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Ceropegia semifusca (Apocynaceae), a novel species from Yunnan, China

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ABSTRACT: *Ceropegia semifusca* P.R.Luo & J.D.Ya, a new species from Aziying Township, Panlong District, Kunming, central Yunnan, China, is described and illustrated. It resembles *C. sinoerecta* M.G.Gilbert & P.T.Li and *C. sunhangiana* P.R.Luo & T.Deng, but differs by its leaf shape, indumentum, and a corolla throat about twice as wide as the inflated basal tube. Based on its rootstock, the species is assigned to *C.* sect. *Chionopegia*. Its chromosome number and genome size are also reported for the first time. Both molecular phylogenetic analyses and morphological evidence provide strong support for the distinctiveness of *C. semifusca*.

KEY WORDS: Central Yunnan, *Ceropegia sinoerecta*, *Ceropegia sunhangiana*, endemic, molecular evidence, Southwest China.

INTRODUCTION

The genus *Ceropegia* L., in its traditional circumscription, comprises approximately 230 species predominantly distributed in seasonally arid to semi-arid habitats across the Old World (Li *et al*., 1995; Bruyns *et al*., 2017; Endress *et al*., 2018). However, phylogenetic analyses based on molecular data have demonstrated that *Ceropegia* sensu stricto does not constitute a monophyletic group (Meve and Liede-Schumann, 2007), thereby casting doubt on the current delimitation of the genus. To address this issue and preserve monophyly within the tribe Ceropegieae, Bruyns *et al*. (2017) proposed an expanded generic concept—*Ceropegia* sensu lato—which consolidates nearly all genera and species within tribe Ceropegieae (32 genera, 498 species), with the exception of ten early-diverging genera comprising 45 species. Under this revised framework, *Ceropegia* would become the most speciose genus within Apocynaceae, encompassing 63 sections and exceeding 700 species. More recently, taxonomic reassessment has advocated the exclusion of the clearly monophyletic stem-succulent stapeliads (at least 31 genera, 357 spp.) from *Ceropegia* s.l. largely on grounds of taxonomic stability and practical usability, while supporting the inclusion of the genus *Brachystelma* R.Br. (Gilbert, 2020). Consequently, the circumscription of *Ceropegia* remains controversial, with two contrasting approaches currently in use. A broadly defined concept (sensu lato) emphasizes strict molecular monophyly, often resulting in substantial morphological heterogeneity, whereas a narrower or moderately expanded concept (sensu stricto) prioritizes morphological coherence and practical usability, while tolerating limited paraphyly. Given the pronounced morphological convergence and corolla plasticity within tribe Ceropegieae, both approaches are defensible. Here, we adopt the latter circumscription as a working hypothesis, pending further integrative phylogenomic and morphological studies.

The continued taxonomic exploration of *Ceropegia* in China underscores the influence of the region's complex geological history and climatic heterogeneity within the broader Eurasian context (Chen *et al*., 2018). Based on the recent taxonomic revision, five new species of *Ceropegia* were described, *Ceropegia paohsingensis* Tsiang & P. T. Li was synonymized, and previously synonymized *Ceropegia angustilimba* Merr. was reinstated as a distinct species from *Ceropegia trichantha* Hemsl.. Thus, the total number of recognized *Ceropegia* species in China remains at 25 (Wu *et al*., 2019; Ma *et al*., 2022a,b., 2023; Luo *et al*., 2023, 2024; Xie *et al*., 2023). This includes 21 species that belong to *C.* sect. *Chionopegia*, 4 species belong to *C.* sect. *Tiloris*, with 2 species formerly placed in *Brachystelma* are included.

During a recent flora investigation in Aziying Township (formerly part of Songming County), Kunming, Yunnan Province, southwest China, an unknown species of *Ceropegia* was collected. This species belongs to *C.* sect. *Chionopegia* as it presents no tuber but fleshy roots, a corolla with a slender tube, globose at the base, and lobes coherent at the apex. The leaves of this species are sparsely pubescent only along the margins and on the abaxial midvein. In addition, the outstanding feature is the corolla throat that is approximately twice the length of the inflated basal tube, and the corolla lobes are dark brown in the distal half. Considering that in China only members of *Ceropegia* sect. *Tiloris*, which have usually compressed and disc-like tubers, and sect. *Chionopegia*, characterized by slightly fusiform roots, are distributed. This species is related to the *Ceropegia sinoerecta* M.G.Gilbert & P.T.Li and the *Ceropegia sunhangiana* P.R.Luo & T.Deng, yet it can be distinguished by lifestyle or corolla characteristics from

both. We were unable to match our specimens with any known species of *C.* sect. *Chionopegia*. Therefore, it is described here as a new species.

MATERIALS AND METHODS

Morphological observation

Morphological characterization was carried out on both living plants and dried specimens using stereomicroscopes, a high-resolution extended depth-of-field imaging system, and precision vernier calipers. To ensure taxonomic accuracy, we conducted an extensive review of the relevant literature, including major monographs and recent publications on *Ceropegia* (Li *et al*., 1995; Wu *et al*., 2019; Ma *et al*., 2022b, 2023; Luo *et al*., 2023). Specimens deposited in KUN and PE were physically examined, while those in other herbarium were accessed virtually via the Chinese Virtual Herbarium (CVH, http://www.cvh.ac.cn) as high-resolution scans. Protologue data were retrieved from literature in the Biodiversity Heritage Library (BHL, https://www.biodiversitylibrary.org), and specimen records were cross-referenced through CVH and JSTOR Global Plants (https://jstor.botanicalgarden.cn). Comparative morphological features distinguishing the new species from its closest relatives, *C. sinoerecta* M.G.Gilbert & P.T.Li *and C. sunhangiana* P.R.Luo & T.Deng, are presented in Figs 1, 2 and summarized in Table 1.

Molecular analyses

To investigate the phylogenetic position of *Ceropegia semifusca* sp. nov., we conducted a phylogenetic analysis based on complete chloroplast genome sequences. In this study, we newly sequenced and assembled chloroplast genomes of eleven *Ceropegia* samples: *C. sunhangiana, C. sinoerecta, C. salicifolia, C. dolichophylla, C. pubescens, C. aridicola, C. jinshaensis* and this *C. semifusca* are included. DNA sequences used for the phylogenetic analyses included both newly generated and previously published data. Newly generated sequences of *Ceropegia* species were deposited in Figshare (Luo, 2025; https://doi.org/10.6084/m9.figshare.30884621.v1), while available sequences from GenBank were incorporated to improve taxon sampling. Specifically, GenBank accessions OP133586 (*C. longifolia*), OP133580 (*C. dolichophylla*), OP133584 (*C. nilotica*), OR260539 (*C. sunhangiana*), and MT365042 (*Apocynum venetum* L.) were included as related taxa (Wang *et al*., 2023). All sequences were aligned and analyzed together for phylogenetic reconstruction. Following the sectional classification proposed by Bruyns *et al*. (2017), our dataset comprised 16 representative species from four closely related sections: *C.* sect. *Chionopegia*, *C.* sect. *Callopegia*, and *C.* sect. *Tiloris.* All chloroplast genomes were aligned using MAFFT v7.490 with default parameters (Katoh and Standley, 2013), and the alignment was trimmed with trimAl v1.4 to remove ambiguously aligned regions (Capella-Gutiérrez *et al*., 2009). Phylogenetic inference was performed using the maximum likelihood (ML) method implemented in RAxML-NG v1.2.2 under the GTR+G substitution model (Kozlov *et al*., 2019), and the Bayesian inference (BI) method implemented in MrBayes as integrated in Geneious (Kearse *et al*., 2012; Ronquist *et al*., 2012). For the BI analysis, the HKY85 substitution model with gamma-distributed rate variation was used. The Markov chain Monte Carlo (MCMC) analysis was run for 1,100,000 generations with four chains (heated chain temperature = 0.2), sampling every 200 generations, and discarding the first 100,000 generations as burn-in. The outgroup was set as MT365042 (*A. venetum*), and a random seed of 4641 was used to ensure reproducibility.

Chromosome karyotyping and flow cytometry

Root tips were pretreated in 0.002 mol/L 8-hydroxyquinoline solution at 25 °C in darkness for 3 hours, followed by rinsing five times with ultrapure (UP) water (2 minutes each rinse). Pre-treated root tips were then fixed in Carnoy's fixative (absolute ethanol:glacial acetic acid = 3:1) on ice for 2 hours at 4 °C, followed by another five washes with UP water (2 minutes each). After fixation, the root tips were hydrolyzed in a 1:1 (v/v) mixture of 45% glacial acetic acid and 1 mol/L HCl at 60 °C for 5 minutes, rinsed again five times with UP water (2 minutes each), and then incubated in UP water for 2 hours for hypotonic treatment. The root tips were stained with modified carbol fuchsin solution for 10–15 minutes before squashing. Well-spread metaphase chromosomes were observed under a LEICA DM1000 optical microscope at 20× magnification and photographed at 100× magnification. Genome size estimation was performed using flow cytometry, with *Zea mays* and *Solanum lycopersicum* serving as internal reference standards (Doležel and Bartoš, 2005).

RESULTS

Morphology and taxonomy

After examining specimens of *Ceropegia* in major herbaria across China, no authentic specimens attributable to *C. sinoerecta* were found. However, we collected a specimen *P.R.Luo* 671 (KUN) from the type locality, Heqing County, which represents a recent collection of this species. The morphological comparisons presented here are mainly based on the holotype specimen P00639940 (Muséum National d'Histoire Naturelle) and our collection *P.R.Luo* 671 (KUN). Besides, we found *C. sinoerecta* photographed near its type locality in the Plant Photo Bank of China database (PPBC, https://ppbc.iplant.cn/sp/220971), so it has also been included as a reference for morphological description. Based on the available morphological evidence, the species status of *C. sinoerecta* is here reaffirmed.

Table 1. Diagnostic characters of ***Ceropegia semifusca*** and comparison with other related species of sect. ***Chionopegia***.

Characters	***C. semifusca***	***C. sinoerecta***	***C. sunhangiana***
Stem	erect, to 0.35 m long, puberulent	erect, to 0.2 m long, uniformly fine puberulent	twining, to 1.5 m, pilose
Leaf shape	blade elliptic, base broadly cuneate, apex acute	blade elliptic, base narrowly cuneate, apex narrowly acute	leaf blade ovate, apex abruptly acute to long acuminate
Leaf size	20–30 × 10–20 mm	20–50 × 6–16 mm	20–60 × 15–30 mm
Peduncle	absent	4–17 mm long, sparsely pilose	5–10 mm, pilose
Pedicel	5–10 mm long, glabrous	5–17 mm long, glabrous	8–20 mm, sparsely pilose
Corolla length	25–40 mm	36–43 mm	25–40 mm
Corolla shape and color	Basal swelling ovoid; lobes gradually widening at base; corolla yellow-green with lavender stripes or dots	Basal swelling ovoid; lobes gradually widening; tube dark purple basally, pale apically	Basal swelling ovoid; lobes gradually widening; corolla yellow-green, throat white
Width of lobe ovoid cage	1.5 times as wide as the inflated basal tube	as wide as the inflated basal tube	as wide as the inflated basal tube
Corolla lobes	Linear to narrowly oblong, glabrous below, dark brown and pubescent from midpoint, fused at apex	Linear to narrowly lanceolate, dark nearly to base, minutely puberulent, slightly curved at base, apex sharply incurved	Linear to narrowly oblong, slightly revolute along midrib, coherent at apex, strongly folded outwards, glabrous, light green to reddish brown

It appears to be most closely related to *C. mairei*; however, *C. mairei* represents a species complex with considerable morphological variation, and its circumscription requires further taxonomic investigation.

Morphologically, *C. semifusca* differs from *C. sinoerecta* primarily in the coloration and proportions of the corolla lobes. In *C. semifusca*, the distal half of the corolla lobes is dark brown, whereas in *C. sinoerecta* they are uniformly black throughout. Additionally, in *C. sinoerecta*, the width of the corolla lobes at the base is approximately equal to that of the corolla tube at its basal swelling, while in *C. semifusca*, the lobes are 1.5 to 2 times broader than the tube at its widest point.

In comparison with *Ceropegia sunhangiana*, *C. semifusca* exhibits distinct morphological differences. The former is an erect herb, whereas *C. sunhangiana* is a twining species. In addition, *C. semifusca* differs by having elliptic leaves with an acute apex 20–40 mm long, in contrast to the abruptly acute to long-acuminate leaf apex 20–60 mm long in *C. sunhangiana*. (Figs. 1, S1, Table 1).

Phylogenetic analyses

The matrix of complete chloroplast genome sequences was analyzed using Bayesian inference (BI) and maximum likelihood (ML) methods, which produced congruent topologies (Fig. 2). The BI tree is shown with Bayesian posterior probabilities (PP) and ML bootstrap support values (BS) indicated at the nodes. *C. semifusca* was placed within *C.* sect. *Chionopegia*, and its phylogenetic position was resolved between *C. sunhangiana* and *C. sinoerecta*, with strong support in both BI and ML analyses. This result demonstrates that morphologically similar species exhibit close phylogenetic relationships, providing molecular evidence for the recognition of *C. semifusca* as a new species.

Chromosome karyotype analysis and genome size estimation

The somatic chromosome number of *Ceropegia semifusca* was determined to be $2n = 22$ (Fig. 3). Metaphase chromosomes were small and morphologically similar, with an average length of approximately 5 μm. The karyotype was symmetrical, indicating a relatively conserved chromosomal structure within the genus *Ceropegia*.

Genome size estimation based on flow cytometry revealed that *C. semifusca* possesses a haploid genome size of approximately 0.61 Gb. Using *Zea mays* L. and *Solanum lycopersicum* L. as internal standards, the fluorescence intensity ratios between the sample and the references were 0.27 and 0.68, respectively, yielding consistent estimates. The close agreement between the two reference-based measurements supports the reliability of the result. These findings provide fundamental cytogenetic and genomic data for *C. semifusca*, which are valuable for understanding its evolutionary relationships and comparative genome characteristics within the genus *Ceropegia*.

TAXONOMIC TREATMENT

Ceropegia semifusca P.R.Luo & J.D.Ya**, *sp. nov.***

滇中吊灯花 Fig.1

Diagnosis: *Ceropegia semifusca* is characterized by its erect habit, elliptic leaves with an acute apex (20–40 mm long), and a corolla with lobes 1.5–2 times broader than the tube at its widest point. It differs from *C. sinoerecta* by the dark brown distal halves of the corolla lobes (vs. uniformly black in *C. sinoerecta*) and from *C. sunhangiana* by its non-twining and shorter stem, less acuminate leaf apex.

Type: CHINA. Yunnan Province: Panlong District, Aziying Township, 25°19'N, 102°48'E, 2142 m a.s.l., 11 Aug. 2024, *J.D. Ya & Y.R. Ding 24CS25948* (holotype KUN!, isotype CSH!).

***Description*:** Perennial, erect herb, up to 350 mm. Roots 8–15, white, fleshy, fusiform, fascicled, 80–200 mm long, 2–6 mm in diameter. Stem slender, terete, greenish or brown, branched, 1–2 mm in diameter, uniformly fine

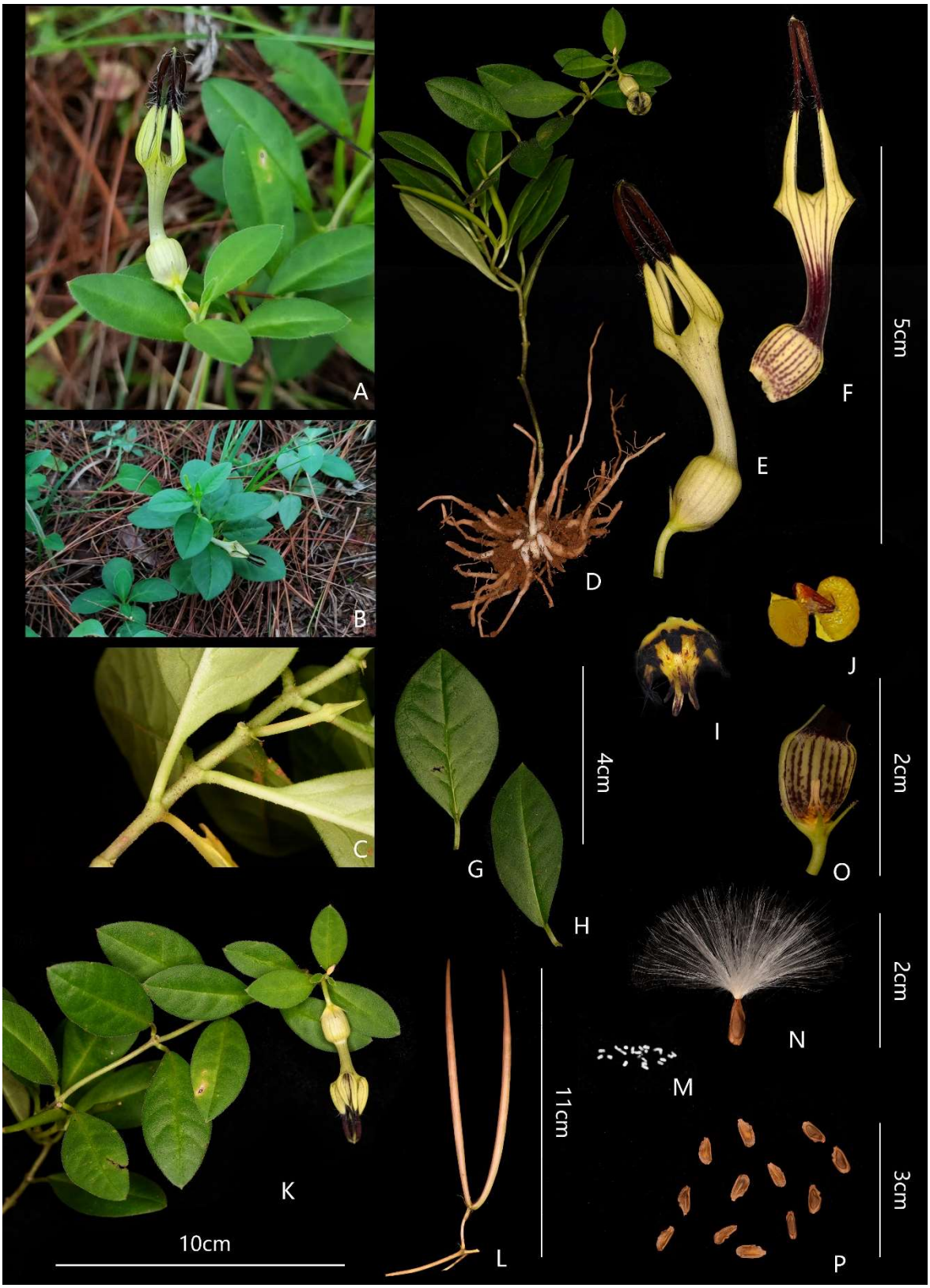

Fig. 1. ***Ceropegia semifusca*** P.R.Luo & J.D.Ya **A**−**B**, habit. **C**, stem and abaxial leaf showing the pubescence. **D**, plant showing the root. **E**−**F**, corolla tube dissected showing corolla interior and corona position. **G**−**H**, adaxial leaf. **I**, gynostegium. **J**, pollinarium. **K**, corolla position. **L**, follicles. **M**, chromosome number: 2*n*=22. **N**, seed with hair. **O**, pedicel, calyx and corona. **P**, seed. Scale bars: L = 110 mm; K = 100 mm; E,F = 50 mm; H = 40 mm; P = 30 mm; O,N = 20 mm.

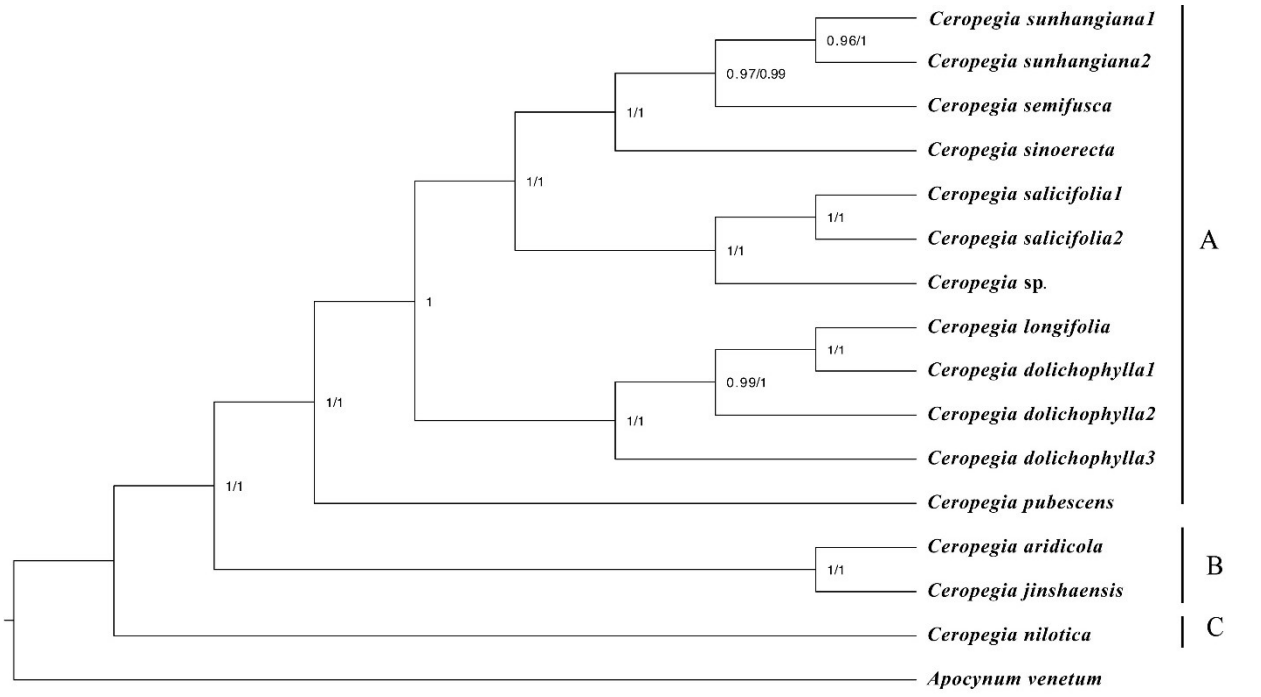

Fig. 2. Phylogenetic tree based on the complete chloroplast sequences. Numbers in the branches are Likelihood bootstrap support (BS) from ML, Bayesian posterior probability (PP) from BI. **A**. ***Ceropegia*** sect. ***Chionopegia***. **B**. ***C.*** sect. ***Tiloris***. **C**. ***C.*** sect. ***Callopegia***.

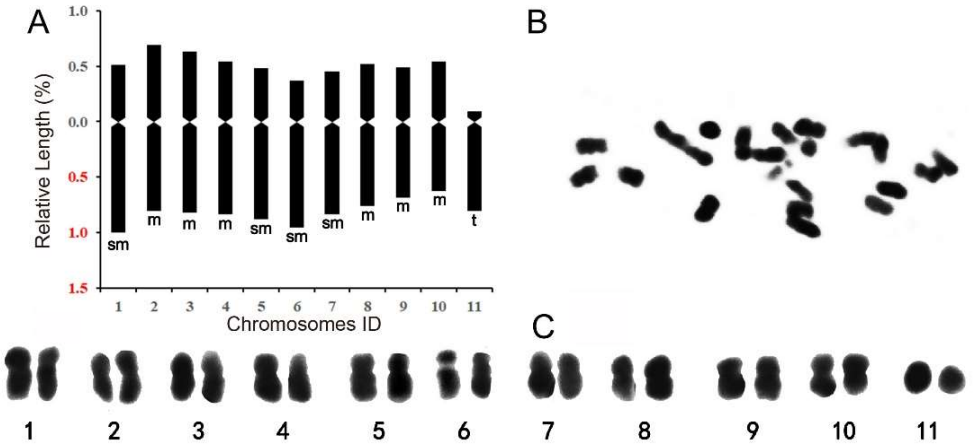

Fig. 3. Chromosome karyotype analysis of ***C. semifusca***. **A**. Chromosome Pattern. **B**–**C**. Chromosome number and characteristics.

puberulent; internodes 10–40 mm long. Leaves opposite; petiole terete, 10–15 mm long, ca. 1 mm in diameter, sparse pilose, adaxially grooved; leaf blade elliptic, 20–30 × 10–20 mm, adaxially green, sparsely pubescent on adaxial leaves, abaxially light green, pilose along midvein, base broadly cuneate; midvein adaxially flat or slightly depressed; lateral veins in 4–6 pairs, obliquely ascendant, adaxially flat, abaxially slightly convex. Flowers solitary next to the axils; pedicel 5–10 mm long, ca. 1 mm in diameter, glabrous; bracts 3–5, subulate to lanceolate, 2–4 mm long, greenish, acuminate at apex. Calyx 5, subulate to lanceolate, 3.0–5.0 × 0.5–1.0 mm, acuminate at apex, glabrous. Corolla tubular, 25–40 mm long, tube 15–20 mm long, 3–5 mm in diameter, basal swelling ovoid, 5–10 mm long, 3–6 mm in diameter, gradually narrowed and increasing from the middle of tube gradually to 4–7 mm at corolla throat as 1.5 times wide as the inflated basal tube, externally yellowish-green with lavender stripes or dots, glabrous, inside yellowish-green with dark purple stripes; corolla lobes linear to narrowly oblong, 8.0–20.0 × 1.0–3.0 mm, gradually narrowing from the throat, glabrous below, becoming dark brown and pubescent from about halfway up, and fused at the apex; Corona biseriate; interstaminal corona lobes 5, each ca. 2 mm long, deeply divided into two triangular teeth; lobes orange, sparsely covered with white hairs, apex cuspidate; Staminal corona lobes 5, linear-ligulate, ca. 3.5 mm long, translucent and light yellow, glabrous, marked

with purple spots and longitudinal streaks. Pollinia orange, ovoid, ca. 0.25 × 0.30 mm, attached to a brownish corpusculum by short translator arms. Ovary conical, ca 2 mm long, 0.5 mm diameter in the middle, glabrous. Seeds ellipsoid ca 50 × 30 mm with a coma at the apex.

Chromosome number and genome size: 2*n*=22, genome size 0.61 Gb.

Etymology: *Ceropegia semifusca* is named for the corolla lobes being half dark-coloured (*semi* = half, *fuscus* = dark), with the distal halves dark brown. Vernacular name: the Chinese name is given as "滇中吊灯花" (diān zhōng diào dēng huā), referring to the distribution of *C. semifusca* in the central Yunnan.

Phenology: The flowering period is from June to September.

Distribution and habitat: This new species is currently known from Aziying Township (formerly part of Songming County), Panlong District, Kunming City, Yunnan Province, at altitudes 2000 m to 2250 m, growing around stones in the grassy areas of forest understories.

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LITERATURE CITED

Bruyns, P.V., Klak, C., Hanáček, P. 2017 A revised, phylogenetically-based concept of *Ceropegia* (Apocynaceae). S. Afr. J. Bot. **112:** 399–436.

Capella-Gutiérrez, S., Silla-Martínez, J.M., Gabaldón, T. 2009 TrimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics **25(15):** 1972–1973.

Chen, Y.-S., Deng, Z.T., Gou, Z., Sun, H. 2018 Is the east asian flora ancient or not? Nat. Sci. Rev. **5(6):** 920–932.

Doležel, J., Bartoš, J. 2005 Plant DNA flow cytometry and estimation of nuclear genome size. Ann. Bot. **95(1):** 99–110.

Endress, M.E., Meve, U., Middleton, D.J., Liede-Schumann, S. 2018 Apocynaceae. In: Kadereit, J.W., Bittrich, V. (eds.), Flowering Plants. Eudicots 207–411pp. Springer International Publishing, Cham.

Gilbert, M.G. 2020 *Ceropegia*. In: Goyder, D.J., Gilbert, M.G., Venter, H.J.T. Apocynaceae (part 2). Flora Zambesiaca [García MA (ed.)] **7(3)**: 92–190. Royal Botanic Gardens, Kew.

Katoh, K., Standley, D.M. 2013 Mafft multiple sequence alignment software version 7: Improvements in performance and usability. Mol. Biol. Evol. **30(4)**: 772–780.

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Meintjes, P., Drummond, A. 2012 Geneious basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics **28(12)**: 1647–1649.

Kozlov, A.M., Darriba, D., Flouri, T., Morel, B., Stamatakis, A. 2019 Raxml-ng: A fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. Bioinformatics **35(21)**: 4453–4455.

Li, P.-T., Gilbert, M., Stevens, W. 1995 Asclepiadaceae. In: Wu, Z., Raven, P. (eds.), Flora of China **16**: 189–270. Science Press, Beijing & Missouri Botanical Garden.

Luo, P.-R., Rong, S.-T., Zhao, X.-J., Huang, X.-H., Chen, J.-T., Liu, Q., Zhang, X.-J., Jiang, K.-Z., Yang, W.-G., Huang, G.-Y., Deng, T. 2023 *Ceropegia sunhangiana*, a new species of Apocynaceae from southwest China. Nord. J. Bot. **2023(9)**: e03999.

Luo, P.-R., Yang, Q.-Y., Huang, X.-H., Zhang, X.-J., Tan, J.-B., Tu, T.-Y., Goyder, D.J., Gilbert, M.G., Deng, T., Sun, H. 2024 Lectotypification of *Ceropegia driophila* (Apocynaceae) and proposal of *Ceropegia paohsingensis* as a heterotypic synonym. Nord. J. Bot. **2024(12)**: e04489.

Ma, X.-D., Wang, H.-C., He, K.-H., Shi, J.-P., Shen, J.-Y. 2022a *Ceropegia luzhiensis*, a new species of Apocynaceae from Yunnan, China. Nord. J. Bot. **2022(4)**: e03505.

Ma, X.-D., Xing, Y.-W., Tan, Y.-H., Li, J.-W., Zhou, S.-S., Ding, H.-B., Shen, J.-Y. 2022b *Ceropegia jilongensis*, a new species of Apocynaceae from Xizang, China. Taiwania **67(1)**: 93–96.

Ma, X.-D., Wang, W.-G., Shi, J.-P., Shen, J.-Y. 2023 *Ceropegia eshanensis*, a new species of Apocynaceae from Yunnan, China. Taiwania **68(1)**: 75–78.

Meve, U., Liede-Schumann, S. 2007 *Ceropegia* (Apocynaceae, Ceropegieae, Stapeliinae): Paraphyletic but still taxonomically sound. Ann. Mo. Bot. Gard. **94(2)**: 392–406.

Ronquist, F., Teslenko, M., Van Der Mark, P., Ayres, D.L., Darling, A., Höhna, S., Larget, B., Liu, L., Suchard, M.A., Huelsenbeck, J.P. 2012 Mrbayes 3.2: Efficient bayesian phylogenetic inference and model choice across a large model space. Syst. Boil. **61(3)**: 539–542.

Wang, Y., Zhang, C.-F., Ochieng Odago, W., Jiang, H., Yang, J.-X., Hu, G.-W., Wang, Q.-F. 2023 Evolution of 101 Apocynaceae plastomes and phylogenetic implications. Mol. Phylogenet. Evol. **180**: 107688.

Wu, Z.-K., Cai, J., Cai, L., Liu, D.-T. 2019 *Ceropegia jinshaensis* (Apocynaceae), a new species from northwestern Yunnan, China. PhytoKeys **130:** 41–48.

Xie, G., Nong, D.-X., Meng, T., Huang, Y.-S. 2023 Notes on *Ceropegia* (Apocynaceae) in south China. J. Trop. Subtrop. Bot. **31(2)**: 263–271.

Supplementary materials are available from Journal Website