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Research Article

Petrocodon gracilis (Gesneriaceae) is a synonym of *P. mirus* based on morphological and molecular data

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Petrocodon gracilis T.Ding & B.Pan and *P. mirus* X.Z.Shi, J.X.Fu & Li H.Yang are two recently described species exhibiting nearly identical morphology. To determine whether they represent the same taxon, we compared their type localities, type materials, and morphological features and conducted phylogenetic analyses using the nuclear internal transcribed spacer (ITS) and five plastid regions (*atpI-H*, *matK*, *rps16*, *trnH-psbA* and *trnL-F*). Morphological comparisons and type information revealed that both species originated from the same population and are indistinguishable in key traits. Molecular phylogenetic analysis further showed that four samples of *P. gracilis* and *P. mirus* form a strongly supported monophyletic clade. Combined morphological and molecular evidence confirmed their conspecificity. We therefore treat *P. gracilis* as a synonym of *P. mirus*.

Keywords: morphology, *Petrocodon gracilis*, phylogeny, synonymy, taxonomy

Introduction

Petrocodon Hance, a genus of Gesneriaceae, was established for *P. dealbatus* Hance (1883, p. 167) and remained small until 2011 (Wang et al. 1998, Wei 2007, Wang et al. 2011). Molecular phylogenetic analyses have since expanded the genus considerably (Wang et al. 2011, Weber et al. 2011). According to the Gesneriaceae Resource Centre (GRC 2025), *Petrocodon* now comprises 59 species and one variety, exhibiting remarkable morphological diversity (Li et al. 2025a). However, two recently described species, *P. mirus* X.Z.Shi, J.X.Fu & Li H.Yang (Shi et al. 2024, p. 4) and *P. gracilis* T.Ding & B.Pan (Ding et al. 2024, p. 8), share almost identical morphological features. Their publication dates differ by less than two months, suggesting independent descriptions of the same taxon. Examination of their type materials confirmed that they are

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morphologically and geographically identical. To test whether these morphologically identical taxa could represent cryptic species, we conducted multilocus phylogenetic analyses. As described in detail below, both morphological and molecular evidence support the conclusion that *P. gracilis* is conspecific with *P. mirus* and should be treated as its synonym.

Material and methods

Both *P. mirus* and *P. gracilis* (Ding et al. 2024, Shi et al. 2024) are known only from type materials deposited in IBSC, IBK and PE. We compared their type specimens, photographs of living plants, and distributional data.

Phylogenetic relationships were reconstructed using nuclear ITS and five plastid regions (*atpI-H*, *matK*, *rps16*, *trnH-psbA* and *trnL-F*). Datasets from Ding et al. (2024) were retrieved from the National Center for Biotechnology Information (NCBI) and the sampling information can be found in Ding et al. (2024). Two *P. mirus* accessions from Shi et al. (2024) and Qi et al. (2025) were also included. For *P. mirus* accession SXZ339 (Shi et al. 2024), ITS and *trnL-F* sequences were obtained from GenBank, and four additional chloroplast regions (*atpI-H*, *matK*, *rps16* and *trnH-psbA*, NCBI accessions PV361529–PV361532) were amplified from the same DNA sample as used by Shi et al. (2024) to cover the genomic regions employed by Ding et al. (2024). The primers for the four chloroplast regions were retrieved from Qiu et al. (2015). PCR was performed under the following conditions: initial denaturation at 94°C for 5 min; 35 cycles of denaturation at 94°C for 30 s, annealing at 50 °C (for *atpI-H* and *matK*), 54°C (*rps16* and *trnH-psbA*) for 30 s, and extension at 72°C for 1 min; followed by a final extension at 72°C for 10 min. PCR products were bidirectionally sequenced by Sangon Biotech (Shanghai, China). For the other accession (voucher QYC24051001) of *P. mirus* in Qi et al. (2025), the complete chloroplast genome and raw sequencing data were available. We extracted the five chloroplast regions and assembled the ITS (NCBI accession PV422805) using GetOrganelle ver. 1.7.7 (Jin et al. 2020). Six loci (ITS, *atpI-H*, *matK*, *rps16*, *trnH-psbA* and *trnL-F*) were integrated into the phylogenetic matrix from Ding et al. (2024). Phylogenetic analyses were conducted using maximum likelihood (ML) method as implemented in RAxML ver. 8.2.X (Stamatakis 2014) with 1000 rapid bootstrap replicates employing GTRGAMMA model.

Results

Collection data confirmed that *P. mirus* and *P. gracilis* were obtained from the same locality. After publication, the describing authors communicated and verified that both species were collected from the same population. Morphological comparisons revealed complete concordance, including suborbicular leaves, short pedicels, pale-pink corollas with slender tubular tubes, linear reflexed adaxial lobes, oblanceolate abaxial lobes, and fully included stamens and pistils (Fig. 1). Both species exhibit a chiritoid stigma, previously unreported in *Petrocodon*. However, as demonstrated by Ding et al. (2024), the stigma of *P. gracilis* initially develops as a left-right-bilobed structure, consistent with other *Petrocodon* species, and finally turns into a chiritoid shape. This observation clarifies that both species undergo a developmental transition: their stigmas begin as bilobed structures in early developmental stages and later mature into the chiritoid form. Therefore, both species possess stigmas that are essentially consistent with other *Petrocodon* species.

Phylogenetic analyses revealed that the two *P. gracilis* samples are sister to one *P. mirus* accession (QYC24051001), while the *P. mirus* (SXZ339) is further sister to the other three samples, together forming a clade with maximum support (Fig. 2; bootstrap = 100). Branch lengths within the clade are short, and sequence comparison showed near identity among the four samples, differing by only two mutations apart from terminal missing. This strong molecular similarity aligns with their morphological uniformity. Collectively, these data confirmed that the two names refer to the same species. Accordingly, *P. gracilis* is synonymized under *P. mirus* following the International Code of Nomenclature (Turland et al. 2025).

Taxonomic treatment

Petrocodon mirus X.Z.Shi, J.X.Fu & Li H.Yang (Shi et al. 2024, p. 4).

Type: China, Guangxi Zhuang Autonomous Region, Tiandeng County, Shangying Town, 23°03′6″N, 106°58′8″E, 630 m a.s.l., 27 Apr. 2024, X. Z. Shi & J. X. Fu SXZ339 (holotype: IBSC1021453; isotypes: IBSC1021454, IBSC1021455, IBSC1021456).

Synonym: *Petrocodon gracilis* T.Ding & B.Pan (Ding et al. 2024, p. 8). syn. nov. Type: China, Guangxi Zhuang Autonomous Region, Tiandeng County, Shangying Town, 23°04′5″N, 106°59′6″E, 600 m a.s.l., 4 May 2024, T. Ding & B. Pan LPW2024022 (holotype: IBK; isotypes: IBK IBSC PE).

Description

Perennial herb. Rhizome thick, with conspicuous leaf scars, 0.5–4.0 (20) cm long, 0.5–1.8 cm in diameter; internodes inconspicuous. Leaves 3–9, clustered at rhizome apex; petioles cylindrical, 2–13 cm long, 0.3–0.7 cm in diameter, villous and glandular-villous; blades slightly leathery when dry, broadly ovate to suborbicular, 4.0–16.0 × 3.5–15.0 cm, at both surfaces villous and glandular-villous, rounded to obtuse at apex, cordate at base, with entire to serrate margin; lateral veins 3–6. Cymes erect, axillary, 1–11, 1–3-branched, 4–64-flowered; peduncles 5–25 cm long, densely brown-villous and glandular-villous; bracts 2, opposite, narrowly triangular, with entire margin, 3.0–6.0 × 1.0–1.6 mm, densely pubescent and glandular pubescent. Pedicels 1–4 mm long,

Figure 1. Morphology of *Petrocodon mirus* (A–B) and *P. gracilis* (C–D). (A) isotype of *P. mirus*, (C) holotype of *P. gracilis*. Field photographs (B) and (D) by Xi-Zuo Shi and Bo Pan, respectively. Holotype of *P. mirus* was published in Shi et al. (2024).

densely glandular- and eglandular- pubescent. Calyx 5-parted to base; segments equal, narrowly triangular, 5–11 × 1–2 mm, glandular-pubescent to pubescent externally, sparsely puberulent internally, with entire margin and obtuse to acute apex. Corolla pale pink, densely villous and glandular-villous; throat with bluish purple or white vermicular hairs; tube narrowly tubular, 8–12 (15) mm long, slightly swollen at base, 2–3 mm in diameter at base and 3–4 mm in diameter at mouth; limb white, densely villous and glandular-villous, distinctly 2-lipped; adaxial lip 2-lobed from base with lobes linear to narrowly triangular, 6–8 × 1–2 mm, reflexed; abaxial lip 3-lobed to near base with lobes oblanceolate, 7–10 (14) × 2–4 mm. Stamens 2, included, adnate to 6 mm above the abaxial side of the corolla tube base; filaments white, 2–3 mm long, glabrous; anthers coherent face to face, divaricate, 1.5 mm long, glabrous. Lateral staminodes 2, 0.4 mm long, retrorse, glabrous, adnate to 4–5 mm above the corolla base; adaxial staminode invisible. Disc annular, with repand margin, 1 mm high, glabrous. Pistil 6.0–9.5 mm long; ovary narrowly ovoid, 2–3 mm long, densely glandular-pubescent; style linear, 4–6 mm long, glandular-pubescent; stigma chiritoid-like with a lower stigma lobe lamellar with a slightly bilobed apex, 0.4 mm long. Capsule linearly ovoid, 5–8 mm long, loculicidally dehiscing. Seed unappendaged, ellipsoid, fusiform, 0.4–0.6 mm long, 0.2 mm in diameter.

Phenology

Petrocodon mirus was observed flowering in April–May, and fruiting from May–June.

Distribution and ecology

Petrocodon mirus is endemic to Tiandeng County, Guangxi Zhuang Autonomous Region, China, growing growing in limestone habitats beneath evergreen broad-leaved forests.

Conservation status

Approximately 150 mature individuals are known from two subpopulations in Shangying, Guangxi, China (Shi et al. 2024). No evidence of decline or extreme fluctuations has been observed. As an endemic restricted to karst habitats

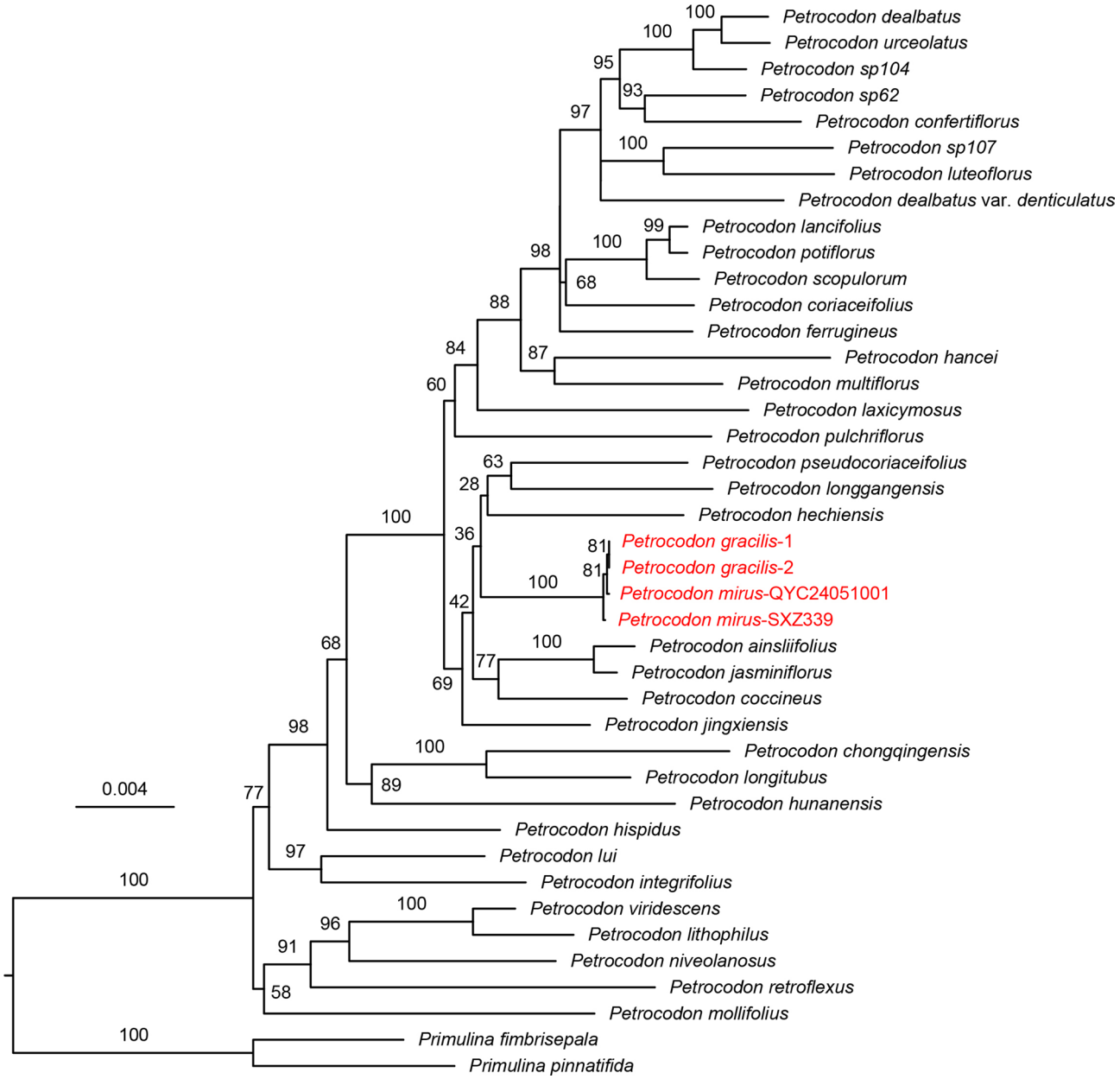

Figure 2. Maximum likelihood tree based on concatenated ITS and five chloroplast regions (*atpI-H*, *matk*, *rps16*, *trnH-psbA* and *trnL-F*). Numbers besides the nodes are bootstrap values.

near the China-Vietnam border (Ding et al. 2024), potential undocumented populations may exist in contiguous limestone habitats. Pending further field surveys, *P. mirus* should be classified as data deficient (IUCN 2022).

Specimen examined

Guangxi, Tiandeng, Shangying, 27 Apr. 2024, X. Z. Shi & J. X. Fu SXZ339 (holotype: IBSC-1021453; isotypes: IBSC-1021454, IBSC-1021455, IBSC-1021456); same locality, 4 May 2024, T. Ding & B. Pan LPW2024022 (IBK, IBSC, PE); same locality, 10 May 2024, Y. C. Qi QYC24051001 (IBK).

Notes

Differences in recorded coordinates between *P. mirus* and *P. gracilis* result from weak mobile signals at the remote type locality, leading to approximate GPS readings. Discrepancies in reported individual counts are due to rough population estimate rather than precise counts.

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Author contributions

Nan Li: Data curation (lead); Formal analysis (lead); Investigation (equal); Methodology (lead); Resources (lead); Software (lead); Validation (equal); Writing – original draft (lead). **Xi-Zuo Shi**: Data curation (equal); Formal analysis (equal); Investigation (equal); Methodology (equal); Resources (equal); Validation (equal); Visualization (equal); Writing – original draft (equal). **Yan-Lin Zhao**: Data curation (equal); Formal analysis (equal); Investigation (equal); Methodology (equal); Software (equal); Validation (equal); Writing – original draft (equal). **Yan-Xiang Lin**: Conceptualization (lead); Data curation (equal); Funding acquisition (lead); Investigation (equal); Methodology (equal); Project administration (lead); Supervision (lead); Validation (equal); Visualization (equal); Writing – original draft (equal).

Data availability statement

We deposited sequencing data in the National Center for Biotechnology Information with accession numbers PV361529–PV361532.

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