**ORIGINAL ARTICLE**

**Blumea chishangensis** sp. nov. (Asteraceae: Inuleae) from Taiwan and new insights into the phylogeny of *Blumea*

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**Abstract**

*Background:* *Blumea* plants are widely distributed in the tropical areas of Asia, Africa, and Australia, especially tropical Asia. Limited studies left the taxonomy and infrageneric phylogeny of *Blumea* insubstantial. Here, a new species, *Blumea chishangensis* S. W. Chung, Z. H. Chen, S. H. Liu & W. J. Huang, from Taiwan is described, and an extended phylogeny is reconstructed to provide new perceptions of *Blumea* evolution.

*Results:* The new species is distinguished from *B. hieraciifolia* by the following features: leaf blade sparsely pilose or glabrescent (vs. silky villous), the leaves margins regularly remote mucronulate (vs. double serrate or dentate), capitula pedicelled (vs. capitula sessile or subsessile), and leaves basal rosette or sub-basal rosette and a few cauline (vs. mostly cauline). Phylogenetic analysis based on the ITS, *trnL-trnF*, and *trnH-psbA* regions places the new species in the sub-clade II in *B. lacera* clade and shows a close relationship with *B. axillaris* and *B. oxyodonta*. A key to *Blumea* species in Taiwan and the studied species in the subclade II is provided. Moreover, the evolutionary inferences of *B. conspicua*, *B. linearis*, and *B. sinuata* are also revealed for the first time.

*Conclusions:* Both morphological and molecular data support that *B. chishangensis* is a new species. Our phylogeny highlights the need for further taxonomic and evolutionary studies on *Blumea*.

**Keywords:** *Blumea chishangensis*, Compositae, Taiwan, Taxonomy, Molecular phylogeny

**Background**

*Blumea* DC. is one of the largest genera in the Tribe Inuleae, comprising approximately 100 species (Randeria 1960; Anderberg and Eldenäs 2007; Pornpongrungrueng et al. 2016) distributed in tropical Asia, Africa, and Australia, with the highest diversity occurring in tropical Asia (Pornpongrungrueng et al. 2016). *Blumea* is characterized by its disciform capitula, presence of one large oxalate crystal in each cell of the cypselae epidermis, radial anther endothecium thickenings, and tailed anthers. Despite being common in southeast Asia, the taxonomy of *Blumea* has not been thoroughly studied (Randeria 1960; Grierson 1972; Koyama 1984). The number of taxonomic revisions regarding this genus is still limited, with only a partial revision of 49 species of *Blumea* worldwide by Randeria (1960) and another revision of 27 species in continental southeast Asia by Pornpongrungrueng et al. (2016). In addition to the lack of taxonomic studies, the inconsistent and indistinct traits among some species and the heterogeneity of the genus increase the difficulty of determining the boundaries between different species (Pornpongrungrueng et al. 2016).

Previous phylogenetic studies had revealed that *Blumea* is a sister group of the genus *Caesulia* Roxb. (Anderberg et al. 2005; Pornpongrungrueng et al. 2007; Zhang et al. 2019). Combining evolutionary information...
of the ITS, trnL-trnF, and trnH-psbA regions from 30 Blumea species, Pornpongrungrueng et al. (2007, 2009) were the first to examine the infrageneric relationships of Blumea and identified three clades in the genus—B. lacerata clade, B. densiflora clade, and B. balsamifera clade. Their phylogeny showed that the relationships among the three clades were unresolved and pointed out that several taxa were not monophyletic. Zhang et al. (2019) investigated the infrageneric relationships of 22 Chinese Blumea taxa with the ITS and trnL-trnF regions, recognized two clades. The clade I, which contained B. densiflora clade and B. balsamifera clade recognized by Pornpongrungrueng et al. (2007, 2009), however, had low supports in Zhang et al. (2019) phylogenies. The clade II was equal to B. lacerata clade in Pornpongrungrueng et al. (2007, 2009). Within clade II (hereafter call B. lacerata clade), Zhang et al. (2019) identified three subclades and two single species.

Twelve species of Blumea were recorded in Flora of Taiwan, including B. aromatica, B. balsamifera, B. conspicua, B. formosana, B. hieracifolia, B. lacera, B. laciniate, B. lanceolaria, B. axillaris, B. oblongifolia, B. riparia var. megacephala and one endemic species, B. linearis (Leu and Peng 1998). During the fieldwork in the southeast of Taiwan in 2019, the authors found a Blumea population from Chishang Township which did not match any of the known Blumea species (Henry 1896; Randeria 1960; Leu and Peng 1998; Chen and Anderberg 2011; Pornpongrungrueng et al. 2016). After careful examination of relevant literature and specimens in Taiwanese herbaria, we conclude that it is an undescribed species (Figs. 1, 2). Hence, it is proposed as a new species with detailed morphological descriptions. A key to Blumea in Taiwan is also provided.

To understand the evolutionary position of the new species as well as to give new insights into the infragenic relationships of Blumea with additional taxa and molecular data, phylogenetic analysis based on nuclear ITS and two plastid DNA sequences was conducted in this study.

**Methods**

**Plant materials and morphological investigation**

For morphological comparison, the living materials of all 12 Taiwanese Blumea species (Leu and Peng 1998) and Blumea specimens preserved in HAST, TAI, and TAIF were carefully observed, photographed, and measured. For taxa whose materials are not available in Taiwan, their morphological data were adopted from literature, chiefly the latest monographic work of Pornpongrungrueng et al. (2016). Digital specimen images available in the online databases of IBSC, IBK, K, KUN, P, and PE were also consulted for reference.

For molecular phylogenetic analyses, the new species and the majority of Taiwanese Blumea taxa were collected from the field and planted in the research greenhouse of Taipei Botanical Garden. The fresh leaf materials for the following molecular analyses were dried in silica gel immediately right after collection. The vouchers applied for our morphological investigation were deposited in the TAIF herbarium for further studies.

**Genomic DNA isolation, PCR, and sequencing**

Genomic DNA of the newly collected Blumea young leaf materials was isolated with the Plant Genomic DNA Extraction Miniprep System (Viogene, Taipei, Taiwan) and kept at −20 °C before the amplifications. Following the earlier studies focusing on Blumea (Anderberg et al. 2005; Pornpongrungrueng et al. 2007, 2009; Zhang et al. 2019; Abdullah et al. 2021), both nuclear ITS (ITS1 + 5.8S + ITS2) and chloroplast (trnL-trnF and trnH-psbA spacers) regions were used in the present study to infer the phylogenetic positions of the described Taiwanese Blumea taxa and the new species. With seven sets of primers (Table 1), all three regions were successfully amplified for all newly collected Blumea samples. The primer sequences, sources, optimal conditions for the PCR reactions, and PCR product sizes of the studied DNA regions are shown in Table 1. Each PCR mixture contained 1 μL genomic DNA, 1 μL 10 μM forward primer, 1 μL 10 μM reverse primer, 5 μL 5 × FIREPol Master Mix (Solis BioDyne, Tartu, Estonia), and 17 μL nuclease-free water. The PCR product purifications and DNA sequencing in an ABI 3730xl DNA Analyzer were then conducted commercially with the services at the Genomics BioSci & Tech. Co., Ltd. New Taipei City, Taiwan.

To understand the phylogenetic positions of Taiwanese Blumea taxa, additional 101 sequences from 26 Blumea taxa and 12 sequences from four taxa in the close relative genera (Aster L., Caesalia, Laggera Sch. Bip. ex Benth. & Hook. f., and Pluchea Cass.) were downloaded from the NCBI. The GenBank accession numbers of the studied sequences and sampled taxa are available in Additional file 1.

**Sequence assembly, alignment, and phylogenetic analyses**

Sequence reads were trimmed and assembled using both the De Novo Assemble and Map to Reference tools implemented in Geneious Prime 2022.1 (https://www.geneious.com) with the default settings. The ITS, trnL-trnF, and trnH-psbA regions from Blumea oxyodonta (NCBI accessions EU195665 and BK013128) were served as the references when the Map to Reference tool was applied. Two assembling tools generated identical sequences in all of our samples.
The initial sequencing results showed no ambiguous base in the newly generated *Blumea* ITS sequences. Therefore, no cloning was conducted.

Sequence alignments for the studied regions were carried out applying Clustal W (Larkin et al. 2007) implemented in Geneious Prime 2022.1 and then visualized with Mesquite 3.7 (Maddison and Maddison 2021). As the earlier studies focused on *Blumea* plants (Pornpangrungrueng et al. 2007, 2009; Zhang et al. 2019), we then concatenated the alignments of ITS, *trnL-trnF*,...
*trnH-psbA* regions for the following analyses using Mesquite 3.7.

Many studies have suggested that taxa with extensive missing data would mislead the topology (e.g., Wiens 1998; Lemmon et al. 2009; Simmons 2012). Therefore, only the taxa with both ITS region and at least one chloroplast region will be applied in this study.
The best-fit nucleotide substitution model for the concatenated alignment was estimated with jModeltest 2.1.10 (Darriba et al. 2012). Both the maximum likelihood (ML) and Bayesian inference (BI) algorithms were then performed to infer the phylogenetic relationships among the studied Blumea taxa. The ML tree was reconstructed using RAxML-VI-HPC (Stamatakis 2006) in Geneious Prime 2022.1 with 1000 rapid bootstrap procedures and the best-fit nucleotide substitution model. The BI tree was generated utilizing MrBayes 3.2.6 (Huelsenbeck and Ronquist 2001; Ronquist et al. 2012) available in the CIPRES Science Gateway 3.3 (Miller et al. 2010) with the best-fit nucleotide substitution model and two independent Markov Chain Monte Carlo (MCMC) runs. A total of $5 \times 10^6$ generations were executed in each MCMC run, and trees were sampled every 1000 generations. The posterior probabilities (pp) on the consensus BI tree were given by summing the last 75% of trees ($\text{burnin-frac} = 0.25$). Above all, the ML and BI trees were drawn using FigTree 1.4.4 (Rambaut 2018).

### Results and discussions

#### Phylogenetic analyses and insights

In total, 140 Blumea sequences—including 39 newly generated and 101 downloaded sequences—representing 32 Blumea taxa and 12 sequences representing four closely related outgroups were investigated in the present study (Additional file 1). Note that these numbers do not include the other six Blumea taxa which had been dismissed from the following analyses because these six taxa have only ITS region or only one chloroplast region (Additional file 1). The ML and BI trees were reconstructed based on the combined alignment (ITS, trnL-trnF, and trnH-psbA regions) with a length of 2054-bp. The maximum parsimony statistics and evolutionary model are provided in Table 2. Both ML and BI trees show the same topology (Additional file 1) and hence only ML is shown here (Fig. 3). Our phylogeny (Fig. 3) supports Pornpongrungrueng et al. (2007, 2009)'s works that Blumea taxa are clustered in three groups—B. lacer a clade, B. densiflora clade, and B. balsamifera clade. The relationships among the three

### Table 1

The PCR primers, optimal annealing temperatures, and product sizes of ITS, trnL-trnF, and trnH-psbA regions in this study

| DNA regions          | Primers | Primer Sequences (5′→3′) | Primer sources | Annealing temperature (°C) | Product size (bp) |
|----------------------|---------|--------------------------|----------------|----------------------------|-------------------|
| Nuclear region       |         |                          |                |                            |                   |
| ITS (ITS1 + 5.8S + ITS2) | ITS_4   | TCC TCGGCTTATCGATATGC    | White et al. 1990 | 55 | 662–666 |
|                      | ITS_5   | GGAAGTTAAAGTCGTTAACAGG   | White et al. 1990 |                |                   |
|                      | ITS_L   | TCGTTAACAGGTTTTCCTAGTGT  | Hsiao et al. 1994 | 60 | 662–666 |
|                      | ITS_Scleria | ATGCTTTAATCTACGCGGGTA | Liu et al. 2021 |                |                   |
| Chloroplast regions  |         |                          |                |                            |                   |
| trnL-trnF            | trnL_c  | CGAAATCGGGTAGGCTACCG     | Taberlet et al. 1991 | 60 | 829–895 |
|                      | trnL_f  | ATTTGAACTGGTGACAGGAG    | Taberlet et al. 1991 |                |                   |
|                      | trnL_d  | GGGGATAGGAGGGCTTGAGAC   | Taberlet et al. 1991 | 60 | 466–471 |
|                      | trnL_e  | ATTTGAACGGTGACAGGAG     | Taberlet et al. 1991 |                |                   |
|                      | trnL_f  | GGTTCAGTCCCTCTATCC     | Taberlet et al. 1991 | 59 | 369–383 |
| trnH-psbA            | psbAF   | GTTATGCATGAAGCTATGCTCG  | Sang et al. 1997 | 64 | 460–494 |
|                      | trnH2   | CGCCGACAGGGTGACACATTCC  | Tate and Simpson 2003 |                |                   |
|                      | trnH2   | CGCCGATGCTGGTACACATTCC  | Tate and Simpson 2003 | 63 | 505–637 |
|                      | psbABL  | AGCTGCTGGCGCTGATAG     | This study |                |                   |

| Table 2

Characteristics, maximum parsimony statistics, and evolutionary model of the studied alignment

| DNA alignment        | Number of outgroups/Blumea accessions | Length (bp) | Evolutionary model | Number of parsimony-informative sites [%] | CI/RI/RC/HI |
|----------------------|--------------------------------------|-------------|--------------------|----------------------------------------|-------------|
| All combined         | 4/49                                 | 2054        | GTR + I + G        | 385 (282 + 36 + 67) [18.74% (42.28% + 4.21% + 12.62%)] | 0.704/0.848/0.597/0.296 |

CI consistency index; RI retention index; RC rescaled consistency index; HI homoplasy index
clades remain unclear. Within the B. lacera clade, our data support Zhang et al. (2019)’s work that three subclades and two single species are recognized (Fig. 3).

The phylogenetic positions of five Blumea taxa (B. chishangensis, B. conspicua, B. linearis, B. sinuata, and B. formosana) are discussed in the following paragraphs, and the evolutionary information of the former three are firstly provided in this study.

Our results suggest that the new species, B. chishangensis, described here is a member of the subclade II in B. lacera clade (Fig. 3). This species is closely related to B. oxyodonta and B. axillaris, and all three species together are the sister group of B. hamiltonii. Interestingly, B. axillaris, B. hamiltonii, and B. oxyodonta are widely distributed, while B. chishangensis is one of the endemic Blumea taxa in Taiwan and has a restricted distribution. Blumea axillaris is the most widespread Blumea taxon distributed in tropical Asia (including Taiwan), tropical Africa, and northern Australia. Both B. hamiltonii and B. oxyodonta occur in southwest China, Indochinese Peninsula, and the Indian subcontinent, but not in Taiwan (Merrill 1910; Randeria 1960; Leu and Peng 1998; Chen and Anderberg 2011; Pornpongrungrueng et al. 2016).

Blumea chishangensis is morphologically similar to B. hieraciifolia (see the following discussion), and both species are members of subclade II. However, B. chishangensis and B. hieraciifolia had different evolutionary histories. The former is grouped with B. oxyodonta and B. axillaris while the latter shares the same ancestor with B. macrospathya (Fig. 3). The conflicts between molecular and morphological data are not rare in plants (e.g., Bremer and Struwe 1992; Schuster et al. 2018; Lu et al. 2021). These conflicts might infer some convergent evolution and/or hybridization in the evolutionary history (e.g., Ran et al. 2018; Soreng and Davis 2000; Liu et al. 2020).

Blumea conspicua occurs only on Ryukyu arc islands, Japan, Orchid Island, and Taiwan, and B. linearis is endemic to Orchid Island and Taiwan (Hayata 1911; Leu and Peng 1998; Peng and Leu 1999; Chen and Anderberg 2011). Our phylogeny points out that B. conspicua and B. linearis are sister taxa, and both of them belong to the B. densiflora clade (Fig. 3). These two species are closely related to B. canalensis and B. arfakiana, which distributions are also limited to some islands in the West Pacific Rim (Martelli 1883; Moore 1921). Additional samplings and/or DNA regions will be required to fully understand the diversification of this West Pacific Rim clade (e.g., Petersen and Hughes 2007; Chiang et al. 2014; Shaw et al. 2015).

With three samples, our phylogeny suggests that B. sinuata belongs to the B. lacera clade, but it is not a monophyletic taxon (Fig. 3). One B. sinuata sample is grouped with B. oblongifolia and B. saussureoides [pp = 1.00; bootstrapping value (bs) = 100], while another sample is sister to B. sessiliflora (pp = 1.00; bs = 100). Moreover, our data indicates that B. formosana belongs to the B. densiflora clade and it is clustered with B. densiflora, B. martiniana, and the West Pacific Rim Blumea clade (Fig. 3). However, Zhang et al. (2019)’s study suggested that B. formosana was grouped in the subclade III in B. lacera clade and sister to B. saxatilis, which had been asserted as a paraphyletic taxon in Pornpongrungrueng et al. (2009)’s study. Integrating Zhang et al. (2019)’s work and our work, it is likely that B. formosana is also a paraphyletic taxon. In fact, Pornpongrungrueng et al. (2009) had recognized several paraphyletic Blumea taxa—including B. lacera, B. axillaris, B. saxatilis, and B. riparia var. megacephala. Here, we report two more paraphyletic Blumea taxa, B. formosana and B. sinuata. All of the six paraphyletic taxa are relatively widespread. There might be some cryptic diversifications or taxa within a widely distributed taxon (e.g., Dick et al. 2003; Gottlieb 2004). Hybridization, introgression, and gene exchange with local taxa might also be the potential mechanisms that result in a widespread, but paraphyletic, taxon (e.g., Liu et al. 2018; Wen et al. 2020). Further taxonomic and molecular works will be demanded to provide a comprehensive classification and better understanding of the evolutionary history of Blumea.

Morphological investigation on the new species
Detailed comparisons showed that this unknown taxon is morphologically similar to B. hieraciifolia, which is distributed to southeastern Asia and China (Leu and Peng 1998; Pornpongrungrueng et al. 2016), but still distinct in following features: leaves basal rosette or sub-basal rosette and a few cauline (vs. mostly cauline), leaf blade sparsely pilose or glabrescent (vs. silky villous), and capitula pedicelled (vs. capitula sessile). Additionally, B. oxyodonta, B. axillaris, and B. hamiltonii are included in the B. lacera clade (Pornpongrungrueng et al. 2007, 2009), also share similar gross morphology with the unknown taxon. However, B. oxyodonta can be clearly distinguished by its procumbent habit, spinous-toothed...
Fig. 3 (See legend on previous page.)
leaves, and mostly abortive anthers; B. axillaris differs in having purple flowers, distinctly petiolate leaves; B. hamiltonii is also distinct by having tomentose to wooly stem and leaf surface with glandular hairs and branch-tailed anthers bases. As the morphological characteristics of the unknown Taiwanese population could not match well with any described Blumea taxa, we consider it as a new species and propose the name “B. chishangensis” (see “Taxonomic treatment” section below). A key to Blumea species in Taiwan and the allies of B. chishangensis is also provided.

**Taxonomic treatment**

*Blumea chishangensis* S. W. Chung, Z. H. Chen, S. H. Liu & W. J. Huang sp. nov. (Fig. 1, Fig. 2).

**Diagnosis**

*Blumea chishangensis* is closely allied to *B. hieraciifolia* in morphological appearance but not in the evolutionary relationship (Fig. 3). The new species could be distinguished by the following features: sparsely pilose or glabrescent (vs. silky villous) leaves, the leaves margins regularly remote mucronulate (vs. double serrate or dentate), capitula with pedicelled (vs. capitula sessile or subsessile), and leaves basal rosette, sub-basal rosette or sometimes cauline (vs. mostly cauline).

**Type**

TAIWAN. Taitung County: Chishang Township, Fuxing wetland, 250 m, 26 September 2019, S. W. Chung 14025 (holotype TAIF!).

**Description**

Perennial herb, erect, 30–60 cm high, with a fibrous rootstock. Stems simple, purple, usually unbranched, terete, 2–4 mm in diameter, puberulous or sometimes glabrate on basal part; leaves basal rosette or sub-basal rosette and a few cauline. Lower leaves larger, coriaceous, (5.5–10–17.9) cm long, (1.2–)2–2.8 cm wide, spathulate to obovate-oblong, obtuse or acute at apex, the base attenuate into winged petiole, the margins regularly remote mucronulate, the upper surface often rugose and glabrescent when mature, the lower surface puberulous or glabrescent, veins 6–8 pairs. Capitula dense to lax pani -

**Distribution and habitat**

*Blumea chishangensis* is endemic to Taiwan, recorded around the south and southeast region of Taiwan at elevations of 250–300 m. Plants grow on open grassland along the trail.

**Phenology**

The flowering of *Blumea chishangensis* is observed from August to October and fruiting from September to November.

**Etymology**

The epithet “chishangensis” refers to the name of the Chishang Township, Taitung County, Taiwan, where the novel species was discovered. Vernacular names, “池上艾纳香” and “Chishang Blumea”, are also proposed.

**Conservation status**

Endemic. Known from two restricted locations and one was only recorded once by Henry (1896) in Kaohsiung City over a hundred years ago. The present existing population would be negatively affected by an increase in human activities. AOO is less than 10 km², and 100 individuals at most. We, therefore, evaluated it as Vulnerable [CR C2a] based on the latest IUCN guidelines (IUCN Standards and Petitions Committee 2022).

**Additional specimens examined (paratypes)**

TAIWAN. Taitung County: Chishang Township, Fuxing wetland, 2 August 2019, Z.H.Chen1847 (TAIF!).

Key to *Blumea* species in Taiwan. (Include all studied taxa in the Subclade II of *B. lacera* Clade; Taiwan’s species are highlighted in bold).

1. Plants scandent; heads 10–15 mm across...............

2. Leaves nearly glabrous on both surfaces........................... *B. lanceolaria*.

3. Pappus reddish ........................................... *B. balsamifera*. 
3. Petiole without appendages, pappus white

4. Leaves distinctly petiolate; lobes of disc corolla purplish or pink .............................................. *B. axillaris*.

4. Leaves sessile or subsessile; corollas yellow or rarely pinkish..........................................................5.

5. Involucres glandular hairy only, involucral bracts recurved at tips....... *B. aromatica*.

5. Involucres both glandular hairy and villous; involucral bracts appressed or ascending..............................5.

6. Plants 1.5–3 m tall; leaves 30–45 cm long.........................................................6.

6. Plants less than 1.5 m tall; leaves less than 25 cm long ......................................................7.

7. Leaves linear or linear-lanceolate, 2.5–3.5 cm wide; corolla lobes of central florets without multi-cellular hairs.............. *B. linearis*.

7. Leaves obovate or lanceolate, 10–15 cm wide, corolla lobes of central florets without multi-cellular hairs.............. *B. conspica*.

8. Plant prostate or procumbent, leaves spinous-toothed......................................................*B. oxyodonta*.

8. Plant erect, leaves not spinous-toothed .................................................................................8.

9. Inflorescence a loose panicle .................................................................................9.

9. Inflorescence a dense panicle or a terminal glose cluster.........................................................................10.

10. Leaf base acuminate, margin serrulate..............................11.

10. Leaf base acute, margin coarsely dentate ......................................................11.

11. Leaves irregularly laciniate or lyrate at base ......................................................12.

11. Leaves remotely serrate, not lobed................................................................................12.

12. Leaves lyrate, usually pinnatipartite at base; receptacles pubescent, pilose, rarely glabrous..........................*B. oblongifolia*.

12. Leaves obovate, slightly lyrate; receptacles glabrous...........................................................................*B. sinuate*.

13. Anther tails branched ......................................................................13.

13. Anther tails unbranched ......................................................................13.

14. Capsule 3–4 mm diam.; cypselas 5-ribbed...................................................*B. macrostachya*.

14. Capsule 6–10 mm diam.; cypselas 10-ribbed..............................................................*B. chishangensis*.

15. Leaves mostly cauline, silky villous, margins double serrate or dentate, capitula sessile..............................*B. hieracifolia*.

15. Leaves mostly cauline, silky villous, margins double mucronulate, capitula pedicelled..............................*B. chishangensis*.

Abbreviations

| BI | Bayesian inference |
| bs | Bootstrapping value |
| HAST | Academia Sinica, Herbarium |
| IBK | Guangxi Institute of Botany, Herbarium |
| IBSC | South China Botanical Garden, Herbarium |
| K | Royal Botanic Gardens, Herbarium |
| KUN | Kunming Institute of Botany, Chinese Academy of Sciences, Herbarium |
| MA | Maximum likelihood |
| PE | Institut de Botany, National Taiwan University, Herbarium |
| TAIF | Taiwan Forestry Research Institute, Herbarium |

**Supplementary Information**

The online version contains supplementary material available at [https://doi.org/10.1186/s40529-022-00350-z](https://doi.org/10.1186/s40529-022-00350-z).

Additional file 1: Table S1. List of the studied *Blumea* taxa, their GenBank accession numbers, and voucher information.

**Additional file 2:** Alignments and trees of the phylogeny of genus *Blumea*.

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**Author contributions**

ZHC is the first person to collect *Blumea chishangensis*. SWC and ZHC initialed this study. SWC and WJH conducted the morphological investigation. SHL collected the molecular data and performed phylogenetic analyses. SWC, SHL, and WJH prepared the manuscript. All authors read and approved the final manuscript.

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**Availability of data and materials**

All data generated and analyzed during this study are included in this published article and its supplementary information files.

**Declarations**

**Ethics approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable.

**Competing interests**

The authors declare that they have no competing interests.

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