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Author-formatted, not peer-reviewed document posted on 28/06/2022

DOI: <https://doi.org/10.3897/arphapreprints.e89376>

# ***Phalaenopsis yarlungzangboensis* (Orchidaceae: Epidendroideae, Vandeeae), a new species from Xizang, China**

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***Phalaenopsis yarlungzangboensis* (Orchidaceae: Epidendroideae, Vandaeae), a new species from Xizang, China**

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**Abstract**

A new species of Orchidaceae, *Phalaenopsis yarlungzangboensis* from Motuo, Xizang, is described and illustrated based on morphological characters and molecular phylogenetics. *Phalaenopsis yarlungzangboensis* is distinguished from its relatives by its column foot with triangular wings, subrectangular lateral lobes concave, lower part white with a deep purplish red spot and hairy and upper part pale yellow with densely rusty spots, rhombic middle lobe with a fleshy horned appendage at base, disc grooved. Molecular phylogenetic analyses and morphological characters indicated that *P. yarlungzangboensis* is closed to *P. deliciosa*, *P. gibbosa* and *P. lobbii*.

**Keywords:** *Phalaenopsis yarlungzangboensis*, new species, Xizang, Orchidaceae

## Introduction

The genus *Phalaenopsis* Bl. comprises of approximately 63 species, distributed from India and Southeast Asia to Australia and New Guinea with centers of diversity in Indonesia and the Philippines (Deng et al. 2015; Pridgeon et al. 2014). Based on molecular and morphological evidence, seven genera, including *Kingidium*, *Nothodoritis*, *Doritis*, *Lesliea*, *Ornithochilus*, *Hygrochilus* and *Sedirea*, have been transferred to *Phalaenopsis* s.l. (Cribb and Schuiteman 2012; Kocyan and Schuiteman 2014; Tsai et al. 2010). *Phalaenopsis* s.l. was redefined and a new infrageneric classification was proposed, comprising of four subgenera, namely subgen. *Parishianae* (Sweet) Christenson, subgen. *Phalaenopsis* Blume, subgen. *Hygrochilus* (Pfitzer) Kocyan & Schuiteman, and subgen. *Ornithochilus* (Lindl.) Kocyan & Schuiteman (Aung and Jin 2021; Kocyan and Schuiteman 2014; Li et al. 2016; Pridgeon et al. 2014).

There are about 24 species of *Phalaenopsis* in China (Zhou et al. 2021). During our fieldwork in Motuo County, Linzhi city, Xizang, China in 2022, a unknown species of *Phalaenopsis* was found in evergreen broad-leaved forest along the Yarlungzangbo River. Based on morphological characters and molecular evidence, it was identified as a new species of *Phalaenopsis* and described below.

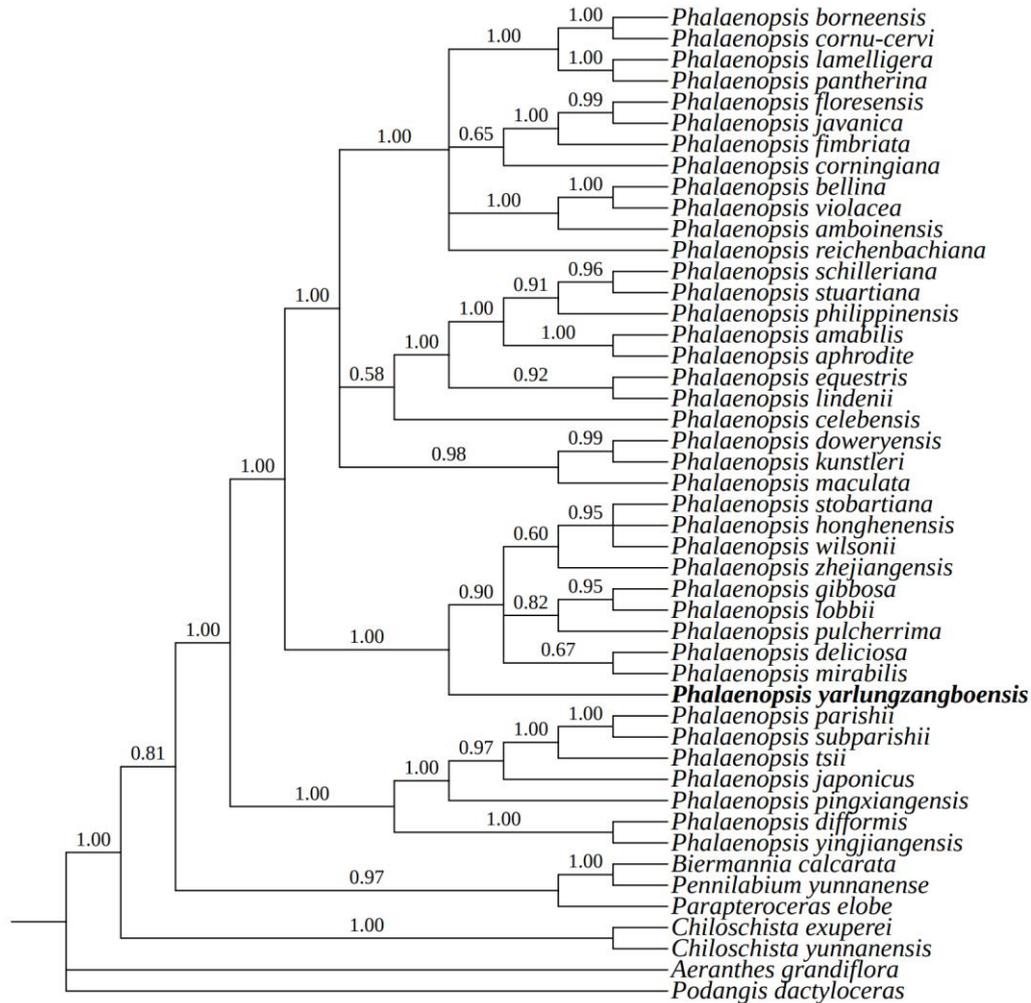
## Materials and methods

Morphological characters of the specimens were observed, measured and photographed based on living plants in Motuo, Tibet. Four markers including one nuclear marker (nrITS) and three plastid markers (*matK*, *trnL*, and *trnL-F*) were used in molecular phylogenetics. Primers and amplification procedures were performed following Deng et al. (2015). Molecular phylogenetics included 40 species in *Phalaenopsis* and 7 related species of Aeridinae (Table S1 in Appendix). The incongruence length difference test (ILD) was used to quantify the conflicts between nrDNA and plastid DNA data in PUPA (Darlu and Lecointre 2002). Two species, *Aeranthes grandiflora* Lindley and *Podangis dactyloceras* (Reichenbach) Schltr., were used as the outgroup based on previous results (Chase et al. 2015). Sequences were edited independently and assembled using SeqMan (<https://www.dnastar.com/>). Sequence alignment, model selection and super matrix construction were performed in the Phylosuit (Zhang et al. 2020). Bayesian inference were inferred with MrBayes v. 3.2.7a on XSEDE in CIPRES Science Gateway online web server (Miller et al. 2010). Partition selection of the model was found in ModelFinder (Kalyaanamoorthy et al. 2017) with Corrected Akaike Information Criterion (AICc). GTR+F+I+G4 was selected as the best models for ITS and GTR+F+G4 for three plastid markers. Two separate Markov-chain Monte Carlo (MCMC) analyses were performed, proceeding for 1,000,000 generations, and sampling every 1000 generations. Maximum likelihood analyses and model selection were performed in IQ-Tree 2 (Minh et al. 2020). Support values for the clade were estimated using 1,000,000 bootstrap replicates.

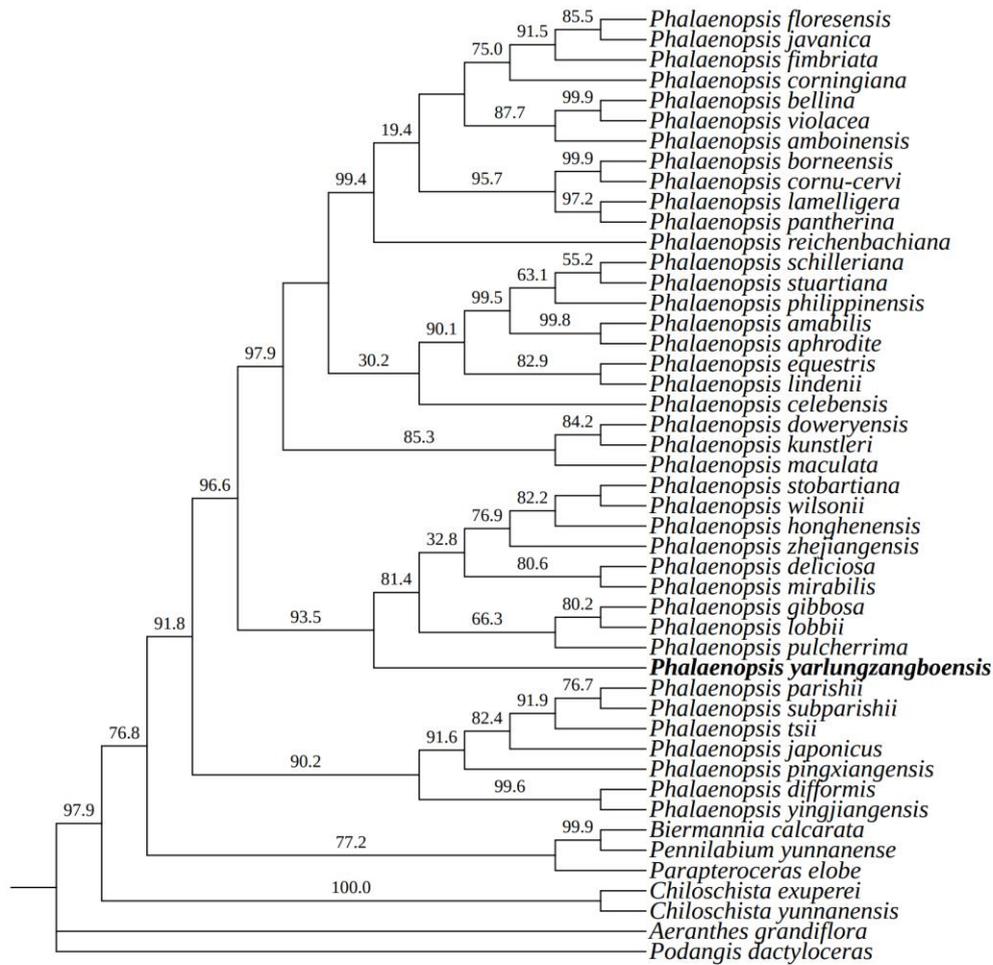
## Results

*P. yarlungzangboensis* belongs to subgen. *Parishianae* and close to *P. deliciosa*, *P. gibbosa* and *P. lobbii* based on morphological characters. ILD Test indicated that plastid DNA and nuclear DNA were not suitable for combined analysis. The Bayesian

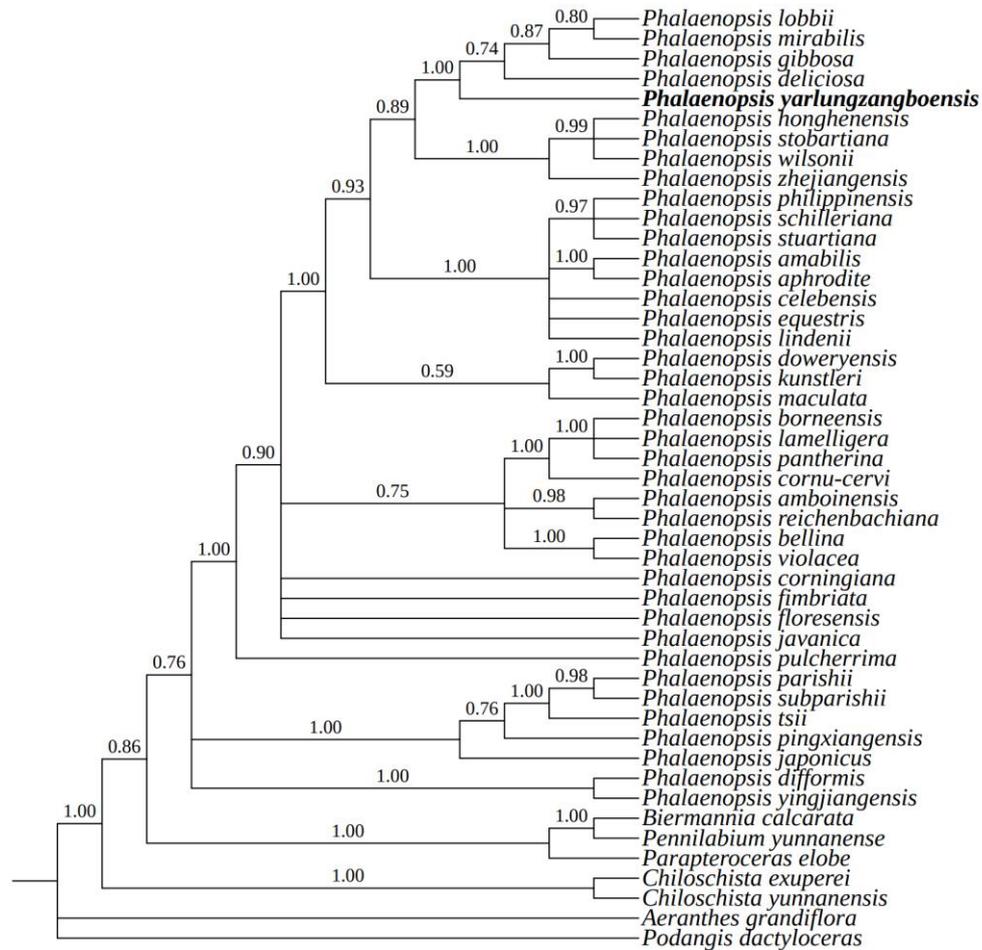
inference and ML analyses of ITS showed that *P. yarlungzangboensis* belongs to subgen. *Parishianae* with middle to high support (Figs. 1, 2; PP=1, BS<sub>ML</sub>=93.5). The Bayesian inference of three plastid markers showed that *P. yarlungzangboensis* is sister to group including *P. deliciosa*-*P. lobbii* with high support (PP=1, Fig. 3). All these results indicated that *Phalaenopsis yarlungzangboensis* was nested with in subgen. *Parishianae*.



**Fig. 1.** Phylogram of Bayesian inference based on nrDNA ITS. Numbers above branches indicate posterior probabilities (PP).



**Fig. 2.** Phylogram of maximum likelihood of nrDNA ITS. Numbers at nodes are bootstrap support ( $BS_{ML}$ ).



**Fig. 3.** Phylogram of Bayesian inference based on plastid sequences (*matK*, *trnL* and *trnL-F*). Numbers above branches indicate posterior probabilities (PP).

### Taxonomy

*Phalaenopsis yarlungzangboensis* X.H. Jin & C.B. Ma, *sp. nov.* (雅鲁藏布蝴蝶兰) (Figs. 4-5)

**Type:** CHINA. Xizang Autonomous Province, Linzhi City, Motuo County, elev. 800, 18 Apr. 2022, Xiaohua Jin, Chongbo Ma & Tiankai Zhang 38519 (holotype PE!, isotype, PE!).

**Diagnosis:** *Phalaenopsis yarlungzangboensis* is distinguished from its relatives by its column foot having triangular wings, subrectangular lateral lobes concave, lower part of lateral lobes white with a deep purplish red spot and hairy, upper part pale yellow with dense rust spots, rhombic middle lobe with a fleshy horned appendage at base and grooved in centre.



**Fig. 4.** *Phalaenopsis yarlungzangboensis*. The habitat and plants of *P. yarlungzangboensis*.



**Fig. 5.** *Phalaenopsis yarlungzangboensis* X.H. Jin & C.B. Ma, *sp. nov.*

A. Front view of flowers. B. Lateral view of flower. C. Front view of flower, showing basal part of lip. D. Lateral view of column, ovary and pedicel. E. Lip, side view. F. Lip, dorsal view. G. Column and column foot. H. Middle sepal. I. Petal. J. Lateral sepal. K. Anther cap. Photographed by Xiaohua Jin and Chongbo Ma.

Epiphytic plants. Roots greenish, elongate, flattened and prostrate along the twigs or trunk, densely verrucose. Stem inconspicuous. Leaf 1, oblong-elliptic, 7–10 × 3–4 cm. Inflorescences 1 or 2, suberect or arching, ca. 12 cm long, unbranched, laxly 5–6-flowered; floral bracts ovate-triangular, 5–6 mm long. Flowers 1–1.2 cm in diameter, yellow; sepals and petals pure yellow, without spots or other coloration. Middle sepal similar to petals, elliptic, ca. 7–8 × 5 mm; lateral sepals broadly triangular, ca. 10 × 6

mm; petals long elliptic, ca.  $9 \times 5$  mm; lip 3-lobed; lateral lobes subrectangular, concave into boat-shaped,  $2 \times 4$  mm, lower part white with a deep purplish red spot and hairy, upper part pale yellow with dense rust spots; mid-lobe rhombic, ca.  $10 \times 7$  mm, disk grooved, base with a fleshy protuberant appendage; appendage 2–3 teeth on either side and apex with two long horns. Column subparallel to middle lobe of lip, ca. 5 mm long; column foot ca. 4 mm long, with triangular wings on both sides; anther cap yellow, hemi-spherical. Fl. Mar-Apr.

**Etymology:** The name “*yarlungzangboensis*” refers to the type locality of the new species, Yarlungzangbo River, Linzhi City, Xizang Autonomous Province, China.

**Distribution and habitat:** *Phalaenopsis yarlungzangboensis* is currently known only from the type locality in Motuo, Tibet, China. During our field investigation in Motuo, about twenty plant specimens were found epiphytic on trunks and twigs at elevations of 700-900 m.

**Phenology:** Flowering in March to April.

**Conservation status:** *Phalaenopsis yarlungzangboensis* grows in tropical season rain forest in Motuo County. At least one population was discovered during our fieldwork. For the time being, the current conservation status of the new species is Data Deficient (DD) according to the IUCN guidelines (IUCN 2019).

### Acknowledgements

Funds were provided by Project of Orchid Biodiversity Survey of China, National Forestry and Grassland Administration (2019070714, 2020100707).

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