

A new endophytic species and a new host record of *Periconia* (Periconiaceae, Pleosporales) from Brazilian biomes

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Article info

Received: 2 Jun. 2026
Revision received: 18 Jul. 2026
Accepted: 18 Jul. 2026
Published: 21 Oct. 2026

Associate Editor

Marcin Piątek

Abstract. Species of *Periconia* are cosmopolitan and occur as saprobes, endophytes and plant pathogens on a wide range of hosts. During a survey of endophytic fungi associated with *Brosimum gaudichaudii* (Moraceae) in the Brazilian Cerrado and *Mimosa tenuiflora* (Fabaceae) in the Caatinga, four isolates with morphological features typical of *Periconia* were obtained. Morphological observations and phylogenetic analyses based on ITS, LSU, and *tef1-α* sequence data showed that two isolates represent a new species, described here as *Periconia cerradoensis*, while two other isolates are identified as *P. igniaria*. *Periconia cerradoensis* is phylogenetically close to *P. dicranopteridis*, but differs by producing well-developed conidiophores and smaller conidia. The *P. igniaria* isolates represent a new endophytic record from *M. tenuiflora* in Brazil. Our findings expand current knowledge of *Periconia* in South America and highlight the importance of investigating endophytic fungi in underexplored Brazilian biomes.

Key words: Caatinga, Cerrado, fungal endophytes, phylogeny, taxonomy

Introduction

The genus *Periconia* was first described by Tode (1791), with *Periconia lichenoides* designated as the type species. Currently, the genus is classified in the family Periconiaceae (Pleosporales, Dothideomycetes), although its taxonomic placement has undergone several revisions over time (Hyde et al. 2013; Hongsanan et al. 2020). Initially assigned to Periconiaceae (Nannizzi 1934), *Periconia* was later treated as incertae sedis due to the absence of molecular data for the generic type, with its placement

in Dothideomycetes mainly supported by morphological similarities between *P. lichenoides* and species of *Periconia* s.str., such as *Periconia byssoides*, *Periconia cookei*, *Periconia igniaria*, and *Periconia digitata* (Markovskaja & Kačergius 2014; Tanaka et al. 2015; Wood 2019; Yang et al. 2022). Subsequently, the genus was transferred to Massarinaceae after phylogenetic analyses demonstrated that *Periconia* formed a distinct, but closely related, clade to this family (Hyde et al. 2013; Phukhamsakda et al. 2016). Periconiaceae was re-established within Pleosporales based on molecular phylogenetic evidence (Tanaka et al. 2015) and later consolidated in global taxonomic frameworks (Wijayawardene et al. 2022), which synthesized the available literature. More recent phylogenetic updates have refined the circumscription of the family, excluding previously included genera, such as *Bambusistroma* and *Noosia*, and restricting Periconiaceae to *Periconia* and *Flavomyces* (Hyde et al. 2024).

Currently, 253 names are listed for *Periconia* in Index Fungorum (2026), while a recent global checklist compiled 349 molecularly confirmed records from 47 countries, highlighting its broad diversity and worldwide distribution (Madagammana et al. 2024). Species of *Periconia* are commonly reported as saprobic and endophytic fungi, and are occasionally associated with plant diseases (Macko et al. 1992; Ale-Agha et al. 2001; Su et al. 2023; Ren et al. 2024). Several species of *Periconia*

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have been reported from dry environments, where they colonize senescent leaves, branches, and tissues exposed to intense solar radiation and water deficit (Moghaddam et al. 2022; Taghian et al. 2026). Similar to other melanized (dematiaceous) fungi, the presence of melanin in the cell wall may confer protection against ultraviolet radiation, desiccation, and oxidative stress (Lopez et al. 2024). In addition, endophytic associations have been reported between *Periconia* and medicinal plants and grasses, with some species gaining attention for their potential to produce bioactive metabolites (Teles et al. 2006; Verma et al. 2011; Su et al. 2023).

In Brazil, studies involving *Periconia* remain scarce, mostly limited to isolated reports and bioprospecting studies. One of the few reports was of *P. atropurpurea* as an endophyte in leaves of *Xylopia aromatica* (Annonaceae), a native Cerrado species, and the report of its production of bioactive compounds (Teles et al. 2006). More recently, *P. belmontensis* Pommer et al. was described from Brazilian oceanic islands, reinforcing that the genus remains poorly explored in the country (Pommer et al. 2025). However, information concerning the diversity and host association of endophytic *Periconia* species in seasonally dry tropical biomes such as the Cerrado and Caatinga remains extremely limited. These biomes are characterized by marked seasonality, high solar radiation, elevated temperatures, and seasonal water deficit, conditions that strongly influence fungal diversity and may harbor specialized or still-undocumented endophytic communities (Ribeiro & Walter 2008; Higgins et al. 2014; Queiroz et al. 2017).

Brosimum gaudichaudii (Moraceae) and *Mimosa tenuiflora* (Fabaceae) are medicinal woody species widely distributed across the Cerrado and Caatinga, respectively, and both are exposed to marked seasonal water stress (Faria et al. 2015; Dias et al. 2021). In addition, these hosts produce diverse secondary metabolites, including phenolic compounds and flavonoids, which may act as selective factors shaping their associated fungal communities (Bautista et al. 2011; Leite et al. 2018). Despite the ecological and biotechnological relevance of *Periconia*, little is known about its diversity, host association, and occurrence as endophytes in Brazilian seasonally dry ecosystems. Therefore, the aim of this study was to describe a new species of *Periconia* based on morphological and multilocus phylogenetic evidence, and to report its occurrence in *B. gaudichaudii* and *M. tenuiflora* in the Brazilian Cerrado and Caatinga biomes, respectively.

Materials and methods

Endophytic isolates

Branches of *B. gaudichaudii* were collected during the rainy season (April 2022) in a Cerrado area at the School of Agronomy, Samambaia Campus, Universidade Federal de Goiás (UFG, Goiânia, Goiás, Brazil; 16°35'58"S, 49°16'45"W; ~730 m a.s.l.). The region has a tropical savanna climate characterized by hot and humid conditions during the rainy season (Alvares et al. 2013).

Sampling was conducted in the didactic garden (arbo-retum) of the School of Agronomy, where various crop species (e.g., Costa e Silva et al. 2007; Souza et al. 2008) coexist with remnants of native Cerrado. Samples from branches of *M. tenuiflora* were collected during the dry season (April 2013) at the Tamanduá Farm, a private reserve (RPPN) located in Santa Teresinha, Paraíba, Brazil (7°02'20"S, 37°26'43"W; ~340 m a.s.l.). The Tamanduá Farm is located in the semi-arid Caatinga biome – a region characterized by hot and dry climatic conditions – where it preserves native, seasonally dry tropical vegetation and xerophytic plant communities, alongside organic and biodynamic agricultural practices (Guedes et al. 2020) (Fig. 1).

Plant collection was authorized by the Ministério do Meio Ambiente (MMA)/Instituto Chico Mendes de Conservação da Biodiversidade (ICMBio) (SISBIO 40331-1) and the study was registered in the Sistema Nacional de Gestão do Patrimônio Genético (SisGen)/MMA/ Conselho de Gestão do Patrimônio Genético (CGen) (SisGen ACD07BF). Endophytic fungi were isolated from surface-sterilized branches as described by Araújo et al. (2002) and Bezerra et al. (2015). Briefly, plant tissues were sequentially immersed in 70% ethanol (60 s), 2–2.5% sodium hypochlorite (180 s), and 70% ethanol (30 s), followed by three rinses in sterile distilled water. Surface-sterilized branch fragments were plated on Potato Dextrose Agar (PDA) supplemented with chloramphenicol (100 mg/L) and incubated at $28 \pm 2^\circ\text{C}$ under a 12 h light/dark cycle for up to 15 days. A total of 567 branch fragments were analyzed for *B. gaudichaudii*, while 180 fragments were evaluated for *M. tenuiflora*, emerging fungal colonies were purified on PDA and maintained for further identification. Sterilization efficiency was verified by plating 1 mL of the final rinse water onto PDA under the same incubation conditions.

Ex-type cultures are deposited in the URM Culture Collection (URM, Micoteca URM Profa. Maria Auxiliadora Cavalcanti, Recife, Brazil), and the holotype (permanent slide preparation) is deposited in the Herbarium of the Universidade Federal de Goiás (Herbário UFG, Goiânia, Brazil). In addition, all endophytic isolates are deposited in the working collection of the Laboratório de Micologia Ambiental at Universidade Federal de Pernambuco (UFPE) and in the FCCUFG working collection, housed at the Laboratório de Micologia (LabMicol), Instituto de Patologia Tropical e Saúde Pública (IPTSP), UFG.

DNA extraction, PCR amplification, and sequencing

Genomic DNA was extracted from mycelium scraped from 7-day-old cultures grown on PDA using the Wizard® Genomic DNA Purification Kit (Promega Corporation), following the manufacturer's instructions. PCR amplifications were performed for the internal transcribed spacer (ITS) regions, the partial large subunit (LSU, 28S rDNA), and translation elongation factor 1- α (*tef1- α*) using the following primers: ITS5/ITS4 for ITS (White et al. 1990), LR0R/LR5 for LSU (Vilgalys & Hester 1990; Rehner & Samuels 1994), and TEF1-983F/TEF1-2218R for

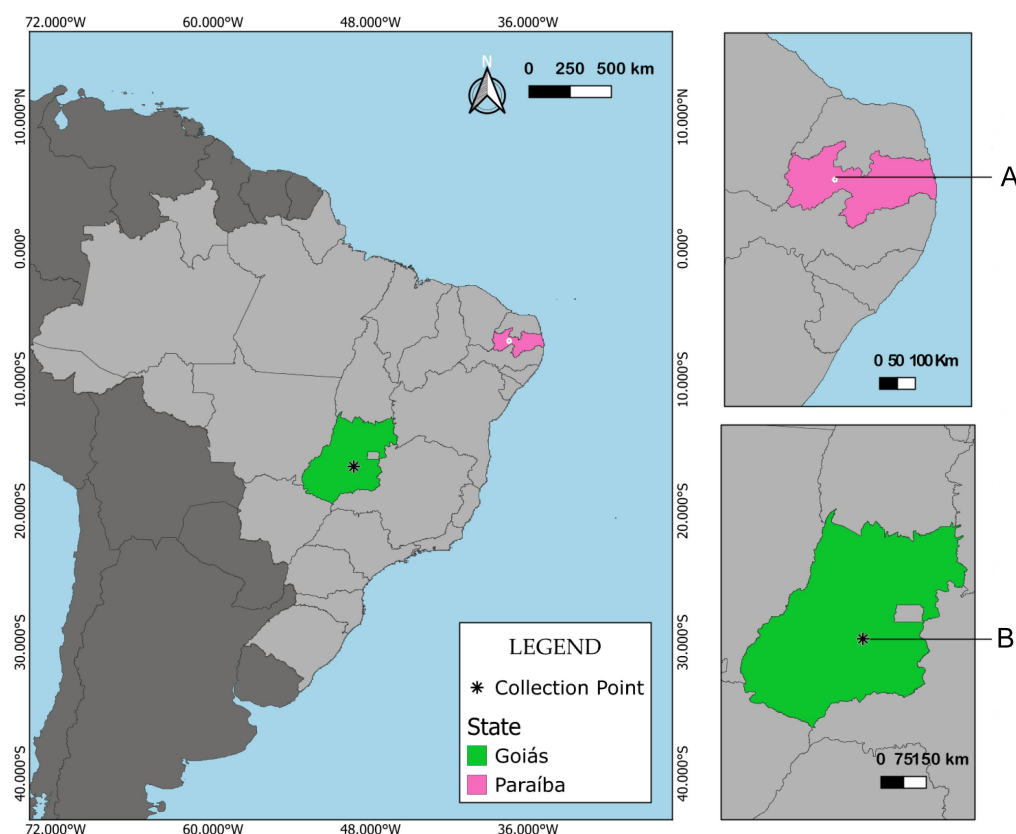


Figure 1. Geographic location of plant sampling sites in Brazil for the isolation of endophytic *Periconia* species, showing areas in the Caatinga and Cerrado domains. A – Farm Tamanduá, a private conservation area (RPPN), Santa Teresinha, Caatinga area; B – Arboretum of the School of Agronomy, Samambaia Campus, Universidade Federal de Goiás, Goiânia municipality, Cerrado area.

tefl-α (Carbone & Kohn 1999). Amplification, sequencing, and sequence editing were performed as described by Ferro et al. (2024). The sequences obtained in this study were deposited in GenBank (Table 1).

Phylogenetic analyses

Phylogenetic analyses were initially performed using our ITS sequences and reference sequences of all species accepted in *Periconia* with available DNA sequences (81 species) and the outgroup (Table 1) following recent publications (e.g., Zhang et al. 2026). Sequences were aligned using the MAFFT v. 7 online interface (Katoh & Standley 2013) and manually edited using MEGA v. 7 (Kumar et al. 2016). Subsequently, we performed a maximum-likelihood (ML) analysis for each gene (ITS, LSU, and *tefl-α*) with the most closely related species (28 species) and the outgroup. We thereafter combined the data using Mesquite v3.61 software (Maddison & Maddison 2009).

The ML analysis was performed using IQ-TREE v. 1.6.12 and involved 5,000 replicates, and the ultrafast bootstrap (UFboot2) method was used to calculate branch support (Hoang et al. 2018). The ModelFinder software, included in IQ-TREE v. 1.6.12 (Kalyaanamoorthy et al. 2017), was used to determine the partitioning strategy and models based on the Akaike information criterion. The combined dataset was also analysed using Bayesian inference (BI) with MrBayes v. 3.2.7a (Ronquist et al. 2012) on the CIPRES Science Gateway, employing the same

models and partitions as in the ML analysis (IQ-TREE). The BI analysis was conducted using 50 M generations and a 25% burn-in, with chains sampled every 1,000 generations. The resulting phylogenetic trees were visualized using FigTree v. 1.4.4 (Rambaut 2012). Values ≥ 0.95 BI posterior probability (BPP) and bootstrap support (BS) from IQ-TREE UFboot2-BS analysis ($BS \geq 70\%$) were plotted near the nodes.

Pairwise homoplasy index

The pairwise homoplasy index (PHI) test was performed using the SplitsTree App (Huson & Bryant 2024), following phylogenetic tree analyses under the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) concept (Taylor et al. 2000), to assess recombination among phylogenetically related species and to complement the analysis of taxonomic novelties. To verify this index, the combined dataset of the three loci (ITS, LSU, and *tefl-α*) was used. The p -value > 0.05 ($p > 0.05$) was interpreted as indicating no significant evidence of recombination. The phylogenetic networks were constructed using the uncorrected p -distance transformation on the distance matrix (Nei & Kumar 2000) and the Neighbor-Net algorithm (Bryant & Huson 2023), implemented in the SplitsTree App (Huson & Bryant 2024). The resulting phylogenetic networks were edited in Adobe Illustrator CS2 v. 12.0.0 (Adobe, USA).

Table 1. GenBank accession numbers for *Periconia* species sequences used in the phylogenetic analyses. All sequences corresponding to currently accepted *Periconia* species available up to May 2026 were included. Isolates and sequences obtained in this study are given in bold. Ex-type strains are marked with (T). Species included in the phylogenetic analyses focused on the clade related to our sequences are marked with (#).

Organism culture	Strain	GenBank accession numbers		
		ITS	LSU	<i>tefl-a</i>
<i>Periconia algeriana</i> #	CBS 321.79	MH861212	MH872979	–
<i>Periconia alishanica</i>	KUMCC 19-0174 = NCYU19-0347	MW063167	MW063231	MW183792
	MFLUCC 19-0145	MW063165	MW063229	MW183790
<i>Periconia ananasi</i> #	MFLUCC 21-0155 ^T	OL753685	OL606153	OL912946
	KUMCC 21-0470	OM102539	OL985955	OM007977
<i>Periconia aquatica</i>	MFLUCC 16-0912 ^T	KY794701	KY794705	KY814760
<i>Periconia areacearum</i>	MFLU 19-0803 = SNT19A ^T	PP592462	PP621090	PP828795
<i>Periconia artemisiae</i>	KUMCC 20-0265 ^T	MW448657	MW448571	MW460898
<i>Periconia atropurpurea</i> #	CBS 381.55	MH857524	MH869061	–
<i>Periconia bambusicola</i>	ZHKUCC 24-1141	PQ276762	PQ276767	–
<i>Periconia baotuenensis</i> #	GMBCC 1980 ^T	PX314711	PX314709	PX310458
<i>Periconia banksiae</i>	CBS 129526 = CPC 17282 ^T	JF951147	NG_064279	–
<i>Periconia belmontensis</i> #	ASPSP3 = VP-2025a ^T	PQ248713	PX600748	PX640513
<i>Periconia byssoides</i>	MFLUCC 17-2292 = KUMCC 18-0272 = C292	MK347751	MK347968	MK360069
	MFLUCC 18-1553 = C457	MK347806	MK348025	MK360068
<i>Periconia caespitosa</i> #	LAMIC 110/16 ^T	MH051906	MH051907	–
<i>Periconia calamagrostidicola</i>	CBS H-25342 = CPC:46238 ^T	PP791432	PP791460	PP780620
<i>Periconia catenata</i> #	GDMCC 3.1041 ^T	PP106201	PP106225	PP112539
<i>Periconia cerradoensis</i> #	URM 9009 = FCCUFG 148 ^T	PV361763	PV364434	PZ324814
	FCCUFG 190	PV361764	PV364435	PZ324815
<i>Periconia chengduensis</i>	CGMCC 3.23930 = UESTCC 22.0126 = W31_1 ^T	OP955987	OP956012	OP961453
	UESTCC 22.0140 = Sarah57	OP955977	OP956002	OP961443
<i>Periconia Chiangraiensis</i> #	KUMCC 21-0471	OM102540	OL985956	OM007978
<i>Periconia chimonanthe</i>	KUMCC 20-0266 ^T	NR_176752	MW448572	MW460897
	UESTCC 22.0133 = LU2_2	OP955964	OP955989	OP961430
<i>Periconia circinata</i> #	CBS 263.37	MW810265	MH867413	MW735660
<i>Periconia citlaltepetlensis</i> #	ENCB 140251 = IOM 325319.1 ^T	MH890645	MT625978	–
	IOM 325319.2	MT649221	MT649216	–
<i>Periconia cookei</i>	MFLUCC 17-1399	MG333490	MG333493	MG438279
<i>Periconia cortaderiae</i>	MFLUCC 15-0451 = MFLU : 16-2579 ^T	KX965734	KX954403	KY429208
	MFLUCC 15-0457 = ICMP 21414 ^T	KX965732	KX954401	KY310703
<i>Periconia cynodontis</i>	CGMCC 3.23927 = UESTCC 22.0127 = LU4 ^T	OP909925	OP909921	OP961434
<i>Periconia cyperacearum</i>	CPC 32138 = CBS 144434 ^T	MH327815	MH327851	–
<i>Periconia delonicis</i>	MFLU 23-0180	OR438355	OR438826	OR500317
<i>Periconia dicranopteridis</i> #	KUN-HKAS129916 = 364-3 ^T	PV138731	PV138587	PV177119
<i>Periconia didymosporum</i>	MFLU 15-0058 = DQD-2015a ^T	KP761734	KP761731	KP761728
<i>Periconia digitata</i>	CBS 510.77 = EF54a	LC014584	AB807561	AB808537
<i>Periconia dujuanhuensis</i>	HKAS 131781 = KUNCC 23-13482 ^T	PQ340469	PP189907	PQ456957
<i>Periconia elaeidis</i>	MFLUCC 17-0087 ^T	MG742713	MH108552	–
<i>Periconia endophytica</i> #	MHZU 23-0245 ^T (ZHKUCC 23-0995) ^T	OR995582	OR995588	PP025968
	ZHKUCC 23-0996	OR995583	OR995589	PP025969
<i>Periconia epilithographicola</i> #	CBS 144017 ^T	NR_157477	–	–
	MFLUCC 21-0153	OL753687	OL606155	OL912948
<i>Periconia festucae</i>	CGMCC 3.23929 = UESTCC 22.0128 = LU7 ^T	OP955973	OP955998	OP961439
<i>Periconia floridana</i>	CPC 45904	PP791420	PP791448	–
<i>Periconia fueloephazae</i>	CBS 135761 ^T	NR_137960	NG_058131	–
<i>Periconia genistae</i> #	CBS 322.79	MH861213	MH872980	–
<i>Periconia guangxiense</i> #	GZAAS 25-0735 ^T	PX118886	PX118882	PX522310
<i>Periconia guizhouensis</i>	GZCC 25-0766 ^T	PX654856	PX654859	PX733136
<i>Periconia heveae</i>	MFLUCC 17-0341	OL780490	OL782069	OL875108
<i>Periconia homothallica</i>	CBS 139698 = JCM 13100 = MAFF 239610 = KT916 = HHUF 29105 = EF58a ^T	AB809645	NG_059397	AB808541
<i>Periconia hongheensis</i>	HKAS 131670 = KUNCC 23-13550 ^T	PQ340467	PP189905	PQ456958
<i>Periconia hydei</i>	ZHKUCC 24-2101	PV434171	PV436640	PV588047

Table 1. Continued.

Organism culture	Strain	GenBank accession numbers		
		ITS	LSU	<i>tefl-α</i>
<i>Periconia hydeiguttulosa</i> #	UESTCC 23.0456	PQ394046	PQ184695	PQ346487
<i>Periconia igniaria</i> #	CBS 298.66	MH858798	MH870438	–
	CBS 379.86	–	AB807566	AB808542
	CBS 845.96	–	GU301841	AB808543
	CBS 583.66	MH858888	MH870553	–
	URM 9010 = FCCUFG 196	PZ295689	PZ295993	PZ324816
	FCCUFG 197	PZ295690	PZ295994	PZ324817
<i>Periconia imperatae</i>	CGMCC 3.23931 = UESTCC 22.0129 = W 236 ^T	OP955984	OP956009	OP961450
	UESTCC 22.0145 = W230_1	OP955979	OP956004	OP961445
<i>Periconia kunmingensis</i>	MFLUCC 18-0679 = RPC 15-017 ^T	MH892346	MH892399	MH908963
<i>Periconia lateralis</i> #	CBS 292.36	MH855804	MH867311	–
<i>Periconia linzhiensis</i>	HKAS 144526 ^T	PQ684989	PQ675408	PQ671465
<i>Periconia longibrachiatum</i> #	GDMCC 3.10435 ^T	PP106205	PP106231	PP112543
<i>Periconia macrospinosas</i> #	CBS 135663 = CPC 22898	KP183999	KP184038	–
	YNE00463	PP106195	PP106219	PP112534
<i>Periconia minutissima</i> #	MFLUCC 15-0245	KY794703	KY794707	–
<i>Periconia miscanthusensis</i>	GZCC 25-0767 ^T	PX654857	PX654860	PX733138
<i>Periconia motuoensis</i>	KUNCC 24-17924	PQ373177	PQ438054	PQ661220
<i>Periconia muchuanensis</i>	HKAS 135150 = CGMCC 3.25599 ^T	PQ067868	PQ067698	PQ278553
<i>Periconia neobritannica</i>	CPC 37903 = CBS 146062 ^T	MN562149	MN567656	–
<i>Periconia neohongheensis</i>	ZHKUCC 24-1140	PQ269733	PQ269739	PQ362733
<i>Periconia neomacrospinosas</i> #	GDMCC 3.1042 ^T	PP106192	PP106212	PP112530
<i>Periconia neominutissima</i>	CPC 42368 = CBS 149514 ^T	OQ628478.1	OQ629060.1	OQ627950
<i>Periconia palmicola</i>	MFLUCC14-0400 ^T	–	MN648327	MN821070
<i>Periconia penniseti</i>	CGMCC 3.23928 = UESTCC 22.0130 = LU5 ^T	OP955971	OP955996	OP961437
<i>Periconia philadelphiana</i>	CPC 42854 = CBS 14968 ^T	OQ628486	OQ629068	OQ627953
<i>Periconia poacearum</i>	CGMCC 3.24545 ^T	PV608571	PV607425	PV626454
<i>Periconia prolifica</i>	CBS 209.64 ^T	NR_160097	MH870050	–
<i>Periconia pseudobyssoisoides</i>	DUCC 0850	MG333491	MG333494	MG438280
	H4151 = MAFF 243868 = EF61a	LC014587	AB807568	AB808544
	H 4790 = MAFF 243874 = TS102 = HHUF 28257 = EF53a	LC014588	AB807560	AB808536
<i>Periconia pseudodigitata</i>	CBS 139699 = JCM 13166 = MAFF 239676 = KT 1395 = HHUF 29730 = EF57a ^T	LC014591	AB807564	AB808540
	JCM 13164 = MAFF 239674 = KT644 = EF55a	LC014589	AB807562	AB808538
<i>Periconia sahariana</i> #	CBS 320.79	MH861211	MH872978	–
<i>Periconia salina</i>	GJ374 = MFLU 19-1235 ^T	MN047086	MN017846	–
<i>Periconia shannanensis</i>	HKAS 134943 = TC-2024a	PP968554	PP968557	PQ226772
<i>Periconia sichuanensis</i>	HKAS 135157 = CGMCC 3.25598 ^T	PQ067867	PQ067697	PQ278551
<i>Periconia spodiopogonis</i>	CGMCC 3.23932 = UESTCC 22.0131 = isolate 2021072818 ^T	OP955963	OP955988	OP961429
<i>Periconia submersa</i>	MFLUCC 16-1098 ^T	KY794702	KY794706	KY814761
<i>Periconia thailandica</i>	MFLUCC 17-0065 ^T	KY753887	KY753888	–
<i>Periconia thysanolaenae</i>	KUMCC 20-0262 ^T	MW442967	MW444850	MW460896
<i>Periconia todei</i>	CGMCC 3.24565 ^T	PV608573	PV607427	PV626456
<i>Periconia variicolor</i> #	CBS 120374 = SACCR 64 ^T	DQ336713	–	–
<i>Periconia verrucosa</i>	MFLUCC 17-2158 ^T	MT310617	MT214572	MT394631
	UESTCC 22.0150 = W232_2	OP955980	OP956005	OP961446
<i>Periconia wurfbainiae</i> #	MHZU 23-0247 ^T (ZHKUCC 23-0999) ^T	OR995586	OR995592	PP025972
	ZHKUCC 23-1000	OR995587	OR995593	PP025973
<i>Periconia xishuangbannaensis</i> #	GZAAS 25-0707 ^T	PX118888	PX118884	PX522312
<i>Periconia yangjiangensis</i> #	MHZU 23-0246 ^T (ZHKUCC 23-0997) ^T	OR995584	OR995590	PP025970
	ZHKUCC 23-0998	OR995585	OR995591	PP025971
<i>Periconia yangtingensis</i>	SICAUCC 23-0047 ^T	PP060663	PP057956	PP061142
<i>Periconia yunnanensis</i> #	HKAS 131727 = KUNCC 23-14259 ^T	PQ340468	PP189906	PQ456960
<i>Lentithecium aquaticum</i>	CBS 123099 ^T	MH863276	GU301823	GU349068.1
<i>Lentithecium cloninum</i>	HHUF 28199	NR_154137	NG_059391	AB808515.1

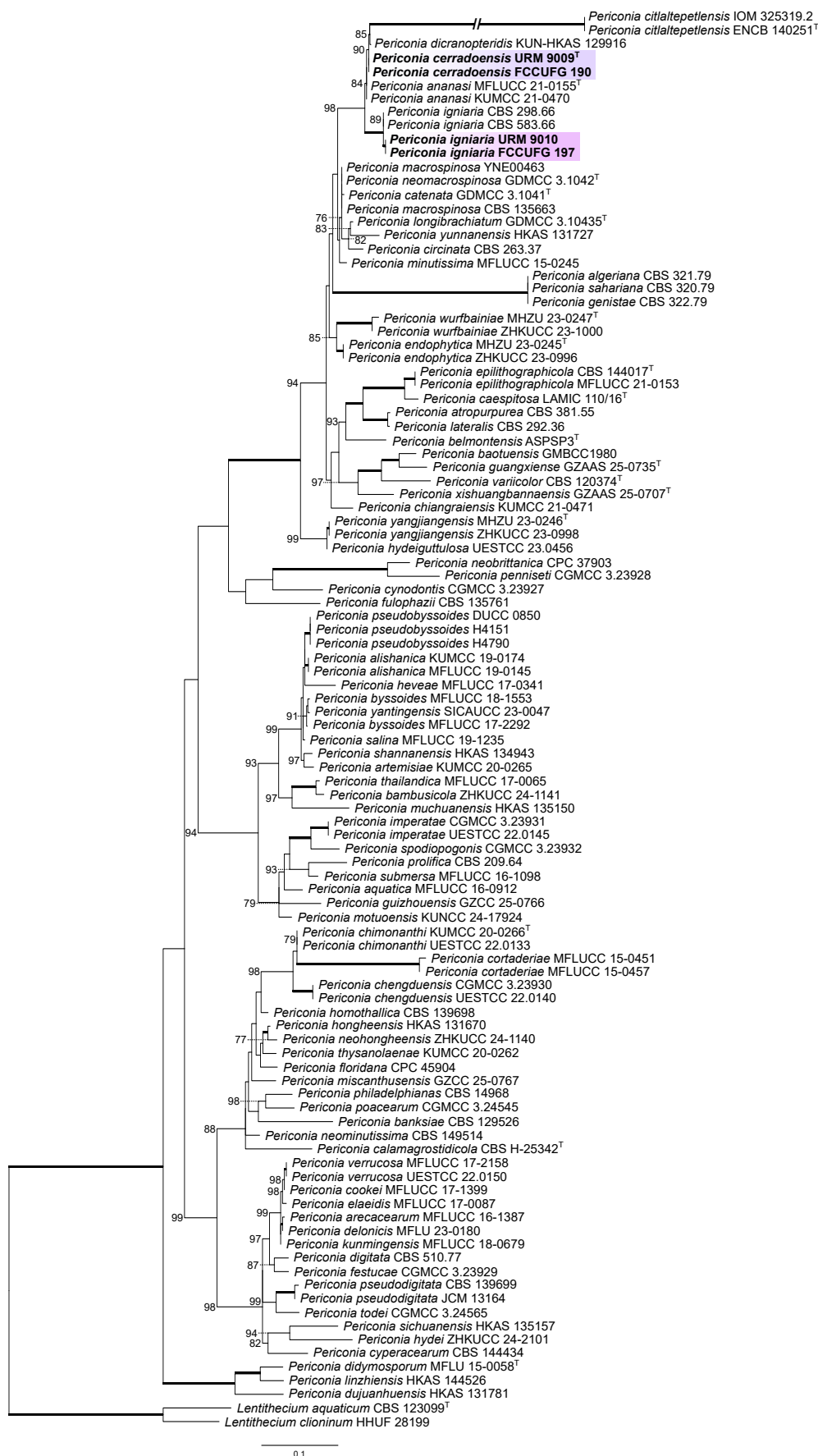


Figure 2. Maximum likelihood phylogenetic tree of *Periconia* species inferred from ITS sequences, including a broad representation of taxa. Bootstrap support values $BS \geq 70\%$ are indicated at the nodes. Thickened branches indicate full statistical support. Isolates obtained in this study are indicated in bold and highlighted in color. Ex-type strains are marked with "T". Long branches were shortened and are indicated by diagonal lines (//). *Lenticitheium aquaticum* (CBS 123099^T) and *L. cloninum* (HHUF 28199) were used as outgroups. Scale bar indicates the number of substitutions per site.

Morphological examination

The isolates were subcultured on potato dextrose agar (PDA) and Malt Extract Agar (MEA) in Petri dishes (90 mm diam.) and incubated for 14 days at 25°C in a 12-hour light/dark cycle to stimulate sporulation. Reproductive structures were mounted in lactic acid (85%), and 30 measurements were obtained for conidia and conidiogenous cells, and at least 10 for conidiophores. Macromorphological characteristics and colony growth were observed and described after 2 weeks of growth at 25°C in the dark. Colony colors (surface and reverse) were analyzed using the color chart of Rayner (1970).

Results

Phylogenetic analyses

We analyzed four *Periconia* isolates based on morphological features, phylogenetic inferences, and the PHI test. Initially, we constructed an ITS matrix using sequences from all accepted species in *Periconia* (Fig. 2). The ITS matrix comprised 104 sequences, including the outgroups *Lentithecium aquaticum* (Yin. Zhang, J. Fourn. & K.D. Hyde) H.W. Shen & Z.L. Luo (CBS 123099) and *Lentithecium clioninum* (Kaz. Tanaka, Sat. Hatak. & Y. Harada) Kaz. Tanaka & K. Hiray. (HHUF 28199), and 580 characters, including gaps, of which 254 were conserved, 300 variable, and 269 parsimony-informative. The ML analysis was used with the GTR+R model, and the matrix contained 342 distinct alignment patterns. The final ML optimisation likelihood value of the best tree was –7189.685, and the estimated base frequencies were: A = 0.214, C = 0.304, G = 0.235, T = 0.247; substitution rates: AC = 2.75210, AG = 3.64945, AT = 2.29873, CG = 1.61726, CT = 6.88209, GT = 1.000000.

Subsequently, individual analyses were performed for each dataset (ITS, LSU, and *tef1-α*) and for the combined matrix of the three genes, based on small alignments constructed using species most closely related to our sequences (Fig. 3, Supplementary Figs S1–S3).

The combined matrix (ITS, LSU, and *tef1-α*) comprised sequences from 44 strains, including the same outgroups, and 2,170 characters, including gaps (560 characters for ITS, 578 for LSU, and 1,032 for *tef1-α*), of which 1,647 were conserved, 523 variable, and 417 parsimony-informative. The ML analysis contained 570 distinct alignment patterns. The final ML optimization likelihood value of the best tree was –8525.193, and the estimated base frequencies were: A = 0.221, C = 0.284, G = 0.272, T = 0.223; substitution rates: AC = 1.40447, AG = 1.93175, AT = 1.40447, CG = 1.00000, CT = 9.37022, GT = 1.000000. The models used for IQTREE ML and BI were GTR+I+G for all the selected partitions. The alignments were deposited in Figshare (<https://doi.org/10.6084/m9.figshare.32098945>).

Based on our phylogenetic analyses (Figs 2, 3 and Figs S1–S3), our endophytes were positioned in a clade with a known species *P. igniaria*, and a clade distinct from the other species included in this analysis; therefore, we introduce a new species for these isolates and

expand the host relationships and geographic distribution of *Periconia* species.

PHI

The PHI test also showed that *P. igniaria* isolates formed a high-identity cluster with our isolates (URM 9010 = FCCUFG 196), grouping closely with reference strains CBS 298.66 and CBS 583.66. In contrast, *P. ananasi*, *P. dicranopteridis*, and the novel species (URM 9009 = FCCUFG 148) were positioned within a central reticulate structure, reflecting narrow genetic boundaries among these species (Fig. 4). The PHI test, based on p-distance, did not detect significant evidence of recombination among the analyzed species ($p = 0.7$). Although limited to a simple distance measure, this result, together with the multilocus phylogeny and morphology, supports recognition of the new species.

Taxonomy

Periconia cerradoensis C.S. Oliveira, L.O. Ferro & J.D.P. Bezerra, sp. nov. (Fig. 5)

Mycobank MB 863941

Diagnosis: *Periconia cerradoensis* differs from *P. dicranopteridis* by producing predominantly well-developed conidiophores and having smaller conidia (5.5–8.5 μm vs 8–11 μm), whereas *P. dicranopteridis* produces only reduced conidiophores.

Type: Brazil, Goiás state, Goiânia municipality, Escola de Agronomia of the Universidade Federal de Goiás (UFG), Campus Samambaia. 16°35'58"S, 49°16'45"W, isolated as an endophyte in branches of *Brosimum gaudichaudii* (Moraceae), April 2022, C.S. Oliveira, T.M. da Silva & J.D.P. Bezerra [holotype UFG 39356 (permanent microscopic slide); ex-holotype culture (URM 9009 = FCCUFG 148)].

Etymology. The name refers to the Cerrado biome, where the fungus was first isolated.

Description. Endophytes on branches of *Brosimum gaudichaudii* (Moraceae). Mycelium partly superficial and partly immersed, composed of branched, septate, smooth, hyaline hyphae, 1.5–3 μm wide. Conidiophores solitary, macronematous, mononematous, predominantly simple, occasionally branched, brown, straight to flexuous, erect, smooth, septate, with a swollen foot-like basal cell, 81–189 × 4–5.5 μm. Reduced conidiophores represented only by conidiogenous cells were occasionally observed. Conidiogenous cells integrated, terminal or lateral, mono- to polyblastic, globose, smooth, arising directly from the stipe, producing simple or branched chains of conidia, 3–5.5 μm diam. Conidia acrogenous, produced in short chains or clusters, with young conidia frequently remaining attached to mature conidia, globose, aseptate, smooth and hyaline when young, becoming verrucose to slightly spiculate and brown with age, 5.5–8.5 μm diam. Sexual morph: undetermined.

Culture characteristics. Colonies on PDA reaching 5.8 cm diam. after 14 days incubation, cottony appearance and regular margin, beige at the beginning and vinaceous pink; reverse greyish black. On MEA, reaching 3.4 cm diam. after 14 days incubation, with a velvety appearance

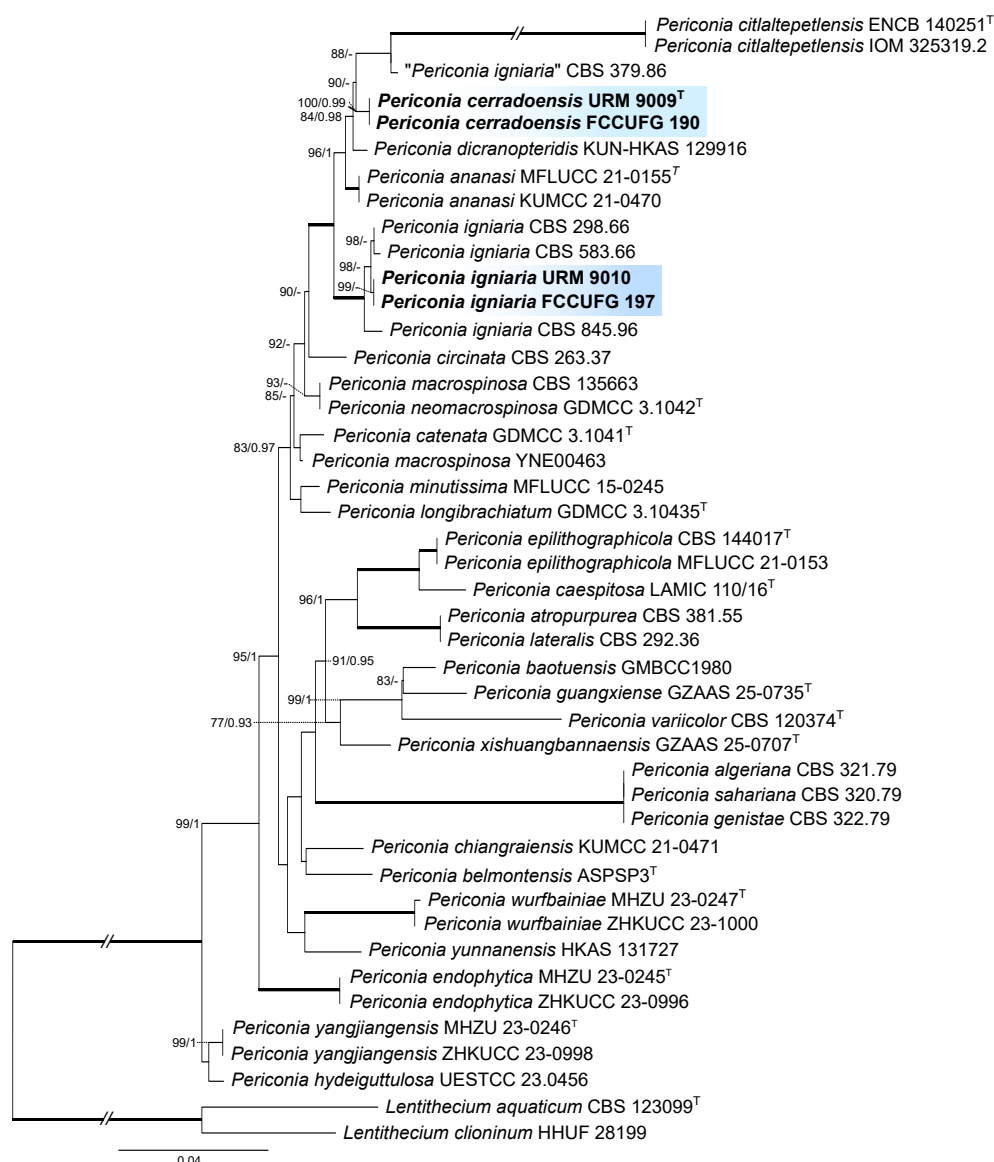


Figure 3. Maximum likelihood phylogenetic tree of *Periconia* species inferred from a combined ITS, LSU, and *tef1-α* dataset. Bootstrap support values $BS \geq 70\%$ and Bayesian posterior probabilities $BPP \geq 0.95$ are shown at the nodes; a hyphen (“-”) indicates lack of statistical support. Thickened branches indicate full statistical support in both analyses. Isolates obtained in this study are indicated in bold and highlighted in color. Ex-type strains are marked with “T”. Long branches were shortened and are indicated by diagonal lines (//). *Lentithecium aquaticum* (CBS 123099^T) and *L. cloninum* (HHUF 28199) were used as outgroups. Scale bar indicates the number of substitutions per site.

and a light salmon color; reverse pinkish-orange with white edges.

Additional specimens examined. Brazil, Goiás State, Goiânia Municipality, Escola de Agronomia, Universidade Federal de Goiás (UFG), Campus Samambaia. 16°35'58"S, 49°16'45"W, isolated as an endophyte from branches of *Brosimum gaudichaudii* (Moraceae), April 2022, C.S. Oliveira, T.M. da Silva & J.D.P. Bezerra (living culture FCCUFG 190).

Notes. *Periconia cerradoensis* is introduced here based on morphological and phylogenetic analyses (Fig. 2 and Figs S1–S3), with *P. dicranopteridis* (KUN-HKAS 129916) as its closest phylogenetic species. The new species is supported by high phylogenetic values (ML = 100%, BPP = 0.99). Based on ITS and LSU sequences, no bp variation was observed, whereas *tef1-α* sequences differ by 13 bp, highlighting *tef1-α* as the primary marker for recognizing new species in *Periconia*. Additionally,

the PHI test revealed no significant recombination event between our strains and the closely related species ($p = 0.7$) (Fig. 4). Morphologically, *P. cerradoensis* differs from *P. dicranopteridis* by producing well-developed conidiophores and smaller conidia (5.5–8 μm vs 8–11 μm in *P. dicranopteridis*) formed in chains or clusters, and initially hyaline. Both were first isolated as endophytes, with *P. dicranopteridis* from the roots of *Dicranopteris pedata* (Gleicheniaceae) in China (Bao et al. 2025). Other morphological differences among phylogenetically related species are highlighted in Table 2.

Periconia igniaria E.W. Mason & M.B. Ellis, Mycol. Pap. 56: 104. 1953. (Fig. 6)

Description. Endophytes in branches of *Mimosa tenuiflora* (Fabaceae). Mycelium partly superficial and partly immersed, composed of branched, septate, smooth,

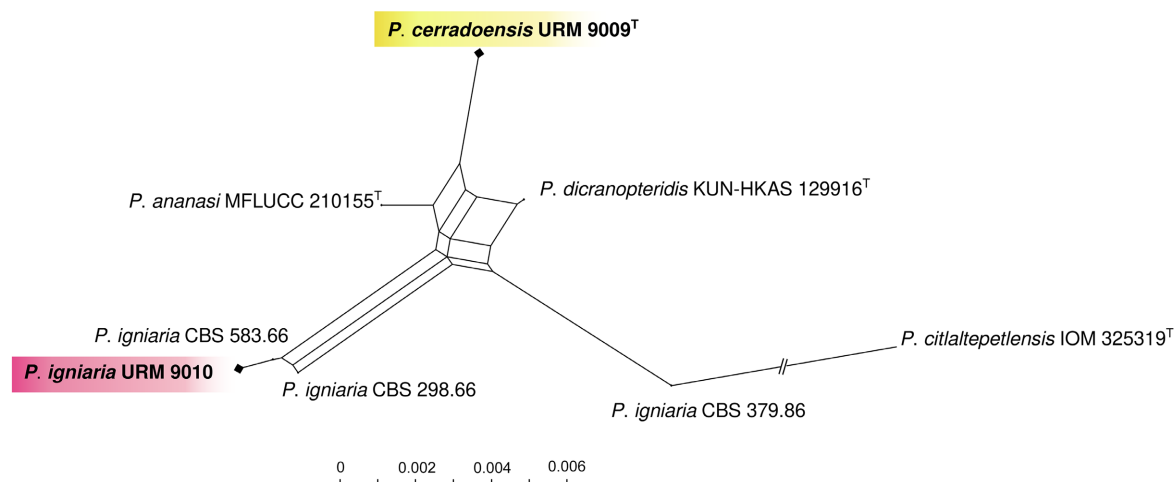


Figure 4. Neighbor-Net phylogenetic network of *Periconia* species based on a combined ITS, LSU, and *tef1-α* dataset calculated using uncorrected p-distances. The network was generated in SplitsTree4 with a fit value of 93. Parallel lines indicate conflicting phylogenetic signals or alternative evolutionary pathways. The PHI test detected no significant evidence of recombination ($p = 0.7$). Isolates obtained in this study are indicated in bold and highlighted with colored boxes. The scale bar represents the number of substitutions per site.

Table 2. Comparison of the main morphological features of *Periconia cerradoensis* and closely related species.

Species	Conidiophores	Conidiogenous cells	Conidia	Host/substrate	Country	Key reference
<i>Periconia ananasi</i>	(415–)545–735 μm long ($\bar{x} = 640 \mu\text{m}$, $n = 25$)	6–11 $\times$ 3–6 μm	6–8 μm diam.	Dead leaves of <i>Ananas comosus</i> (Bromeliaceae)	Thailand	Tian et al. 2022
<i>Periconia cerradoensis</i>	81–189 $\times$ 4–5.5 μm	3–5.5 μm diam.	5.5–8.5 μm diam.	Branch of <i>Brosimum gaudichaudii</i> (Moraceae)	Brazil	This study
<i>Periconia citlaltepeltensis</i>	100–150 $\times$ 5–6 μm	10–12 $\times$ 6–7.5 μm	15–17 μm diam.	High altitude volcanic glacier	México	Calvillo-Medina et al. 2020
<i>Periconia dicranopteridis</i>	Conidiophores reduced to conidiogenous cells	–	8–11 μm diam.	Roots of <i>Dicranopteris pedata</i> (Gleicheniaceae)	China	Bao et al. 2025
<i>Periconia igniaria</i>	300–550 $\times$ 9–13 μm	–	7–10 μm diam.	Palm leaf (Arecaceae)	Great Britain	Cannon 2026

hyaline hyphae, 1.5–2.5 μm wide. Conidiophores solitary, macronematous, mononematous, brown, straight to flexuous, erect, branched, stipe smooth or warty, septate, 32–75 $\times$ 18–30 μm , conidial heads gregarious or branched. Conidiogenous cells polyblastic, light brown to brown, terminal, integrated, branched, smooth and verrucose, 11.5–32 $\times$ 18–30 μm . Conidia acrogenous, in chains or clusters, globose to subglobose, aseptate, light brown to dark brown with age, verrucose, 5.5–8.5 $\times$ 5.5–7.5 μm . Infertile coils were observed. Sexual morph: undetermined.

Culture characteristics. Colonies on PDA measuring 4.5 cm diam. after 14 days incubation, cottony, aerial mycelia scarce, grey to dark grey with irregular white edges; reverse dark grey to grey with beige to white edges. On MEA, measuring 8.8 cm diam. after 14 days incubation, cottony, with irregular edges, brown to progressively lighter, with white edges; reverse dark brown with white edges.

Specimens examined. Brazil, Paraíba state, Santa Teresinha municipality, Fazenda Tamandua (07°02'20"S, 37°26'43"W), isolated as endophytes in branches of *Mimosa tenuiflora*

(Fabaceae), 4 Apr. 2013, J.D.P. Bezerra (living cultures URM 9010 = FCCUFG 196 = O40 and FCCUFG 197 = O9).

Notes. *Periconia igniaria* was introduced by Mason & Ellis (1953) for a fungus obtained from a palm leaf in Great Britain. Our isolates have morphological features and a phylogenetic position (Fig. 2) consistent with sequences designated *P. igniaria* and treated as reference materials for this species, for which we have no available DNA sequences from type material. The morphological characteristics of the examined isolates are consistent with the original description of *P. igniaria*, including branched conidiophores and conidia that are globose, brown to dark brown, and verruculose. However, our isolates showed slightly smaller conidia (5–8 μm in diam.) than reported previously in Morris (1956). To our knowledge, it is the first report of *P. igniaria* as an endophyte of *M. tenuiflora* in Brazil. Previously, *P. igniaria* was reported as an endophyte in *Centaurea solstitialis* L. (Asteraceae) in Russia (Kolomiets et al. 2008), *Cheilocostus speciosus* (Costaceae) in India (D'Souza et al. 2019), *Stephania dielsiana* (Menispermaceae) in China (Lin et al. 2020), and as a phytopathogen of cowpea leaf in Egypt (Abdel-Samad et al. 2024).

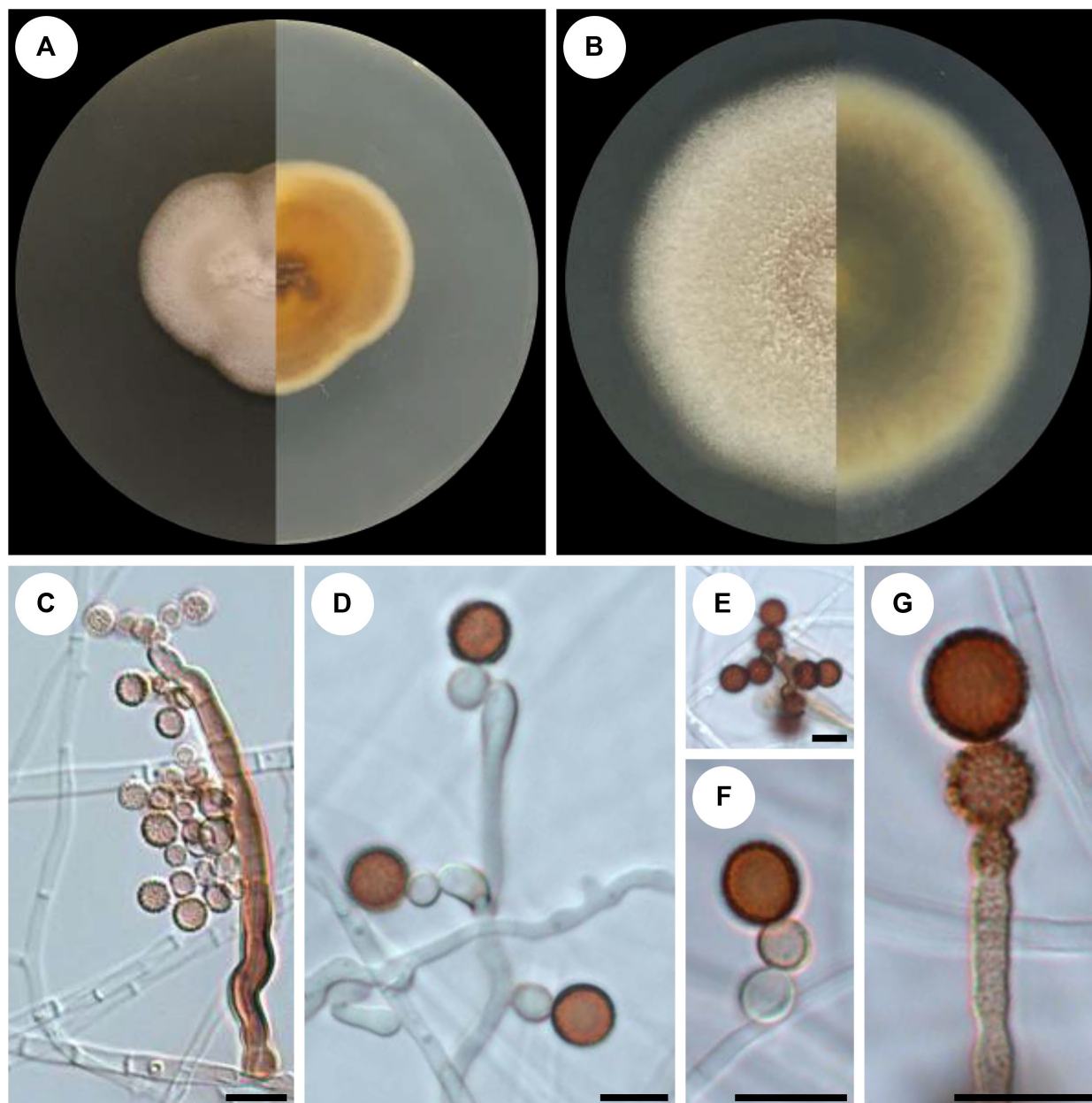


Figure 5. *Periconia cerradoensis* (URM 9009, ex-holotype). A – colonies on MEA after 14 d at 25°C in the dark (surface and reverse); B – colonies on PDA after 14 d at 25°C in the dark (surface and reverse); C – hyphae and conidiogenous cells; D–F – hyphae and conidiogenous cells producing young conidia; G – details of the ornamented conidium. Scales = 10 µm.

Discussion

Reports of *Periconia* in South America remain limited compared with other regions. Despite its broad worldwide distribution and highest species diversity being reported from the USA, with numerous records also reported from Europe and Asia (Madagammana et al. 2024; Li et al. 2026), recent taxonomic studies have considerably expanded knowledge of the genus in China (Su et al. 2023; Liao et al. 2024; Zhang et al. 2025; Zhang et al. 2026). Although several species of *Periconia* are recorded in Brazilian fungal databases, such as Flora e Funga do Brasil (<https://floradobrasil.jbrj.gov.br/>) and speciesLink (<https://specieslink.net/>), these records are mainly concentrated on species especially associated with leaf-litter, e.g., *P. tirupatiensis* Subram. and *P. laxa* Corda. Studies have added new records and species from Brazil, including

P. atropurpurea and *P. belmontensis* (Teles et al. 2006; Pommer et al. 2025). However, information on the diversity, distribution, and ecological roles of *Periconia* in Brazilian ecosystems remains fragmented, particularly for endophytic species associated with native plants in seasonally dry environments such as the Cerrado and Caatinga.

The recognition of *Periconia cerradoensis* as a new species was based mainly on morphological characteristics and multilocus phylogenetic analyses. Phylogenetically, the species formed a distinct lineage closely related to *P. dicranopteridis*, with divergence supported by *tefl-a* sequences, whereas ITS and LSU showed little or no variation. These findings reinforce the importance of protein-coding markers for species delimitation in *Periconia*, particularly among closely related species in which ribosomal markers often provide insufficient

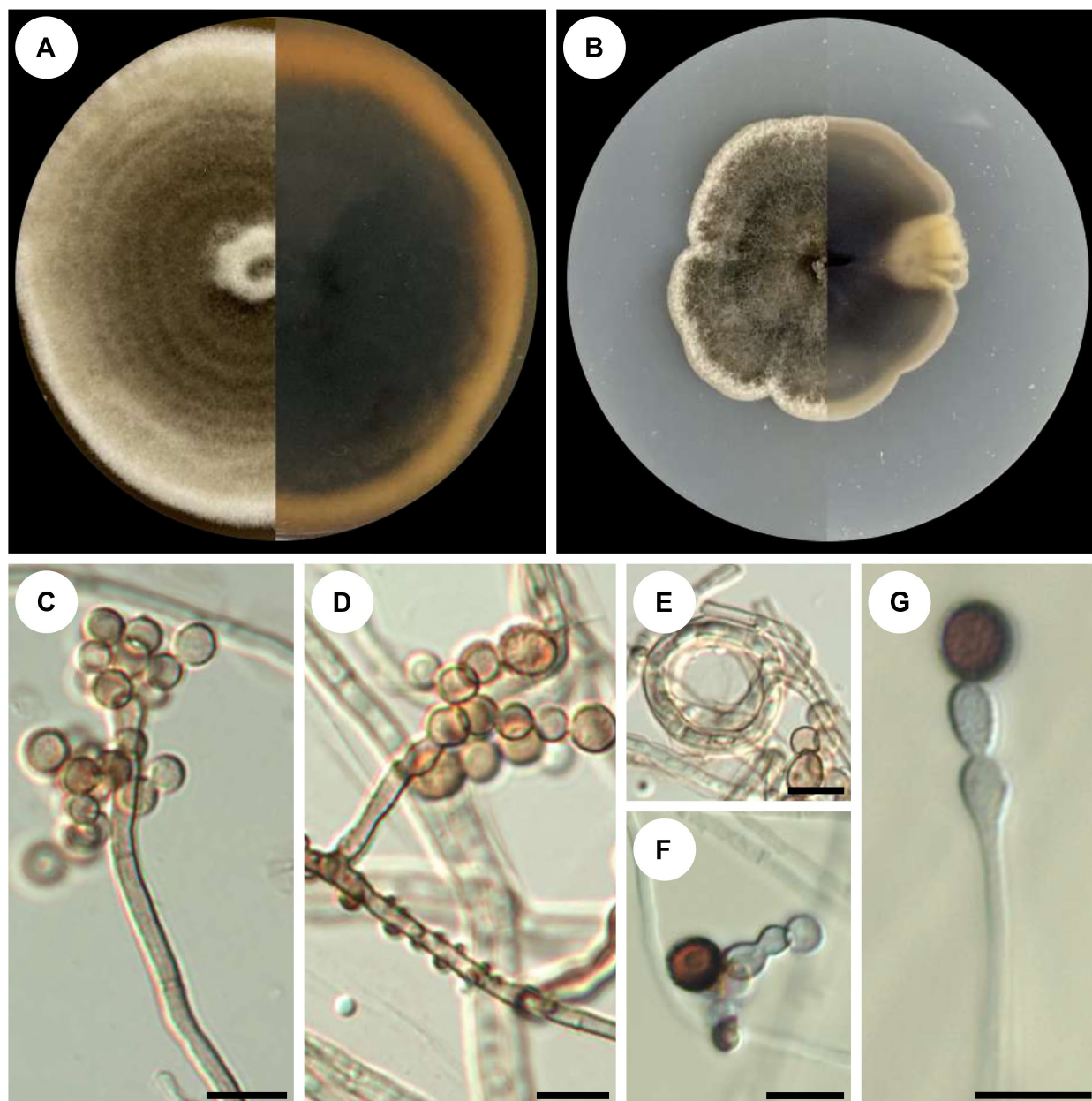


Figure 6. *Periconia igniaria* (URM 9010). A – colonies on MEA after 14 d at 25°C in the dark (surface and reverse); B – colonies on PDA after 14 d at 25°C in the dark (surface and reverse); C – hyphae and conidiogenous cells; D – conidiogenous cell and details of the ornamentation of the hypha; E – coils; F, G – conidium maturation. Scales = 10 µm.

resolution (Liao et al. 2024; Tian et al. 2025). The PHI test also did not detect significant recombination among the analyzed species under the selected parameters. Morphologically, *P. cerradoensis* differs from *P. dicranopteridis* by producing well-developed conidiophores and smaller conidia formed in chains or clusters, which are initially hyaline, and also differs from other related species (Table 2). Together with the morphological differences and multilocus phylogenetic analyses, these results contribute to the delimitation of *P. cerradoensis* as a distinct taxon.

The occurrence of *P. igniaria* as an endophyte of *M. tenuiflora* represents the first report in this host in Brazil and expands the known ecological range of the species. Previous studies have reported *P. igniaria* as an endophyte associated with different plant species in Russia

(Kolomiets et al. 2008), India (D’Souza et al. 2019), and China (Lin et al. 2020), as well as a phytopathogen in Egypt (Abdel-Samad et al. 2024).

The description of *P. cerradoensis* and the new host and the geographical records of *P. igniaria* highlight the importance of the Cerrado and Caatinga as underexplored biomes for endophytic fungi. These seasonally dry tropical ecosystems harbor plant hosts exposed to intense environmental stress, which may favor specialized and still-undocumented fungal communities (Ogola et al. 2025; Xiong et al. 2026). Our findings expand current knowledge of *Periconia* diversity in South America and reinforce the need for integrative taxonomic studies that combine morphology, multilocus phylogeny, ecology, and host-association data for endophytic fungal groups associated with tropical dry environments.

Acknowledgments

We acknowledge financial support from grants provided by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq, process numbers 311187/2022-6; 303939/2022-2; PRO-TAX 445649/2024-0; 316103/2025-0; 310527/2026-0; INCT-PDHN 408678/2024-0; INCT-Fungos do Brasil 409181/2024-2), Fundação de Amparo à Pesquisa do Estado de Goiás (FAPEG, process numbers 202410267001390; 202410267000983; PROTAX 202510267001651; 202510267001150), and Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES - Finance code 001, process numbers FunBioS 88881.986045/2024-01; 88887.146340/2025-00).

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Supplementary electronic materials

Figure S1. Maximum likelihood phylogenetic tree of *Periconia* species inferred from ITS sequences, focusing on taxa closely related to the isolates obtained in this study. Bootstrap support values $BS \geq 70\%$ are indicated at the nodes. Thickened branches indicate full statistical support. Isolates obtained in this study are indicated in bold and highlighted in color. Ex-type strains are marked with “T”. Long branches were shortened and are indicated by diagonal lines (/). *Lentithecium aquaticum* (CBS 123099^T) and *L. clioninum* (HHUF 28199) were used as outgroups. Scale bar indicates the number of substitutions per site. [Download file](#)

Figure S2. Maximum likelihood phylogenetic tree of *Periconia* species inferred from LSU sequences, focusing on taxa closely related to the isolates obtained in this study. Bootstrap support values $BS \geq 70\%$ are indicated at the nodes. Thickened branches indicate full statistical support. Isolates obtained in this study are indicated in bold and highlighted in color. Ex-type strains are marked with “T”. *Lentithecium aquaticum* (CBS 123099^T) and *L. clioninum* (HHUF 28199) were used as outgroups. Scale bar indicates the number of substitutions per site. [Download file](#)

Figure S3. Maximum likelihood phylogenetic tree of *Periconia* species inferred from *tefl*- α sequences, focusing on taxa closely related to the isolates obtained in this study. Bootstrap support values $BS \geq 70\%$ are indicated at the nodes. Thickened branches indicate full statistical support. Isolates obtained in this study are indicated in bold and highlighted in color. Ex-type strains are marked with “T”. Long branches were shortened and are indicated by diagonal lines (/). *Lentithecium aquaticum* (CBS 123099^T) and *L. clioninum* (HHUF 28199) were used as outgroups. Scale bar indicates the number of substitutions per site. [Download file](#)

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