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Unveiling a new species of *Periconia* Tode (Periconiaceae) and its newly identified host in China

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ABSTRACT

A new species *Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov., is described from Gaoligong Mountains of Yunnan province, China, based on morphological features and DNA sequence data. It was isolated from dead leaves of *Ligustrum lucidum* W.T. Aiton, and is characterized by black dark hairy surface colonies on natural substrate, along with large conidiophores and conidia. Multigene phylogenetic analysis of concatenated from LSU, SSU, ITS, and TEF-1α sequences identified *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. as a phylogenetically distinct lineage. The combination of morphological and molecular evidences strongly supports the recognition of *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. as a new species.

KEY WORDS
Biodiversity, fungal taxonomy, Gaoligong Mountains, multigene phylogeny, new species.

RÉSUMÉ

Présentation d'une nouvelle espèce de Periconia *Tode (Periconiaceae) et de son hôte récemment identifié en Chine.*

Une nouvelle espèce, *Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov., est décrite à partir des montagnes de Gaoligong, dans la province du Yunnan (Chine), sur la base de caractéristiques morphologiques et de données de séquences d'ADN. Elle a été isolée à partir de feuilles mortes de *Ligustrum lucidum* W.T. Aiton et se caractérise par des colonies de surface noires et velues sur un substrat naturel, ainsi que par de grands conidiophores et de grosses conidies. Une analyse phylogénétique multigénique des séquences concaténées de LSU, SSU, ITS et TEF-1α a permis d'identifier *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov., comme une lignée phylogénétiquement distincte. La combinaison des preuves morphologiques et moléculaires appuie fortement la reconnaissance de *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov., comme une nouvelle espèce.

MOTS CLÉS
Biodiversité, taxonomie fongique, montagnes de Gaolifong, phylogénie multigénique espèce nouvelle.

INTRODUCTION

The genus *Periconia* Tode (Periconiaceae, Pleosporales) was introduced by H.J.Tode, with *P. lichenoides* Tode as the type species (Tode 1971). There are four genera of Periconiaceae Nann., including three monotypic genera *viz. Bambusistroma* D.Q. Dai & K.D. Hyde, *Flavomyces* D.G. Knapp, Kovács, J.Z. Groenew. & Crous, and *Noosia* Crous, R.G. Shivas & McTaggart, and a polyphyletic genus *Periconia* (Tanaka *et al.* 2015; Wijayawardene *et al.* 2022; Cai *et al.* 2024). Most species of *Periconia* are asexual, and only a few are described as sexual morphs viz. *P. didymospora* (D.Q. Dai & K.D. Hyde) D.Q. Dai & Phookamsak, *P. homothallica* Kaz. Tanaka & K.Hiray., *P. igniaria* E.W. Mason & M.B. Ellis, *P. prolific* Anastasiou, and *P. pseudodigitata Kaz. Tanaka & K. Hiray.* (Tanaka *et al.* 2015; Cai *et al.* 2024). There are currently, 234 records of *Periconia* in the Index Fungorum (2025), of which more than 130 accepted morphological species lacking molecular data (Liao *et al.* 2024). *Periconia* species are mostly saprobes, endophytes, and plant pathogens of herbaceous plants (Markovskaja & Kačergius 2014). They usually have a cosmopolitan distribution and reported in a wide range of habitats, including marine environments, particularly in temperate and tropical regions (Leukel 1948; Rao & Rao 1964; Ellis 1971, 1976; Tanaka *et al.* 2015; Liu *et al.* 2017a; Sarkar *et al.* 2019; Voronin *et al.* 2021; Cai *et al.* 2024). *Periconia* has a broad intercontinental distribution range (Goga 2000; Teles *et al.* 2006; Tanaka *et al.* 2015; Dubey 2017; Crous *et al.* 2018; Phookamsak *et al.* 2019; Calvillo-Medina *et al.* 2020; Gunasekaran *et al.* 2021; Liao *et al.* 2024; Tian *et al.* 2024). In China, numerous *Periconia* species have been reported from the provinces of Guangdong, Sichuan, Taiwan, and Yunnan (Wu *et al.* 2014; Hyde *et al.* 2018; Tennakoon *et al.* 2021; Yang *et al.* 2022; Su *et al.* 2023; Liao *et al.* 2024).

In the present study, specimens were collected from the Gaoligong Mountains, Yunnan Province, China, in October 2024. Comprehensive morphological features and multilocus phylogenetic analyses consistently placed the isolates within *Periconia*, yet distinct from all known species, thereby supporting the recognition of a novel species and host record.

MATERIAL AND METHODS

Collection and examination of specimens

A study survey was conducted of Yunnan province China in 25 October 2024 and the infected leaves of *Ligustrum lucidum* W.T. Aiton were collected from Gaoligong Mountains, Yunnan China. The samples were transferred to the laboratory in Ziplock plastic bags and incubated in boxes cleaned by 75% alcohol and lined with sterile and moist tissue at 25-30°C for three days. The samples were processed and examined following the methods described by Taylor & Hyde (2003). The observations of colonies on the substrate

TABLE 1. — The PCR conditions and the primers used in this study.

Locus	Primer	Sequences	PCR condition	References
LSU	LROR LR5	ACCCGCTGAACTTAAGC TCCTGAGGGAAACTTCG	(1) Initialization for 3 min at 94°C; (2) 40 cycles of denaturation at 94°C for 45s, annealing at 56°C for 50s, and extension at 72°C for 1 min; (3) final elongation at 72°C for 10 min and (4) storage at 4°C.	White *et al.* (1990)
SSU	NS1 NS4	GTAGTCATATGCTTGTCTC CTTCCGTCAATTCCTTTAAG		Vilgalys & Hester (1990)
ITS	ITS4 ITS5	TCCTCCGCTTATTGATATGC GGAAGTAAAAGTCGTAACAAGG		White *et al.* (1990)
TEF1-α	983F 2218R	GCYCCYGGHCAYCGTGAYTTYAT ATGACACCRACRGCRACRGTYTG	(1) Initialization at 95°C for 5 min; (2) 10 cycles of denaturation at 95°C for 30s, annealing at 60°C for 1 min, and extension at 72°C for 50s; (3) followed by 35 cycles of denaturation at 95°C for 30s, annealing at 52°C for 1 min, and extension at 72°C for 50s; (4) final elongation at 72°C for 10 min; (5) storage at 4°C.	Rehner & Buckley (2005)

were carried out using a Motic SMZ 168 Series dissecting microscope. The fruiting bodies were mounted in water for micro-morphological studies and photographed by a Nikon ECLIPSE 80i compound microscope fitted with a Cannon 600D digital camera. Measurements were made with the Tarosoft (R) Image Frame Work program and images used for figures were processed with Adobe Photoshop CS3 software (Adobe Systems, United States).

Fungal isolation was carried out using single spore isolation method on water agar (WA) and then germinated spores were transferred to potato dextrose agar (PDA), following the method described by Chomnunti *et al.* (2014). Isolates are deposited in the Kunming Institute of Botany Culture Collection (KUNCC), China.

DNA extraction, amplification and sequencing

Genomic DNA was extracted by using Fungal DNA Kit (Omega Biotech, CA, United States) according to the manufacturer's protocols and the extracted DNA was stored at –20°C. The partial sequences from the ITS region of the nrDNA were amplified with the primer pair ITS4/ITS5 (White *et al.* 1990). For the SSU region, amplification was performed with the primer pair NS1/NS4 (White *et al.* 1990). The LSU region was amplified with the primer pair LROR/LR5 (Vilgalys & Hester 1990). For the TEF-1α region amplification was performed with the primer pair 983F/2218R (Liu *et al.* 1999). The combination of these genetic regions ITS, SSU, LSU and TEF-1α provides a comprehensive molecular dataset. A 25 mL reaction mixture containing 1.6 mL dNTP mix (2.5 mM/mL), 0.2 mL Taq polymerase (5 µm/mL), 2 mL polymerase buffer (10 /mL), 1 ml forward and reverse primers (10 µm/mL), and 1 mL DNA template was used for PCR experiments following the protocol followed by Sana *et al.* (2025) and the PCR conditions detailed in Table 1. Sangon Biotech (Shanghai) Co., Ltd. sequenced PCR products using the same PCR primers used in amplification operations.

Molecular phylogeny

The newly generated sequences were checked using BioEdit (Hall 1999). A Blast search (https://blast.ncbi.nlm.nih.gov/) was used to locate and retrieve reference sequences from the GenBank nucleotide database. Subsequently, closely related sequences of the taxa that had zero E-values were retrieved from the database to generate the dataset. Sequence alignment was performed using MUSCLE (Edgar 2004), available through the EMBL-EBI Web Services website (http://www.ebi.ac.uk/). In addition, the sequences used in previous studies on *Periconia shannanensis* T. Cai, Shu C. He & Q. Zhao were also retrieved from the database to construct the final phylogenetic tree. *Morosphaeria velatispora* (K.D. Hyde & Borse) Suetrong, Sakay., E.B.G. Jones & C.L. Schoch (KH_221) and *M. ramunculicola* (K.D. Hyde) Suetrong, Sakay., E.B.G. Jones & C.L. Schoch (KH_220) were used as an outgroup in the phylogenetic analyses. Maximum Likelihood tree was constructed using RAxML (Miller *et al.* 2010) based on the GTRG model and 1000 bootstraps available in the CIPRES Science Gateway. Bayesian inference (BI) phylogenetic analysis was performed using MrBayes v. 3.2.1 (Ronquist *et al.* 2012). The Markov Chain Monte Carlo (MCMC) sampling in MrBayes v.3.2.2 (Ronquist *et al.* 2012) was used to determine the posterior probabilities (PP). Four simultaneous Markov chains were run for 1 500 000 generations, and trees were sampled every 1 000th generation. Phylograms were visualized in FigTree v. 1.4.2 (Rambaut 2014). Almost similar topology was obtained for ML and PP trees therefore, only ML tree topology was used for subsequent analysis. Bootstrap values (BS) ≥ 70% and PP ≥ 0.70 were considered as supported and given as branch labels as BS/PP (Fig. 1). The newly generated sequences are presented as violet bold in Fig. 1 and bold in Table 2.

RESULTS

Phylogenetic analysis

The combined dataset included four loci, ITS, LSU, SSU, and TEF1, from 77 isolates of *Periconia* with *Morosphaeria velatispora* (KH 221) and *M. ramunculicola* (KH 220) were used as the outgroup taxon (Table 2). The concatenated alignment comprises 4061 characters (ITS: 1-440; LSU: 441-1728; SSU: 1729-3139; TEF: 3140-4061), including gaps, consisting of 1389 distinct patterns, 804 parsimony-

TABLE 2. — Fungal species used for phylogenetic analyses of *Periconia* Tode including their species names, strains, GenBank accession numbers of the SSU, ITS, LSU and TEF-1α regions. The newly generated sequences for this study are shown in bold. Symbol **–** represents data unavailability while letter "**T**" along with the species name stands for "**type specimen**".

Species	Strain	SSU	ITS	LSU	TEF-1α
Flavomyces fulophazae D.G.Knapp, Kovács, Groenewald & Crous	CBS 135664	KP184081	KP184000	KP184039	–
Flavomyces fulophazae T	CBS 135761	NG_061191	NR_137960	NG_058131	–
Lentithecium aquaticum Ying Zhang, J.Fourn. & K.D.Hyde T	CBS 123099	NG_016507	NR_160229	NG_064211	GU349068
Lentithecium clioninum (Kaz.Tanaka, Sat.Hatak. & Y.Harada) Kaz.Tanaka & K.Hiray. T	KT 1149A	AB797250	LC014566	AB807540	AB808515
Lentithecium clioninum	KT 1220	AB797251	LC014567	AB807541	AB808516
Massarina cisti S.K.Bose T	CBS 266.62	AB797249	–	AB807539	AB808514
Massarina eburnean (Tul. & C.Tul.) Sacc.	CBS 473.64	GU296170	–	GU301840	GU349040
Morosphaeria ramunculicola (K.D.Hyde) Suetrong, Sakay., E.B.G.Jones & C.L.Schoch	KH 220	AB797264	–	AB807554	AB808530
Morosphaeria velatispora (K.D.Hyde & Borse) Suetrong, Sakay., E.B.G.Jones & C.L.Schoch	KH 221	AB797266	LC014572	AB807556	AB808532
Periconia alishanica Tennakoon, C.H.Kuo & K.D.Hyde	KUMCC 19-0174	–	MW063167	MW063231	MW183792
Periconia alishanica T	MFLUCC 19-0145	–	MW063165	MW063229	MW183790
Periconia ananasi X.G.Tian & Tibpromma T	MFLUCC 21-0155	OL606142	OL753685	OL606153	OL912946
Periconia ananasi	KUMCC 21-0470	OL979226	OM102539	OL985955	OM007977
Periconia aquatica Z.L.Luo, Hong Y.Su & K.D.Hyde T	MFLUCC 16-0912	–	KY794701	KY794705	KY814760
Periconia artemisiae E.F.Yang, H.B.Jiang & Phookamsak T	KUMCC 20-0265	MW448658	MW448657	MW448571	MW460898
Periconia banksiae (Crous, R.G.Shivas & McTaggart) H.B.Jiang, Bhat & Phookamsak T	CBS 129526	–	–	NG_064279	–
Periconia byssoides Pers.	KUMCC 20-0264	MW444856	MW444854	MW444855	MW460895
Periconia byssoides	MFLUCC 17-2292	MK347858	MK347751	MK347968	MK360069
Periconia byssoides	MFLUCC 18-1548	MK347902	MK347794	MK348013	MK360070
Periconia byssoides	MFLUCC 18-1553	MK347914	MK347806	MK348025	MK360068
Periconia byssoides T	MFLUCC 20-0172	–	MW063162	MW063226	–
Periconia byssoides	NCYUCC 19-0314	–	MW063163	MW063227	–
Periconia caespitosa Cantillo, Gusmão & Madrid T	LAMIC 110 16	–	MH051906	MH051907	–
Periconia chengduensis Tode T	CGMCC 3.23930	OP956056	OP955987	OP956012	OP961453
Periconia chengduensis	UESTCC 22.0140	OP956046	OP955977	OP956002	OP961443
Periconia chengduensis	UESTCC 22.0142	OP956047	OP955978	OP956003	OP961444
Periconia chimonanthi E.F.Yang, H.B.Jiang & Phookamsak T	KUMCC 20-0266	MW448656	NR_176752	MW448572	MW460897
Periconia chimonanthi	UESTCC 22.0133	OP956033	OP955964	OP955989	OP961430
Periconia citlaltepetlensis Calvillo, Cobos-Villagrán & Raymundo T	IOM 325319	–	MH890645	MT625978	–
Periconia citlaltepetlensis	IOM 325319.2	–	MT649221	MT649216	–
Periconia cookie Tode	MFLUCC 17-1399	–	MG333490	MG333493	MG438279
Periconia cookie	MFLUCC 17-1679	–	–	MG333492	MG438278
Periconia cortaderiae Thambug. & K.D.Hyde	MFLUCC 15-0451	KX986346	KX965734	KX954403	KY429208
Periconia cortaderiae T	MFLUCC 15-0457	KX986345	KX965732	KX954401	KY310703
Periconia cynodontis Tode T	CGMCC 3.23927	OP909920	OP909925	OP909921	OP961434
Periconia cyperacearum Crous T	CPC 32138	–	NR_160357	NG_064549	–
Periconia delonicis Jayasiri, E.B.G.Jones & K.D.Hyde T	MFLUCC 17-2584	NG_065770	–	NG_068611	MK360071
Periconia didymosporum (D.Q.Dai & K.D.Hyde) D.Q.Dai & Phookamsak T	MFLU 15-0058	KP761738	KP761734	KP761731	KP761728
Periconia digitate (Cooke) Sacc.	CBS 510.77	AB797271	LC014584	AB807561	AB808537
Periconia elaeidis T.Sunpapao & K.D.Hyde T	MFLUCC 17-0087	MH108551	MG742713	MH108552	–
Periconia endophytica Tode T	ZHKUCC 23-0995	PP277722	OR995582	OR995588	PP025968
Periconia endophytica	ZHKUCC 23-0996	PP277723	OR995583	OR995589	PP025969
Periconia epilithographicola Coronado-Ruiz, Avendaño, Escudero-Leyva, Conejo-Barboza, P.Chaverri & Chavarría T	CBS 144017	–	NR_157477	–	–
Periconia epilithographicola Coronado-Ruiz, Avendaño, Escudero-Leyva, Conejo-Barboza, P.Chaverri & Chavarría	MFLUCC 21-0153	OL606144	OL753687	OL606155	OL912948
Periconia festucae TodeT	CGMCC 3.23929	OP956042	OP955973	OP955998	OP961439
Periconia philadelphiana Tode T	CPC 42854	–	OQ628486	OQ629068	–
Periconia homothallica Kaz.Tanaka & K.Hiray. T	KT 916	AB797275	AB809645	AB807565	–
Periconia igniaria E.W.Mason & M.B.Ellis	CBS 845.96	AB797277	LC014586	AB807567	AB808543
Periconia imperatae Tode T	CGMCC 3.23931	OP956053	OP955984	OP956009	OP961450
Periconia imperatae	UESTCC 22.0145	OP956048	OP955979	OP956004	OP961445
Periconia imperatae	UESTCC 22.0146	OP956052	OP955983	OP956008	OP961449
Periconia macrospinosa Lefebvre & Aar.G.Johnson	CBS 135663	KP184080	KP183999	KP184038	–
Periconia minutissima Corda	MFLUCC 15-0245	–	KY794703	KY794707	–
Periconia minutissima	MUT 2887	–	MG813227	–	–

TABLE 1. — Continuation.

Species	Strain	SSU	ITS	LSU	TEF-1α
Periconia neobrittanica Crous T	CPC 37903	–	NR_166344	NG_068342	–
Periconia neominutissima Tode T	CPC 42368	–	OQ628478	OQ629060	–
***Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. T**	**KUNCC25-19211**	**PV088447**	**PV088432**	**PV088436**	**PV164601**
***Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov.**	**KUNCC25-19212**	**PV088448**	**PV088433**	**PV088446**	–
Periconia palmicola J.F.Li & Phookamsak T	MFLUCC 14-0400	MN648319	–	NG_068917	MN821070
Periconia penniseti Tode T	CGMCC 3.23928	OP956040	OP955971	OP955996	OP961437
Periconia prolifica Anastasiou	DBOF74	–	JQ724435	–	–
Periconia prolifica	DBOF129	–	JQ724490	–	–
Periconia pseudobyssoides Markovsk. & A.Kačergius	DUCC 0850	–	MG333491	MG333494	MG438280
Periconia pseudobyssoides	KUMCC 20-0263	MW444853	MW444851	MW444852	MW460894
Periconia pseudodigitata Kaz.Tanaka & K.Hiray.	KT 644	AB797272	LC014589	AB807562	AB808538
Periconia pseudodigitata T	KT 1395	NG_064850	NR_153490	NG_059396	AB808540
Periconia spodiopogonis Tode	CGMCC 3.23932	OP956032	OP955963	OP955988	OP961429
Periconia submersa Z.L.Luo, Hong Y.Su & K.D.Hyde T	MFLUCC 16-1098	–	KY794702	KY794706	KY814761
Periconia thailandica N.G.Liu, K.D.Hyde & Hongsanan T	MFLUCC 17-0065	KY753889	KY753887	KY753888	–
Periconia thysanolaenae E.F.Yang, H.B.Jiang & Phookamsak T	KUMCC 20-0262	MW448659	MW442967	MW444850	MW460896
Periconia variicolor S.A.Cantrell, Hanlin & E.Silva T	SACCR-64	–	DQ336713	–	–
Periconia verrucosa Phukhams., Ertz, Gerstmans & K.D.Hyde T	MFLUCC 17-2158	MT226686	MT310617	MT214572	MT394631
Periconia verrucosa	UESTCC 22.0149	OP956045	OP955976	OP956001	OP961442
Periconia verrucosa	UESTCC 22.0150	OP956049	OP955980	OP956005	OP961446
Periconia wurfbainiae Tode T	ZHKUCC 23-0999	PP277726	OR995586	OR995592	PP025972
Periconia wurfbainiae	ZHKUCC 23-1000	PP277727	OR995587	OR995593	PP025973
Periconia yangjiangensis Tode T	ZHKUCC 23-0997	PP277724	OR995584	OR995590	PP025970
Periconia yangjiangensis	ZHKUCC 23-0998	PP277725	OR995585	OR995591	PP025971
Sporidesmium tengii W.P.Wu	HKUCC 10837	–	–	DQ408559	–

informative, 330 singleton sites, and 3186 constant sites. The RAxML analysis of the combined dataset yielded the best scoring tree (Fig. 1) with a final ML optimization likelihood value of *InL*= –19548.436506. The best-fit evolution models were GTR+I+G for the ITS, LSU, SSU, and TEF1. *Periconia neroscureioniae* (KUNCC 25-19211 and KUNCC 25-19212) forms a monophyletic lineage with strong support values (96% BS/1.00 PP), positioned as a distinct branch within *Periconia*. It diverges from a moderately supported sister clade (72% BS/0.86 PP) comprising *P. byssoides* Pers., *P. thailandica* N.G. Liu, K.D. Hyde & Hongsanan, *P. artemisiae* E.F. Yang, H.B. Jiang & Phookamsak, *P. pseudobyssoides* Markovsk. & A. Kačergius, and *P. alishanica* Tennakoon, C.H. Kuo & K.D.Hyde. The phylogenetic separation of *P. neroscureioniae* from this cluster of closely related taxa, along with its unique morphological features, justifies its recognition as a novel species within the genus *Periconia*.

TAXONOMY

Family PERICONIACEAE (Sacc.) Nann.
Genus *Periconia* Tode

Periconia neroscuroinea M.B. Khan & T.C. Wen, sp. nov. (Fig. 2)

TYPE MATERIAL. — **China** • Yunnan Province, Baoshan City, Gaoligong Mountains; 24.X.2024; *Muhammad Binyamin Khan leg.*; holotype: KUNCC25-19211; GenBank: PV088432-ITS, PV088436-LSU, PV088447-SSU, PV164601-TEF-1α • same data; paratype: KUNCC25-19212; GenBank: PV088433-ITS, PV088446-LSU, PV088448-SSU.

DIAGNOSIS. — *Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. is characterized by solitary, globose, brown to dark brown, verruculose, aseptate conidia (6.5-8.7 µm diam.), and long, curved, unbranched, smooth-walled conidiophores (350-900 × 7-19 µm) with echinulate to verrucose, polyblastic, globose to subglobose conidiogenous cells. Colonies are black, hairy, and effuse on dead leaves of *Ligustrum lucidum*.

ETYMOLOGY. — From Latin, "*nero*" meaning black "*scuroinea*" meaning dark color referring to the distinct black dark colonies on natural substrate.

DISTRIBUTION. — This species is described here for the first time and is so far known only from its type locality in China: Yunnan Province, Baoshan City, Gaoligong Mountains.

SUBSTRATE. — Found on dead leaves of *Ligustrum lucidum*.

MYCOBANK NUMBER. — MB859157.

DESCRIPTION

Saprobic on dead leaves of *Ligustrum lucidum*. Asexual morph: Colonies on natural substrate superficial, effuse, surface, conspicuous, black dark, hairy, surface. Mycelium mostly immersed, septate, smooth, brown, hyaline hyphae 1-2 µm wide. Conidiophores 350-900 µm long × 7-19 µm wide (= 625 × 13 µm, n = 20). Macronematous, mononematous, erect, mostly curved, solitary, broader at the base, unbranched, septate, dark brown to light brown, smooth-walled, 29-66 µm

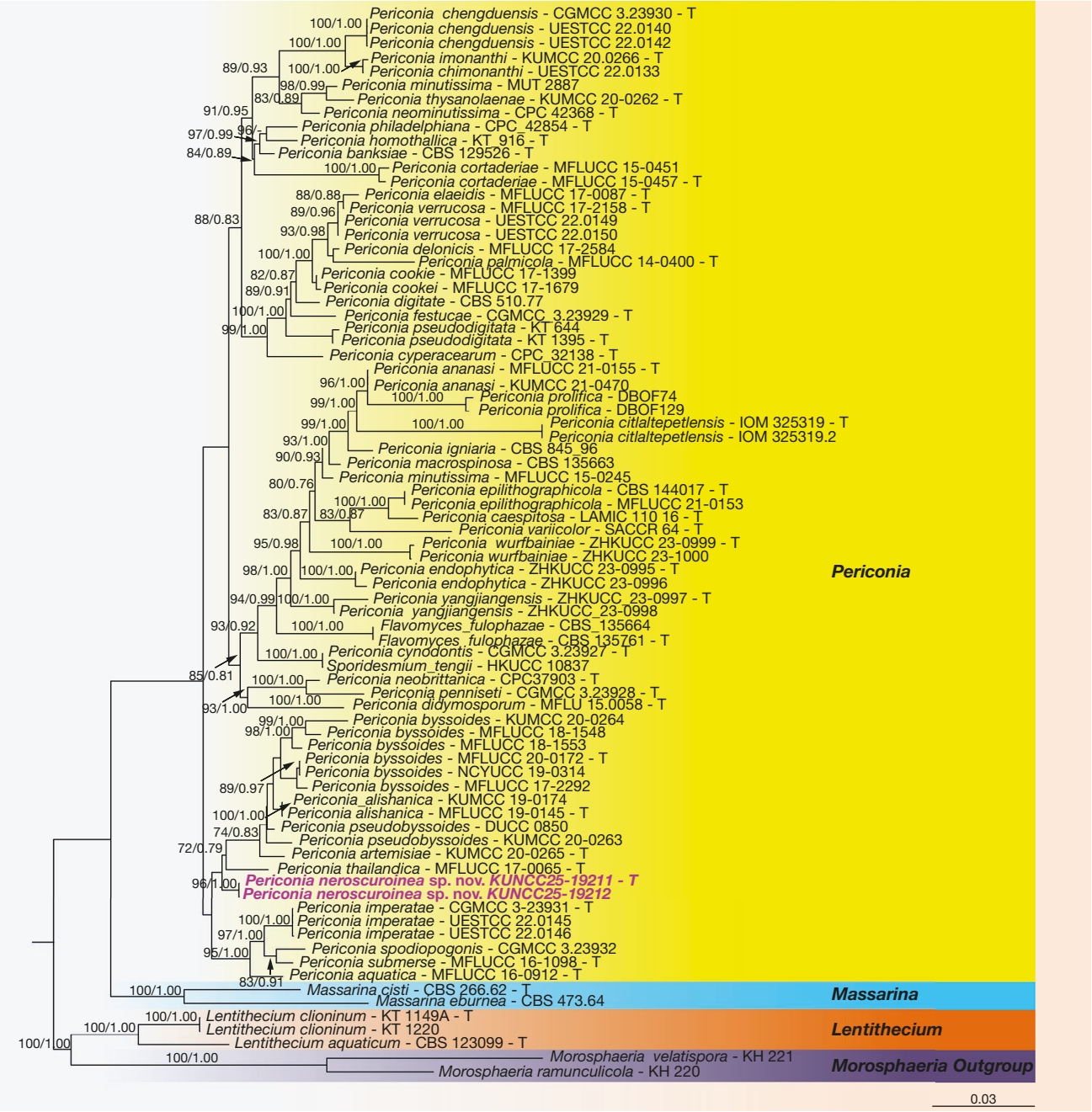

FIG. 1. — Maximum Likelihood and Posterior Probability tree constructed using a combined LSU SSU, ITS and TEF1-α dataset. The *Morosphaeria velatispora* (K.D. Hyde & Borse) Suetrong, Sakay., E.B.G. Jones & C.L. Schoch (KH 221) and *M. ramunculicola* (K.D. Hyde) Suetrong, Sakay., E.B.G. Jones & C.L. Schoch (KH 220) rooted the tree. Bootstrap/Posterior probability values are presented as branch labels. The new species is indicated in **violet bold**. "**T**" denotes the sequences from type specimen.

diam. (= 47.5 µm, n = 10) spherical heads at apex. Conidiogenous cells 10-30 × 5-15 µm (= 20 × 10 µm, n = 20), polyblastic, globose to subglobose, terminal, proliferous, pale brown to brown, echinulate or verrucose, rough. Conidia 6.5-8.7 µm diam. (= 7.6 µm, n = 20) solitary, globose, brown to dark brown, aseptate, distinctly verruculose.

CULTURE CHARACTERS

Conidia germinated on water agar within 24 hours, typically producing one or two germ tubes on either side. On potato dextrose agar (PDA), colonies reached approximately 6 cm in diameter after 5 days, exhibiting sparse, white, superficial mycelium. The reverse side of the colony appeared dark at the center with a white, spinous (spiky) margin.

DISCUSSION

Periconia has a remarkable intercontinental distribution in diverse geographical regions from temperate zones to the

Fig. 2. — *Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov.: **A**, infected leaf of *Ligustrum lucidum* W.T. Aiton; **B**, **C**, colonies on the *Ligustrum lucidum* leaf; **D**, **E**, conidiophores; **F**, **G**, conidiogenous cells and conidia; **H**, conidia; **I**, **J**, colonies in culture media. Scale bars: A-C, 1mm; D-H, 20 um.

tropics. Its broad ecological adaptability enables it to inhabit a wide range of habitats, making it a globally widespread genus (Goga 2000; Teles *et al.* 2006; Tanaka *et al.* 2015; Dubey 2017; Crous *et al.* 2018; Phookamsak *et al.* 2019; Calvillo-Medina *et al.* 2020; Gunasekaran *et al.* 2021; Liao *et al.* 2024; Tian *et al.* 2024). In the phylogenetic analysis based on a combined dataset of four loci (LSU, SSU, ITS and TEF-1α), *P. neroscureioniae* forms a strongly supported monophyletic lineage (96% BS/1.00 PP), positioned as a distinct branch within *Periconia*. It diverges from a moderately supported sister clade (72% BS/0.86 PP) comprising *P. byssoides, P. thailandica*, *P. artemisiae*, *P. pseudobyssoides*, and *P. alishanica*. This clustering confirms the affinity of *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. within a distinct and well-resolved lineage of *Periconia*. *Periconia neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. is morphologically distinct from other species *Periconia* by its dark, hairy surface on the natural substrate and relatively large conidiophores. It shares conidial color (brown to dark brown) with *P. imperatae* but differs in conidiophore and conidial dimensions (Su *et al.* 2023). While it also resembles *P. artemisiae* in substrate affinity, it can be readily separated based on its larger conidiophores and conidia (Yang *et al.* 2022).

Tennakoon *et al.* (2021) described *P. alishanica* with smaller conidiophores (290-400 × 4-5 µm) and conidia (10-12 µm), which are significantly different from those of *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. *P. thailandica*, found on dead bamboo culms, is similar in general morphology and size but differs in having lighter-colored conidia (Liu *et al.* 2017b). Furthermore, *P. pseudobyssoides* can be distinguished from *P. neroscuroinea* M.B. Khan & T.C. Wen, sp. nov. based on the shape and size of its conidiophores and conidia, as well as conidial coloration (Markovskaja & Kačergius 2014).

Data availability

All newly generated sequences included in this study were deposited in GenBank. Specimens of this study were deposited in the herbarium of Cryptogams Kunming Institute of Botany Academia Sinica (HKAS), Kunming, China, and cultures are deposited in the Kunming Institute of Botany Culture Collection China.

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