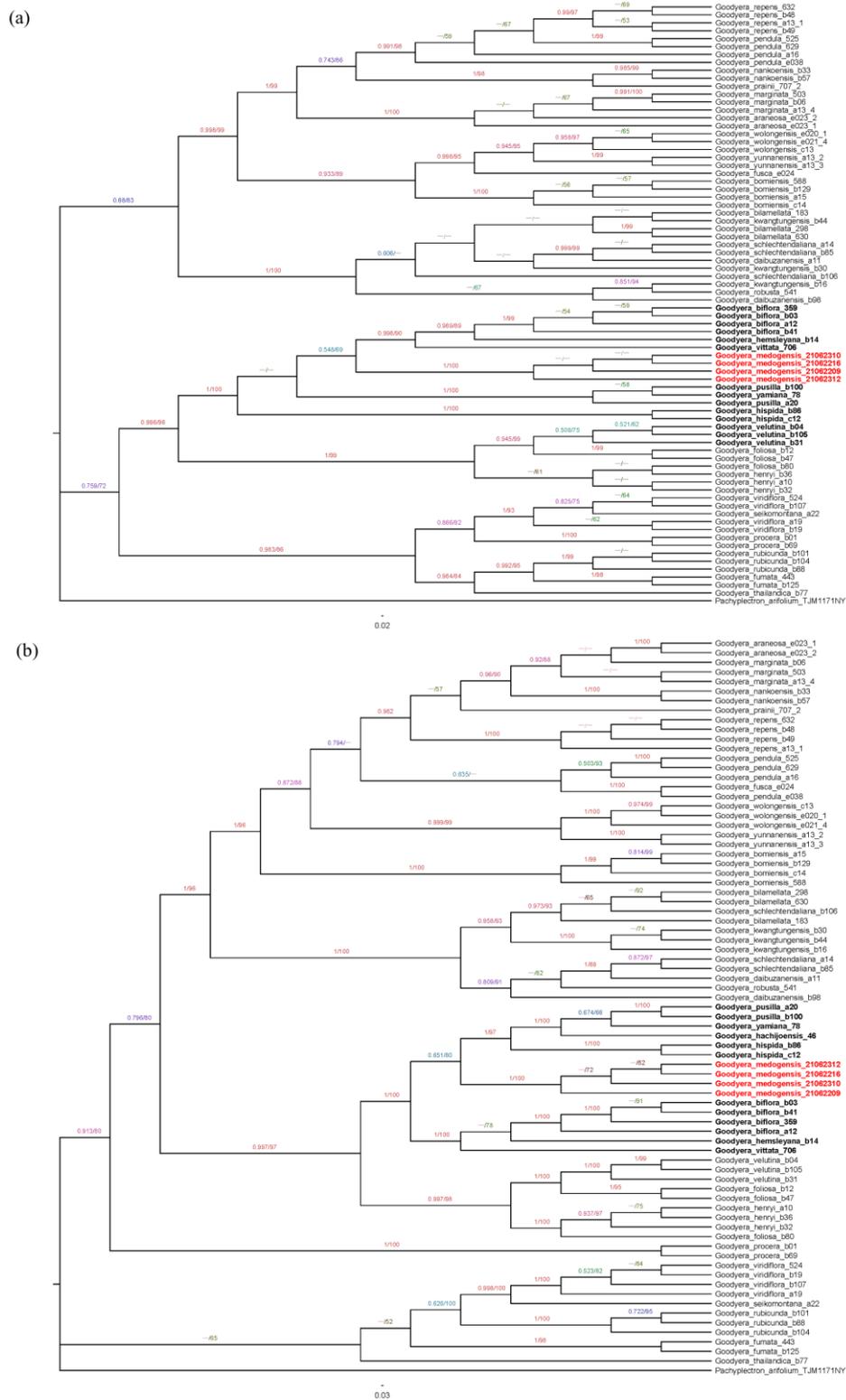
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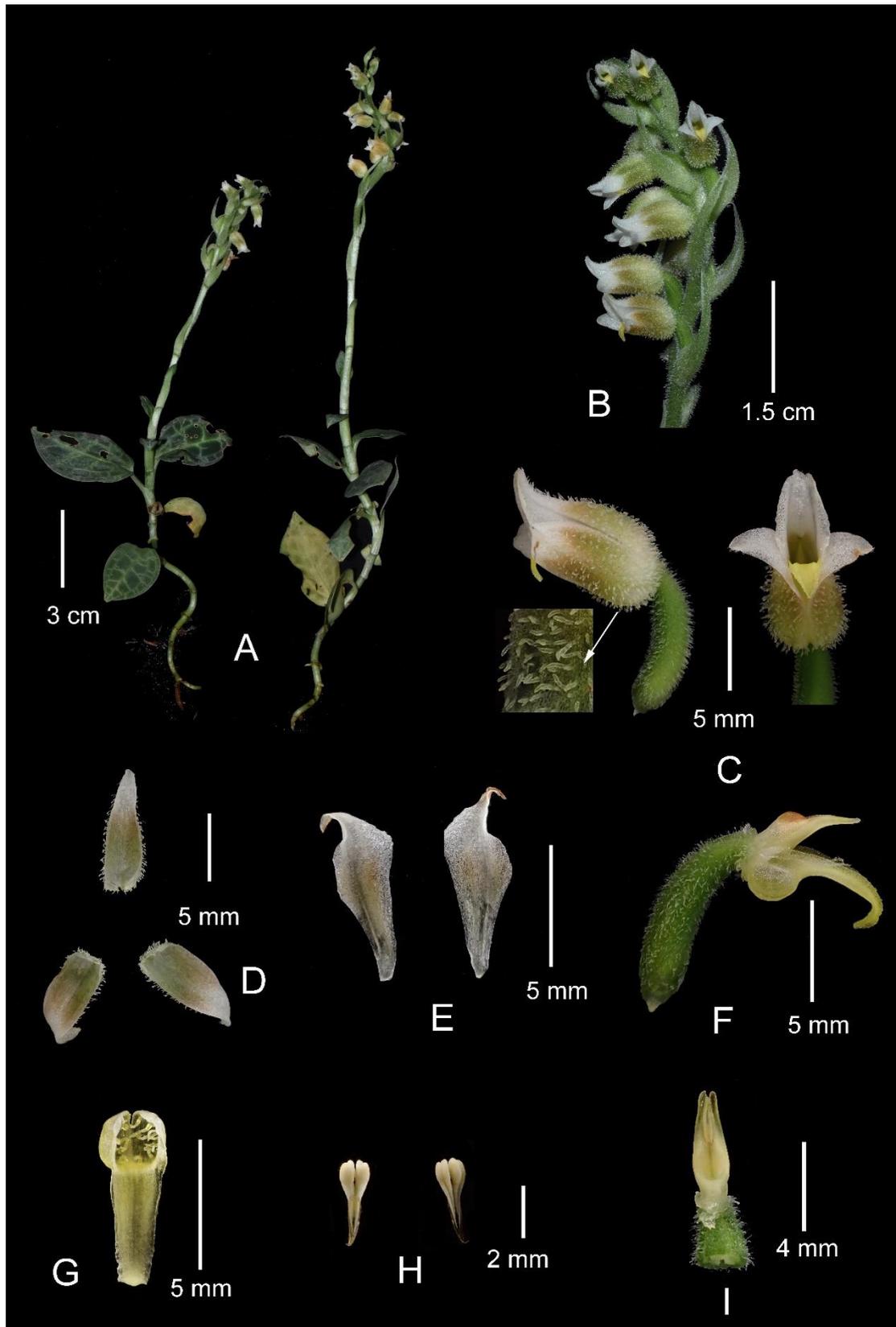
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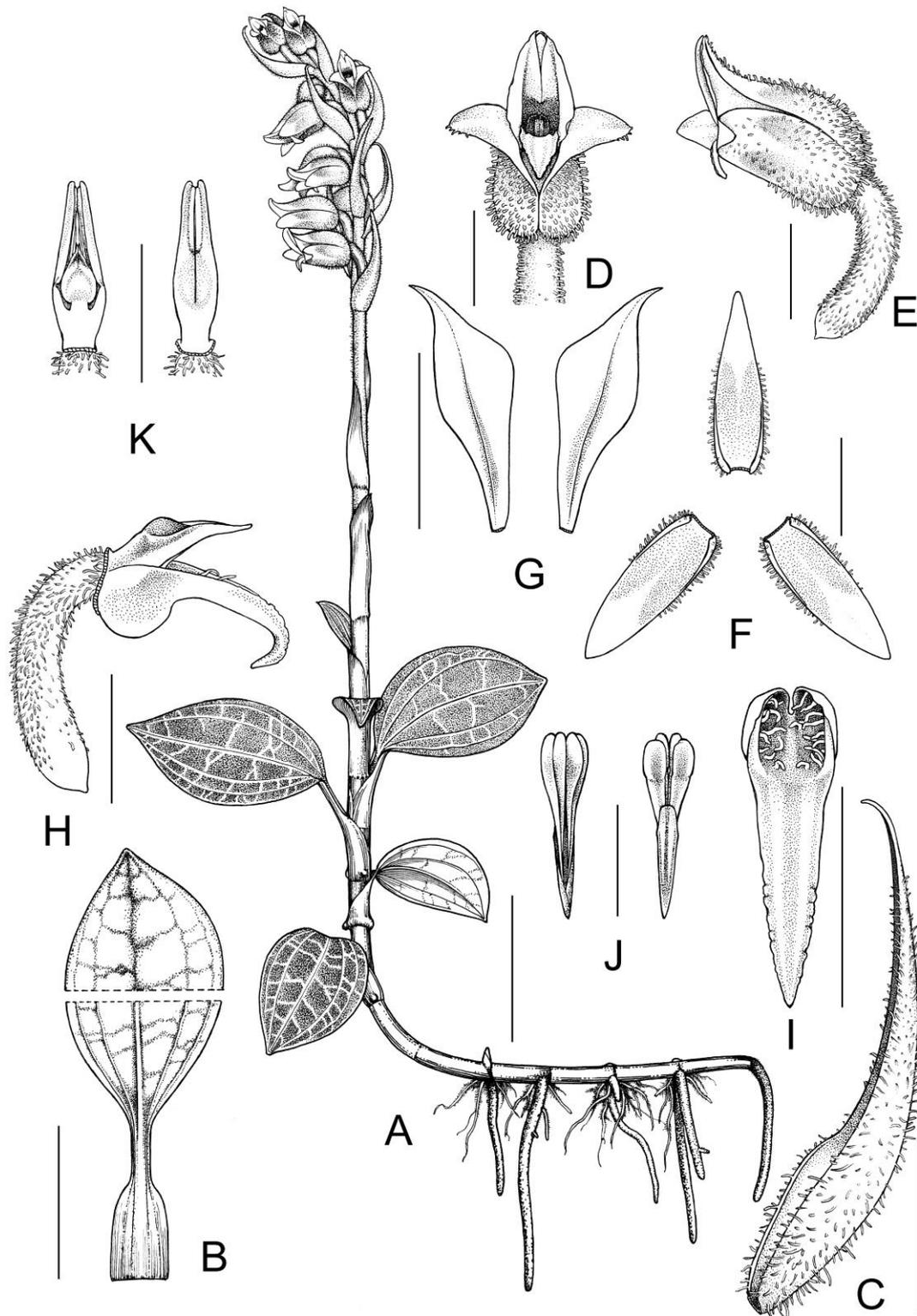


**Figure 1.** Phylogenetic tree of *Goodyera* species inferred by Bayesian analysis and maximum likelihood analyses based on the nrDNA (a) ITS) and cpDNA (b) *matK + trnL-F*) datasets. Posterior probability (PP)  $\geq 0.50$  in BI analysis and bootstrap (BS) values  $\geq 50\%$  in ML analysis are indicated on the left and right of slanting bars above the branches respectively. Dashes means not supported, i.e. the BS value  $< 50\%$  in the ML analysis or PP  $< 0.50$  in the BI analysis. The samples of new species are highlighted in red, and other species of sect. *Reticulum* are highlighted in bold.





**Figure 3.** *Goodyera medogensis*. **A** Habit **B** Inflorescence **C** Flower, lateral (left) and front (right) view, with the arrow showing close-up of trichomes on abaxial surface of sepals **D** Sepals **E** Petals **F** Column with labellum, anther and ovary **G** Labellum **H** Pollinarium **I** Column with a part of ovary. Taken by Y. H. Tong.



**Figure 4.** *Goodyera medogensis*. **A** Habit **B** Leaf **C** Bract **D** Flower, front view **E** Flower, lateral view **F** Sepals **G** Petals **H** Column with labellum, anther and ovary **I** Labellum **J** Pollinarium **K** Column with a part of ovary. Scale bars: 3 cm (**A**); 2 cm (**B**); 5 mm (**C–I**); 4 mm (**K**); 2 mm (**J**).

Table 1. Morphological comparison of *Goodyera medogensis* and *G. hemsleyana*.

Characters	<i>G. medogensis</i>	<i>G. hemsleyana</i>
Grid lines of reticulations on adaxial surface of leaf blades	Thick, margin blurred, transverse ones fewer, 5–7	Thin, margin clear, transverse ones more, 7–17
Number of flowers per inflorescence	(6–)12–15	4–10
Floral bracts	Green	Pinkish green
Trichomes on abaxial surface of floral bracts, sepals and ovary	Non-glandular	Glandular
Sepal	Olive greenish	Pinkish green to pinkish white
Petal	Obliquely obovate-rhombic; white, with reddish or brownish tinge at central part	Obliquely ovate-oblong; pinkish white
Labellum	Yellow or yellowish, without lamella	White, with light greenish to pinkish tinge at apex; with a low bi-lamellate callus

Table S1 Details of materials for phylogenetic study.

Taxon	Voucher	Collector	Locality	nrITS	<i>trnL-F</i>	<i>matK</i>
<i>Goodyera araneosa</i>	e023-1	Tian, Zhang & Zhou	Wangling, Sishuan, China	MN472742	MN544775	MN563606
<i>Goodyera araneosa</i>	e023-2	Tian, Zhang & Zhou	Wangling, Sishuan, China	MN472743	MN544776	MN563607
<i>Goodyera biflora</i>	359	Chung	Hsinchu, Taiwan, China	KT343986	KT385501	KT385588
<i>Goodyera biflora</i>	a12	Tian	Xizang, China	KT343987	KT385498	KT385585
<i>Goodyera biflora</i>	b03	Hu	Linan, Zhejiang, China	KT343988	KT385499	KT385586
<i>Goodyera biflora</i>	b41	Hu&Li	Sangzhi, Hunan, China	KT343989	KT385500	KT385587
<i>Goodyera bilamellata</i>	183	Chung	Hualien, Taiwan, China	KT343990	KT385502	KT385589
<i>Goodyera bilamellata</i>	298	Chung	Taipei, Taiwan, China	KT343991	KT385503	KT385590
<i>Goodyera bilamellata</i>	628	Chung	Hsinchu, Taiwan, China	KT343992	KT385504	KT385591
<i>Goodyera bilamellata</i>	630	Chung	Nantou, Taiwan, China	KT343993	KT385505	KT385592
<i>Goodyera bomiensis</i>	588	Chung	Hsinchu, Taiwan, China	KT343994	KT385506	KT385593
<i>Goodyera bomiensis</i>	a15	Tian	Linzi, Xizang, China	KT343995	KT385507	KT385594
<i>Goodyera bomiensis</i>	b129	Hu&Li	Huoshan, Anhui, China	KT343996	KT385508	KT385595
<i>Goodyera bomiensis</i>	c14	Tang	Xichang, Sichuan, China	KT343997	KT385509	KT385596
<i>Goodyera daibuzanensis</i>	a11	Tian	Chayu, Xizang, China	KT343999	KT385510	KT385597
<i>Goodyera daibuzanensis</i>	b98	Tian	Pingdong, Taiwan, China	KT344000	KT385511	KT385598
<i>Goodyera foliosa</i>	b12	Hu	Malipo, Yunnan, China	KT344004	KT385513	KT385600
<i>Goodyera foliosa</i>	b47	Hu	Guilin, Guangxi, China	KT344005	KT385514	KT385601
<i>Goodyera foliosa</i>	b80	Ye	Simao, Yunnan, China	KT344007	KT385516	KT385603
<i>Goodyera fumata</i>	443	Chung	Taipei, Taiwan, China	KT344010	KT385519	KT385606
<i>Goodyera fumata</i>	b125	Tian&Dong	Wuzhishan, Hainan,	KT344011	KT385520	KT385607

China						
<i>Goodyera fusca</i>	e024	Jin	Yadong, Tibet, China	MK991804	MN013772	MN013778
<i>Goodyera hachijoensis</i>	46	Chung	Cibodas, Indonesia	-	KT385521	KT385608
<i>Goodyera hemsleyana</i>	b14	Hu	Malipo, Yunnan, China	KT344014	KT385522	KT385609
<i>Goodyera henryi</i>	a10	Tian	Cibagou, Xizang, China	KT344017	KT385523	KT385610
<i>Goodyera henryi</i>	b32	Hu	Wenchuan, Sichuan, China	KT344018	KT385524	KT385611
<i>Goodyera henryi</i>	b36	Hu & Li	Emeishan, Sichuan, China	KT344019	KT385525	KT385612
<i>Goodyera hispida</i>	b86	Tian	Motuo, Tibet, China	KT344020	KT385526	KT385613
<i>Goodyera hispida</i>	c12	Jiang		KT344021	KT3855227	KT385614
<i>Goodyera kwangtungensis</i>	b16	Hu	Malipo, Yunnan, China	KT344025	KT385529	KT385616
<i>Goodyera kwangtungensis</i>	b30	Hu & Li	Nanchuan, Chongqing, China	KT344027	KT385531	KT385618
<i>Goodyera kwangtungensis</i>	b44	Hu	Maoershan, Guangxi, China	KT344029	KT385533	KT385620
<i>Goodyera marginata</i>	503	Chung	Chengdu, Sichuan, China	KT344030	KT385534	KT385621
<i>Goodyera marginata</i>	a13-4	Tian	Bomi, Tibet, China	KT344032	KT385535	KT385622
<i>Goodyera marginata</i>	b06	Hu	Dali, Yunnan, China	KT344033	KT385536	KT385623
<i>Goodyera medogensis</i>	21062209	Huang & Sun	Medog, Tibet, China	<a href="#">Waiting to be assigned</a>		
<i>Goodyera medogensis</i>	21062310	Huang & Sun	Medog, Tibet, China			
<i>Goodyera medogensis</i>	21062312	Huang & Sun	Medog, Tibet, China			
<i>Goodyera medogensis</i>	21062216	Huang & Sun	Medog, Tibet, China			
<i>Goodyera nankoensis</i>	b33	Hu & Li	Emeishan, Sichuan,	KT344036	KT385537	KT385624

			China			
<i>Goodyera nankoensis</i>	b57	Ge	Bomi, Xizang, China	KT344037	KT385538	KT385625
<i>Goodyera pendula</i>	525	Chung	Yilan, Taiwan, China	KT344039	KT385539	KT385626
<i>Goodyera pendula</i>	629	Chung	Taitong, Taiwan, China	KT344040	KT385540	KT385627
<i>Goodyera pendula</i>	a16	Tian	Nanling, Guangdong, China	KT344041	KT385541	KT385628
<i>Goodyera pendula</i>	e038	Qin	Maoershan, Guangxi, China	MK991805	MN013773	MN032023
<i>Goodyera prainii</i>	707_2	Tian & Hu	Yingjiang, Yunnan, China	KT344042	KT385542	KT385629
<i>Goodyera procera</i>	b01	Hu	Southern China Botanical Garden, Guangdong	KT344044	KT385543	KT385630
<i>Goodyera procera</i>	b69	Tian & Dong	Wuzhishan, Hainan, China	KT344045	KT385544	KT385631
<i>Goodyera pusilla</i>	a20	Tian	Ruyuan, Guangdong, China	KT344046	KT385545	KT385632
<i>Goodyera pusilla</i>	b100	Tian	Taidong, Taiwan, China	KT344047	KT385546	KT385633
<i>Goodyera repens</i>	632	Chung	Deqing County, Tibet, China	KT344048	KT385547	KT385634
<i>Goodyera repens</i>	a13-1	Tian	Bomi, Xizang, China	KT344049	KT385548	KT385635
<i>Goodyera repens</i>	b48	Wei	Mt. Tianshan, Xinjiang, China	KT344050	KT385549	KT385636
<i>Goodyera repens</i>	b49	Wei	Mt. Tianshan, Xinjiang, China	KT344051	KT385550	KT385637
<i>Goodyera robusta</i>	541	Chung	Mt. Fansipan, Sapa, Viet Nam	KT344054	KT385552	KT385639
<i>Goodyera rubicunda</i>	b88	Tian	Bawangling, China	KT344060	KT385555	KT385642

<i>Goodyera rubicunda</i>	b101	Tian	Taidong, Taiwan, China	KT344058	KT385553	KT385640
<i>Goodyera rubicunda</i>	b104	Tian	Hualian, Taiwan, China	KT344059	KT385554	KT385641
<i>Goodyera schlechtendaliana</i>	a14	Tian	Linzhi, Xizang, China	KT344065	KT385556	KT385643
<i>Goodyera schlechtendaliana</i>	b85	Tian	Linzhi, Xizang, China	KT344067	KT385558	KT385645
<i>Goodyera schlechtendaliana</i>	b106	Tian	Taoyuan, Taiwan, China	KT344066	KT385557	KT385644
<i>Goodyera seikomontana</i>	109	Chung	Yilan, Taiwan, China	KT344068	KT385560	KT385647
<i>Goodyera seikomontana</i>	a22	Tian	Nanling, Guangdong, China	KT344069	KT385559	KT385646
<i>Goodyera thailandica</i>	b77	Ye	Simao, Yunnan, China	KT344070	KT385561	KT385648
<i>Goodyera velutina</i>	b04	Hu	Tianmu mountain, Zhejiang, China	KT344073	KT385562	KT385649
<i>Goodyera velutina</i>	b31	Hu&Li	Sanjiang Ecological Tourist Park, Sichuan, China	KT344075	KT385564	KT385651
<i>Goodyera velutina</i>	b105	Tian	Taoyuan County, Taiwan, China	KT344074	KT385563	KT385650
<i>Goodyera viridiflora</i>	524	Chung	XinZhu, Taiwan, China	KT344080	KT385567	KT385654
<i>Goodyera viridiflora</i>	a19	Tian	Nanling, Guangdong, China	KT344082	KT385568	KT385655
<i>Goodyera viridiflora</i>	b19	Hu	Malipo, Yunnan, China	KT344084	KT385570	KT385657
<i>Goodyera viridiflora</i>	b107	Chung	Philippines	KT344083	KT385569	KT385656
<i>Goodyera vittata</i>	706	Tian & Hu	Yingjing, Yunnan, China	KT344086	KT385572	KT385659

<i>Goodyera wolongensis</i>	c13	Tang	Wanglang, Sichuan, China	KT344087	KT385573	KT385660
<i>Goodyera wolongensis</i>	e020-1	Tian, Zhang & Zhou	Songpan, Sichuan, China	MK991806	MN013779	MN013774
<i>Goodyera wolongensis</i>	e021-4	Tian, Zhang & Zhou	Pingwu, Sichuan, China	MK991807	MN013780	MN013775
<i>Goodyera yamiana</i>	78	Chung	Taidong, Taiwan, China	KT344088	KT385574	KT385661
<i>Goodyera yunnanensis</i>	a13-2	Tian	Bomi, Tibet, China	KT344089	KT385575	KT385662
<i>Goodyera yunnanensis</i>	a13-3	Tian	Bomi, Tibet, China	KT344090	KT385576	KT385663
<i>Pachyplectron arifolium</i>	TJM1171 NY	Motley	–	FJ473334	FJ571286	–

Note: “\_” means missing data.

Table. S2 Primers for sequence amplification and sequencing

Sequenc e	Primers (5'-3')	Reference	Amplification protocol
ITS	18S dir: CGTAACAAGGTTTCCGTAGG ITS4: TCCTCCGCTTATTGATATGC	Venora et al., 2000 <sup>[1]</sup> White et al., 1990 <sup>[2]</sup>	92°C 3min; 95°C 30s, 50°C 30s, 72°C 1min, 30cycles; 72°C 7min
<i>trnL-F</i>	c: CGAAATCGGTAGACGCTACG f: ATTTGAACTGGTGACACGAG	Taberlet et al., 1991 <sup>[3]</sup> Taberlet et al., 1991 <sup>[3]</sup>	94°C 2min; 94°C 1min, 50°C 30s, 72°C 1min, 30cycles; 72°C 7min
<i>matK 1</i>	19F: CGTTCTGACCATATTGCACTATG 834R: AAAGACTCCARAAGATRTTG	Molvray et al., 2000 <sup>[4]</sup> Kocyan et al., 2004 <sup>[5]</sup>	80°C 5min; 95°C 1min, 51°C 1min, 65°C 4min, 30cycles; 65°C 5min
<i>matK 2</i>	731F: TCTGGAGTCTTTCTTGAGCGA trnK2R: AACTAGTCGGATGGAGTAG)	Gervendeel et al., 2001 <sup>[6]</sup> Johnson & Soltis, 1994 <sup>[7]</sup>	The same as <i>matK 1</i>

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