



Morphological and phylogenetic evidence reveal a new species of *Vuilleminia* (Corticiales, Basidiomycota) from China

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Abstract

Wood-decaying fungi, as crucial decomposers in forest ecosystems, have been the subject of meticulous research. In this study, a new wood-decaying fungal species, *Vuilleminia ellipsoidea*, found in Yunnan Province, China, is described and illustrated based on morphological and molecular evidence. It is characterized by producing cream to buff and smooth basidiomata, a monomitic system with clamp connections, cylindrical cystidia, numerous frequently branched dendrohyphidia, cylindrical to tubulate basidia, and thin-walled and ellipsoid basidiospores measuring $10.7\text{--}13 \times 6.3\text{--}7.8\ \mu\text{m}$. Phylogenetic analyses of ITS and nLSU rRNA markers were performed with Maximum Likelihood and Bayesian methods. Inference methods showed that the new species formed a distinct lineage and then grouped with *V. bambusicola* and *V. punctata*. A full description, illustrations, and phylogenetic analysis results of the new species are provided.

Key words: Molecular systematics, New species, Taxonomy, Yunnan Province

Introduction

Fungi play vital roles in forest ecosystems as endophytes, symbionts, pathogens, and saprobes (Dai 2012; Shen *et al.* 2018; Yuan *et al.* 2023; Hyde *et al.* 2024; Liu *et al.* 2025; Song *et al.* 2025). Some cause serious diseases of plants and animals, but others are mutualistic symbionts (for example, mycorrhizae), sources of life-saving drugs (such as statins and antibiotics), and medicinal mushrooms (Zheng *et al.* 2011; Wu *et al.* 2019, 2026; Ghobad-Nejhad *et al.* 2024; Hibbett *et al.* 2025). Wood-decaying fungi destroy our homes, food, and cultural heritage, but their enzymes may provide the keys to next-generation biofuels and aid the decomposition of some toxic substances (Dai *et al.* 2000; Si *et al.* 2011; Wang *et al.* 2013; Hibbett *et al.* 2025). About 165,000 species of fungi have been described (<https://www.indexfungorum.org/>) out of 2.5 million predicted (Niskanen *et al.* 2023), and fungal taxonomists steadily describe about 3,000 new species per year (Dai *et al.* 2015; Hyde *et al.* 2024; Dong *et al.* 2025). Undescribed fungi could therefore represent a massive potential at a time when there is a need to find new sources of food, novel antibiotics, novel metabolites with biotechnological, industrial, and pharmaceutical applications (Hyde *et al.* 2024).

Vuilleminia Maire was introduced by Maire (1902) to accommodate *V. comedens* (Nees) Maire. The genus is characterized by ceraceous to latinous, resupinate basidiomata with a smooth to tuberculate hymenophore, a monomitic hyphal system with clamp connections on generative hyphae, the presence of thin-walled, dendrohyphidia,

and allantoid to ellipsoid basidiospores (Bernicchia & Gorjón 2010). Species of this genus are common in Europe on dead or decaying branches of woody angiosperms (Ghobad-Nejhad *et al.* 2010). Currently, *Vuilleminia* contains 15 species (<http://www.mycobank.org>, accessed on 20 January 2026; <http://www.indexfungorum.org>, accessed on 10 March 2026) (Crous *et al.* 2023; Wijesinghe *et al.* 2025). Among them, two species have been recorded from China (Wijesinghe *et al.* 2025).

Nowadays, DNA sequence-based classification and identification have become the standard approach in fungal taxonomy, and advances in genomic technologies have revolutionized fungal systematics, ushering the field into the phylogenomic era (James *et al.* 2020). Phylogenetic analyses of ITS and nLSU sequences elucidated the taxonomic framework of the genus *Vuilleminia*, in which *V. comedens*, *V. alni* Boidin, Lanq. & Gilles, and *V. megalospora* Bres. formed a polytomy and could not be reliably distinguished based on the ITS sequences (Ghobad-Nejhad *et al.* 2010). Subsequent analyses further expanded the molecular understanding of the genus, in which the integration of the nLSU region with ITS data helped to refine species boundaries and phylogenetic relationships within *Vuilleminia*, *V. comedens*, *V. megalospora* and *V. coryli* Boidin, Lanq. & Gilles grouped together (Ghobad-Nejhad *et al.* 2012). The Bayesian phylogram based on the combined ITS + nLSU + SSU + mtSSU dataset reveals the overall topology of the order Corticiales K.H. Larss., which includes four families: Corticiaceae Herter, Punctulariaceae Donk, Vuilleminiaceae Maire, and Dendrominiaceae Ghob.-Nejh. (Ghobad-Nejhad *et al.* 2021). Phylogenetic inferences based on the combined ITS + nLSU dataset have been consistently employed for species delimitation among *Vuilleminia* and related genera, as demonstrated in independent studies where this molecular approach successfully validated the taxonomic status of novel species (Buyck *et al.* 2022; Wei *et al.* 2022; Crous *et al.* 2023; Wijesinghe *et al.* 2025; Yang *et al.* 2025a).

During investigations on wood-decaying fungi in Yunnan Province, one undescribed species of *Vuilleminia* was discovered and introduced based on morphology and multi-locus phylogeny. This study aims to confirm the taxonomic affinities of the new species and to elucidate the relationships among representative species of *Vuilleminia*.

Materials and methods

Sample collection and fungarium specimen preparation

Samples were collected from Tengchong, Yunnan Province, China. Fresh specimens were photographed in situ using a Huawei P70, and macroscopic features and other important information were recorded in the field (Rathnayaka *et al.* 2024). All photographs were focus-stacked using Helicon Focus software. Specimens were then transported to a field station and dried using an electric food dryer at 40 °C. Once fully dried, the samples were sealed in envelopes and zip-lock plastic bags, labeled, and deposited in the fungarium of the Southwest Forestry University (SWFC), Kunming, Yunnan Province, China.

Morphological studies

The macro-morphology was based on fresh and dried specimens. The color terms in the description followed those of Anonymous (1969) and Petersen (1996). The micromorphological characteristics data were systematically analyzed from dried specimens and observed under a light microscope, in accordance with established methodologies (Dai 2010; Dong *et al.* 2024, 2025; Wijesinghe *et al.* 2025). Sections mounted in 5% KOH and 2% phloxine B dye (C₂₀H₂Br₄Cl₄Na₂O₅). Other reagents were also used, including Cotton Blue and Melzer's reagent. Micromorphology observation follows the method of Wang *et al.* (2024). The following abbreviations were used: CB=Cotton Blue, CB=acyanophilous; KOH=5% potassium hydroxide; IKI=Melzer's reagent, IKI=both inamyloid and indextrinoid; W=mean spore width (arithmetic average for all spores); L=mean spore length (arithmetic average for all spores); Q=variation in the L/W ratios between the specimens studied; n (a/b)=number of spores (a) measured from given number (b) of specimens (Zhao *et al.* 2015; Yang *et al.* 2023; Yang *et al.* 2025b).

DNA Extraction, Polymerase Chain Reaction (PCR), and Sequencing

The CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd., Beijing, China) was used to obtain genomic DNA from the dried specimens according to the manufacturer's instructions. The primer pair ITS5 and ITS4 (White *et al.* 1990) was used to amplify the ITS region. The primer pair LR0R and LR7 was used to amplify

the nuclear nLSU region. The PCR was performed as described by Dong *et al.* (2024). All newly generated sequences were successfully deposited into the National Center for Biotechnology Information (NCBI) GenBank database. All the nucleotide sequences were systematically listed in Table 1.

TABLE 1. List of species, specimens, and GenBank accession numbers of sequences used in this study. The new species are in bold.

Species Name	Sample No.	Country	GenBank Accession No.		References
			ITS	nLSU	
<i>Australovuilleminia coccinea</i>	MG 74	New Zealand	HM046875	HM046930	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Basidiodesertica hydei</i>	SQUCC 15289*	Oman	MW077150	MW077159	Wei <i>et al.</i> (2022)
<i>Corticium roseum</i>	MG 252*	China	MW805872	MW805836	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Corticium thailandicum</i>	MG 242	Thailand	MW805868	MW805831	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Cytidia salicina</i>	MG 49	Finland	GU590881	HM046921	Wei <i>et al.</i> (2022)
<i>Dendrocorticopsis luteoalba</i>	CLZhao 30380*	China	PQ783828	PQ783838	Yang <i>et al.</i> (2025)
<i>Dendrocorticopsis orientalis</i>	He 4195	China	MW580926	MW580921	Wei <i>et al.</i> (2022)
<i>Dendrocorticopsis orientalis</i>	WEI 20-166	China	MW580922	MW580924	Wei <i>et al.</i> (2022)
<i>Dendrocorticium polygonioides</i>	CBS 106.56	France	MH857525	MH869062	Vu <i>et al.</i> (2019)
<i>Dendrocorticium roseocarneum</i>	KUC 20121109-32	Korea	KJ668559	KJ668413	Ghobad-Nejhad & Duhem (2014)
<i>Dendrominia ericae</i>	MG 162	France	JX892938	JX892939	Ghobad-Nejhad & Duhem (2014)
<i>Disporotrichum dimorphosporum</i>	CBS 419.70*	Netherlands	MH859776	MH871538	Vu <i>et al.</i> (2019)
<i>Disporotrichum dimorphosporum</i>	CBS 433.85	USA	MH861895	MH873584	Vu <i>et al.</i> (2019)
<i>Erythrimum hypnophilum</i>	MG 169*	France	MW805858	MW805823	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Erythrimum laetum</i>	MG 72	Finland	GU590875	GU590878	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Erythrimum vernum</i>	FP-133815*	USA	MW805865	MW805828	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Jaapia argillacea</i>	CBS 252.74	Netherlands	GU187524	GU187581	Liu <i>et al.</i> (2022)
<i>Laetisaria fuciformis</i>	CBS 182.49*	Netherlands	MH856485	MH868023	Vu <i>et al.</i> (2019)
<i>Laetisaria roseipellis</i>	CBS 299.82	USA	EU622846	EU622844	Vu <i>et al.</i> (2019)
<i>Marchandiomyces corallinus</i>	JL 128-98*	USA	AY583327	AY583331	DePriest <i>et al.</i> (2005)
<i>Mycobernardia incrustans</i>	CBS 172.36	Canada	MH855759	MH867272	Vu <i>et al.</i> (2019)
<i>Mycobernardia incrustans</i>	Duhem 3613*	France	MW805860	MW805825	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Punctularia atropurpurascens</i>	WEI 17-662	China	MW570883	MW570888	Wei <i>et al.</i> (2022)
<i>Punctularia bambusicola</i>	CLZhao 4133	China	MW559982	MW559984	Guan <i>et al.</i> (2021)
<i>Punctularia fragilis</i>	CLZhao 39788*	China	PV475634	PV490570	Wijesinghe <i>et al.</i> (2025)
<i>Punctularia nigrodontea</i>	CLZhao 30592*	China	PQ783829	PQ783839	Yang <i>et al.</i> (2025)
<i>Punctularia strigosozonata</i>	CBS 345.34	Netherlands	MH855559	MH867064	Vu <i>et al.</i> (2019)
<i>Punctulariopsis efibulata</i>	Burdsall 8824	USA	KR494276	KR494277	Ariyawansa <i>et al.</i> (2015)
<i>Punctulariopsis fissurata</i>	CLZhao 27503*	China	PQ062039	PQ109091	Muhammad <i>et al.</i> (2025)
<i>Punctulariopsis fissurata</i>	CLZhao 27430	China	PQ062036	-	Muhammad <i>et al.</i> (2025)
<i>Punctulariopsis obducens</i>	MG 70	Ethiopia	HM046918	HM046933	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Punctulariopsis subglobispora</i>	FCUG 2535	Argentina	HM046917	HM046932	Guan <i>et al.</i> (2021)
<i>Punctulariopsis yunnanensis</i>	CLZhao 21443*	China	PP425905	PP572972	Muhammad <i>et al.</i> (2024)
<i>Vuilleminia alni</i>	CBS 352.95	France	MH862523	MH874160	Vu <i>et al.</i> (2019)
<i>Vuilleminia bambusicola</i>	CLZhao 39787*	China	PV475632	PV490569	Wijesinghe <i>et al.</i> (2025)
<i>Vuilleminia beltraniae</i>	MA-Fungi 78451	France	OR127125	-	Crous <i>et al.</i> (2023)
<i>Vuilleminia comedens</i>	AFTOL-ID 1247	USA	DQ398959	AF518666	Wei <i>et al.</i> (2022)
<i>Vuilleminia coryli</i>	CBS 751.91*	France	MH862333	-	Vu <i>et al.</i> (2019)
<i>Vuilleminia coryli</i>	MG 136	Turkmenistan	JN387996	JN388005	Ghobad-Nejhad <i>et al.</i> (2021)
<i>Vuilleminia cystidiata</i>	FCUG 2596	Austria	HM046909	-	Ghobad-Nejhad & Ginns (2012)

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TABLE 1 (Continued)

Species Name	Sample No.	Country	GenBank Accession No.		References
			ITS	nLSU	
<i>Vuilleminia cystidiata</i>	KUC 20131022-26	Korea	KJ668433	KJ668285	Wei <i>et al.</i> (2022)
<i>Vuilleminia ellipsoidea</i>	CLZhao 45317	China	PX965995	-	Present Study
<i>Vuilleminia ellipsoidea</i>	CLZhao 45324	China	PX965996	PX966003	Present Study
<i>Vuilleminia ellipsoidea</i>	CLZhao 45325	China	PX965997	PX966004	Present Study
<i>Vuilleminia ellipsoidea</i>	CLZhao 45327*	China	PX965998	PX966005	Present Study
<i>Vuilleminia erastii</i>	MG 96	Canada	JN388000	JN388009	Ghobad-Nejhad & Ginns (2012)
<i>Vuilleminia erastii</i>	MG 97	Canada	JN387998	JN388007	Ghobad-Nejhad & Ginns (2012)
<i>Vuilleminia macrospora</i>	MG 60	Sweden	HM046885	HM046927	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Vuilleminia macrospora</i>	MG 167	France	JX892940	JX892941	Ghobad-Nejhad & Duhem (2014)
<i>Vuilleminia megalospora</i>	MG 83	Iran	HM046886	-	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Vuilleminia nilsii</i>	MG 134	France	JX892945	JX892946	Ghobad-Nejhad & Duhem (2014)
<i>Vuilleminia nilsii</i>	MG 171	France	JX892947	JX892948	Ghobad-Nejhad & Duhem (2014)
<i>Vuilleminia pseudocystidiata</i>	FCUG 2600B	France	HM046916	-	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Vuilleminia pseudocystidiata</i>	MG 69	France	HM046888	HM046928	Ghobad-Nejhad <i>et al.</i> (2010)
<i>Vuilleminia punctata</i>	CLZhao 34434*	China	PV475633	-	Wijesinghe <i>et al.</i> (2025)
<i>Vuilleminia tropica</i>	CAL 1845*	India	NR198144	NG241941	Direct Submission

* is shown type material, holotype.

Phylogenetic analyses

To determine the phylogeny, the ITS and nLSU sequence matrix was constructed, and *Jaapia argillacea* Bres. was selected as the outgroup for Corticiales (He *et al.* 2024). The nucleotide sequences were aligned initially by using MAFFT (<https://mafft.cbrc.jp/alignment/server/>) with the “G-INS-I” strategy, and then manually optimized in BioEdit (Hall 1999). ModelFinder was used to select the best-fit model based on the AIC criterion (Kalyaanamoorthy *et al.* 2017). Best-fit model according to AIC: GTR+F+R3 for Corticiales dataset.

Maximum Likelihood (ML) and Bayesian Inference (BI) analyses were applied to the combined ITS+nLSU datasets, following the approach of Wijesinghe *et al.* (2025). Phylogenetic reconstructions were performed using Maximum Likelihood (ML) tools implemented in the PhyloSuite v2 platform (Zhao *et al.* 2025). Maximum-likelihood phylogenies were inferred with IQ-TREE v2.2.0, with 5,000 ultrafast bootstrap replicates and 1,000 SH-aLRT tests to assess branch support (Nguyen *et al.* 2015). Bayesian inference was performed with MrBayes 3.2.7a (Ronquist *et al.* 2012). Four Markov chains were run for 2 runs from random starting trees for 1.5 million generations for ITS+nLSU (Fig. 1). The first one-fourth of all generations was discarded as burn-in. The majority rule consensus tree of all remaining trees was calculated. Branches exhibiting phylogenetic significance were considered significantly supported if they had a maximum likelihood bootstrap value (BS) $\geq 70\%$ or a Bayesian posterior probability (BPP) ≥ 0.95 (Ma & Zhao 2019; Luo *et al.* 2022; Wang *et al.* 2024; Deng *et al.* 2025; Wijesinghe *et al.* 2025).

Results

Molecular phylogeny

The combined ITS+nLSU dataset (Fig. 1) included sequences from 56 fungal specimens representing 43 taxa. The RAxML analysis of the combined dataset yielded a best-scoring tree (Fig. 1), with a final ML optimisation likelihood value of -16897.944. The alignment contained 2,184 bp. The matrix had 1,120 distinct alignment patterns. Estimated base frequencies; A = 0.247, C = 0.220, G = 0.273, T = 0.260; substitution rates AC = 1.22957, AG = 2.69732, AT = 1.50433, CG = 0.53915, CT = 5.21131, GT = 1.000000. The best BI model for the ITS+nLSU dataset was SYM+I+G4. The average standard deviation of split frequencies in the Bayesian analyses was 0.006594, and the effective sample

size (ESS) across the two runs was double the average ESS (avg ESS) = 836.5. Branches that received bootstrap support for ML and BI $\geq 70\%$ and 0.95, respectively, were considered significantly supported.

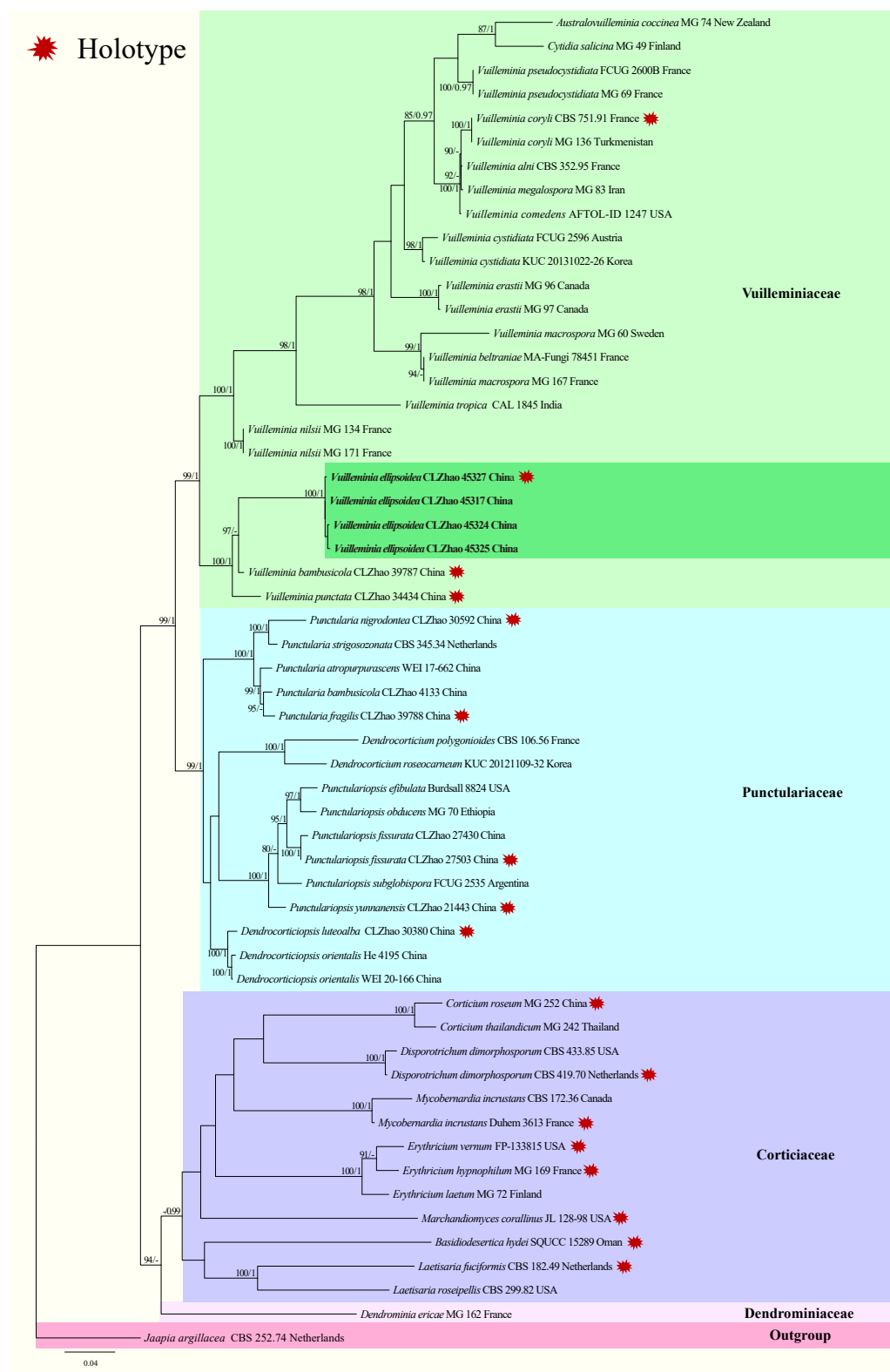


FIGURE 1. Phylogeny of *Vuilleminia ellipsoidea* and related species by ML analysis based on combined ITS+nLSU sequences. Branches are labeled with Maximum Likelihood bootstrap equal to or higher than 70%, and Bayesian Posterior Probabilities equal to or more than 0.95, respectively. *Jaapia argillacea* CBS 252.74 is used as the outgroup. The new species is in bold.

The phylogram inferred from ITS+nLSU sequences within the genus *Vuilleminia* revealed that the presence of one previously undescribed species embedded within the genus, in which *V. ellipsoidea* was grouped with the lineage of *V. bambusicola* L. Wang & C.L. Zhao and *V. punctata* L. Wang & C.L. Zhao (100% BT and 1.00 BPP).

Taxonomy

Vuilleminia ellipsoidea Z.R. Gu & C.L. Zhao, *sp. nov.* Figs. 2–4.

MycoBank no.: MB 862351

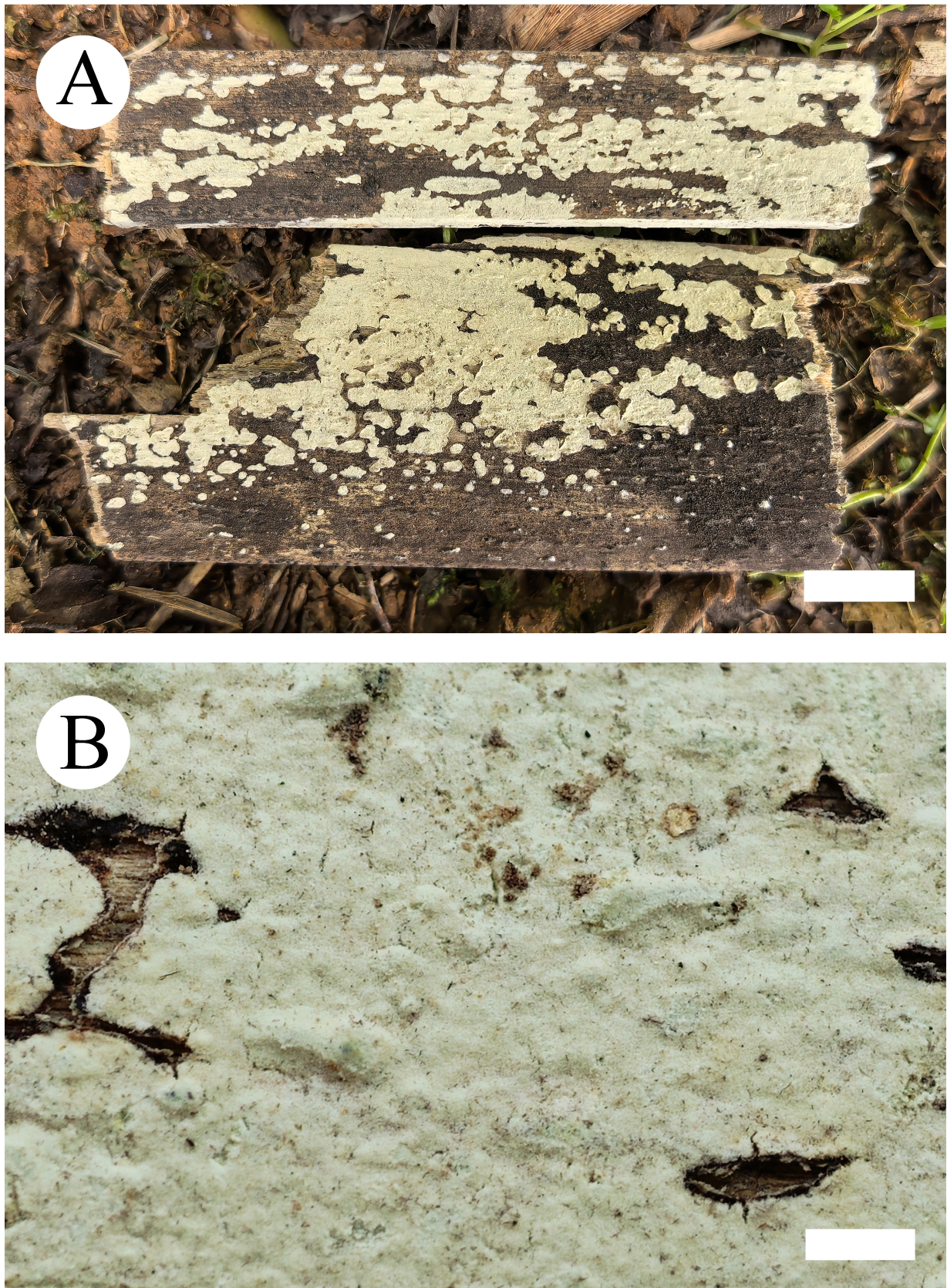


FIGURE 2. Basidiomata of *Vuilleminia ellipsoidea* (holotype, CLZhao 45327). Scale bars: A = 1 cm; B = 1 mm.

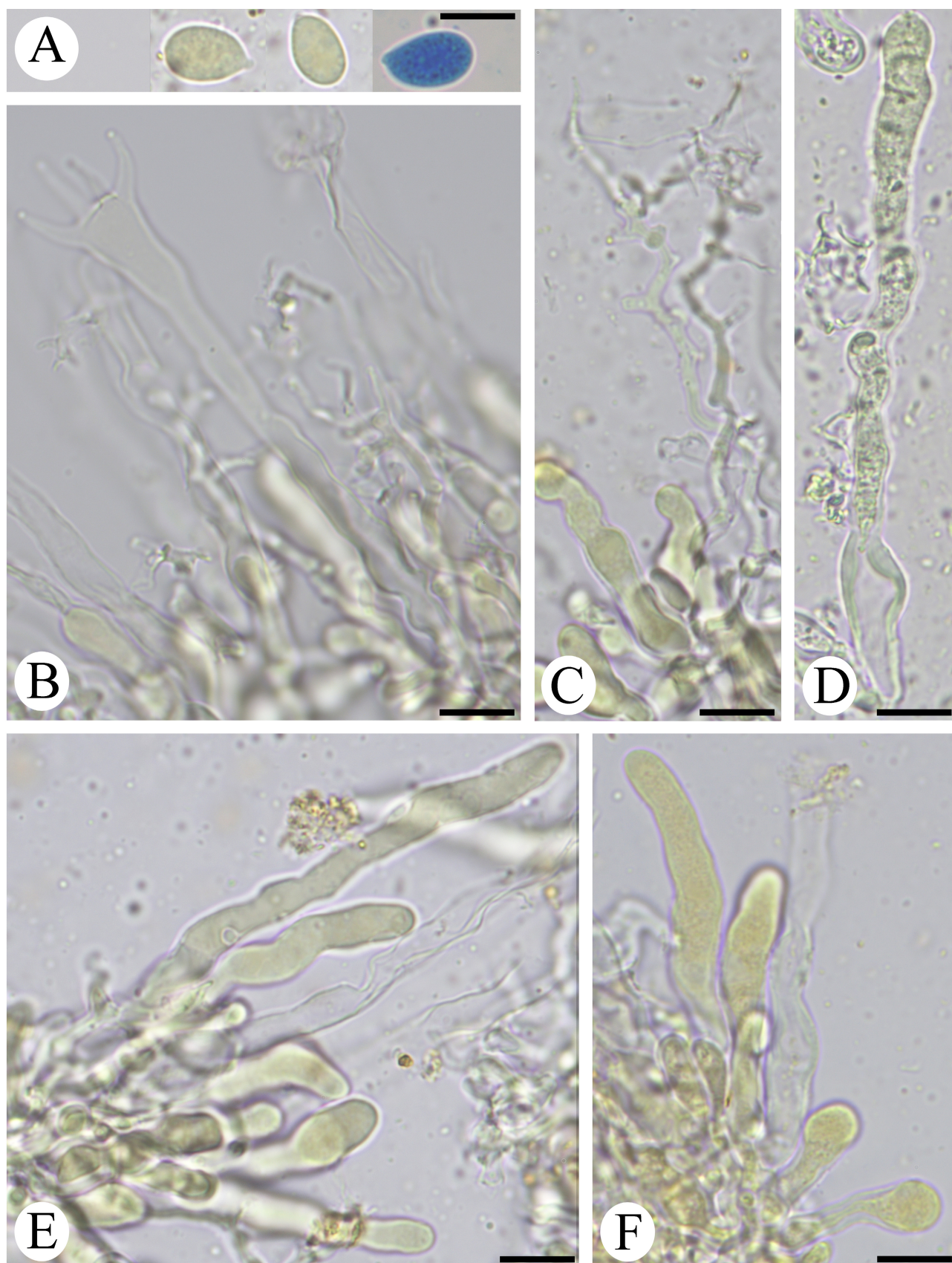


FIGURE 3. Sections of the hymenium of *Vuilleminia ellipsoidea* (holotype, CLZhao 45327). (A) Basidiospores; (B) Basidia and basidioles; (C) Dendrohyphidia; (D) Cystidia; (E–F) A section of the hymenium. Scale bars: (A–F) = 10 μ m, 10 $\times$ 100 Oil.

Diagnosis—Differs from other *Vuilleminia* species by the membranous basidiomata with cream to buff, smooth hymenial surface and ellipsoid basidiospores measuring 10.7–13 $\times$ 6.3–7.8 μ m.

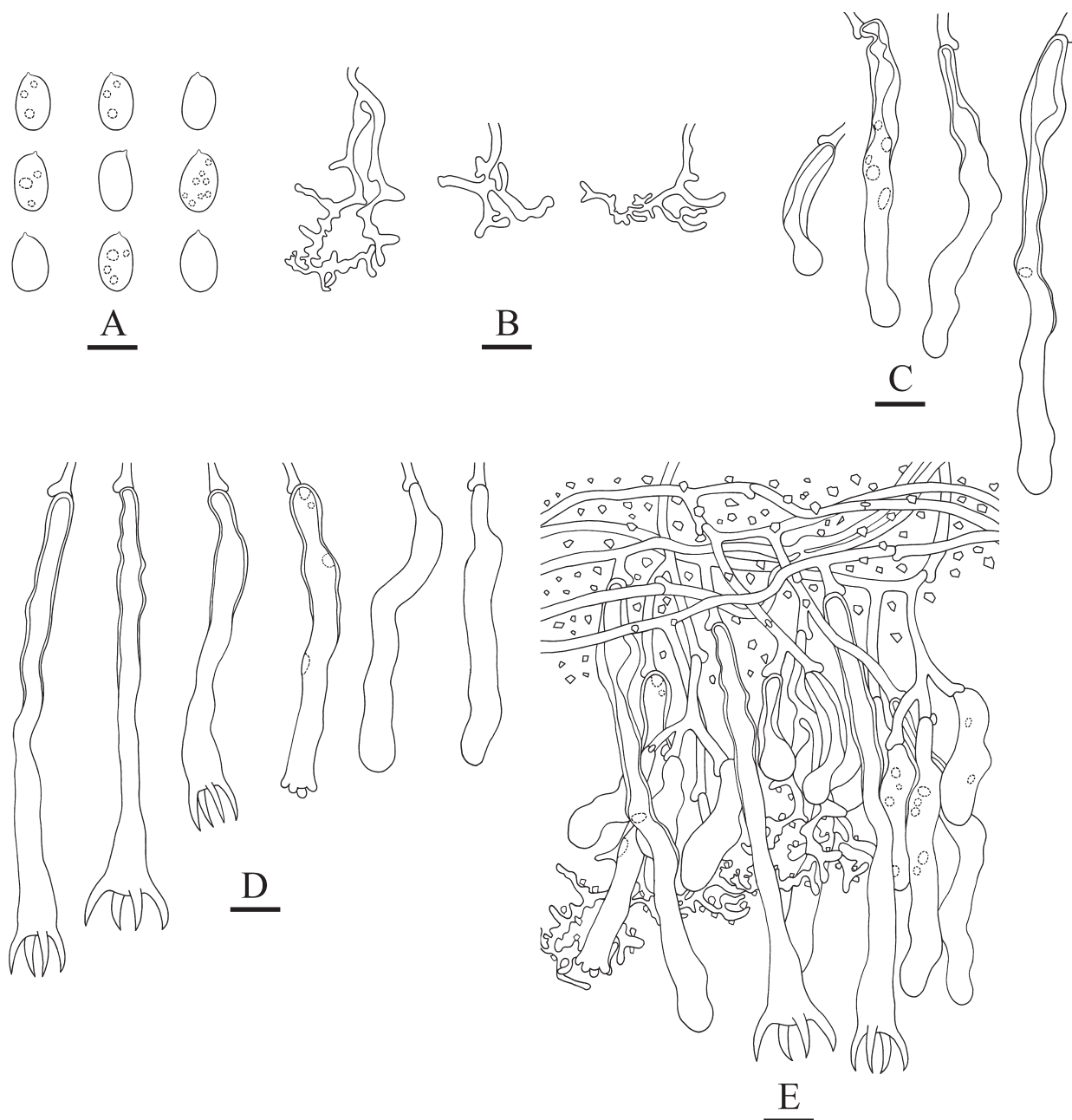


FIGURE 4. Microscopic structures of *Vuilleminia ellipsoidea* (holotype, CLZhao 45327). (A) Basidiospores; (B) Dendrohyphidia; (C) Cystidia; (D) Basidia and basidioles; (E) A cross-section of basidiomata. Scale bars: A –E = 10 μ m.

Etymology—*Ellipsoidea* (Lat.) refers to species having ellipsoid basidiospores.

Holotype—CHINA. Yunnan Province, Tengchong, Beihai Town, Sakura Valley, GPS coordinates 25°06' N, 98°39' E, elev. 1400 m asl., on dead bamboo, 26 March 2025, leg. C.L. Zhao, CLZhao 45327 (SWFC 00045327).

Basidiomata—Basidiomata annual, resupinate, adnate, inseparable from substrate, membranous, without odor or taste when fresh, up to 20 cm long, up to 8 cm wide, and 200 μ m thick at center. Hymenial surface smooth, cream when fresh, turn to cream to buff upon drying. Sterile margin narrow, pale buff, up to 1 mm.

Hyphal system—Monomitic; generative hyphae with clamp connections, IKI–, CB–; tissues unchanged in KOH. Subhymenial hyphae colorless, more or less interwoven, thin-walled, frequently branched, 2–3.2 μ m in diameter; many crystals present among the hyphae.

Hymenium—Cystidia cylindrical, colorless, thin- to thick-walled, apex usually rounded, with large prominent oil-drops, 18–93 $\times$ 5.5–9.7 μ m. Dendrohyphidia numerous, frequently branched, 1.5–3 μ m wide. Basidia cylindrical to tubulate, long clavate, sinuous, with four sterigmata and a basal clamp connection, contents hyaline or with oil droplets, 34.5–92.7 $\times$ 6.5–10.5 μ m, basidioles dominant, in shape similar to basidia, but slightly smaller.

Basidiospores—Ellipsoid, thin-walled, smooth, contents with numerous large guttules, IKI–, CB–, (10–)10.7–13(–13.9) × (5.7–)6.3–7.8(–8.2) µm, L = 11.87 µm, W = 7.04 µm, Q = 1.58–1.81 (n = 120/4).

Additional specimens examined (paratypes)—CHINA. Yunnan Province, Tengchong, Beihai Town, Sakura Valley, GPS coordinates 25°06' N, 98°39' E, elev. 1400 m asl., on dead bamboo, 26 March 2025, leg. C.L. Zhao, CLZhao 45317 (SWFC 00045317), CLZhao 45324 (SWFC 00045324), and CLZhao 45325 (SWFC 00045325).

Discussion

In this study, the new species was discovered in Yunnan Province, China, and is described based on morphological characteristics and phylogenetic analyses.

The phylogram generated from the Maximum Likelihood analysis based on the combined ITS and nLSU sequence data of Corticiales showed that *Vuilleminia* formed a single clade and then grouped with *Dendrocorticopsis* Sheng H. Wu, C.L. Wei & S.H. He, *Dendrocorticium* M.J. Larsen & Gilb., *Punctularia* Pat., and *Punctulariopsis* Ghobad-Nejh (Wijesinghe *et al.* 2025). In the present study, the new taxon was grouped into the genus *Vuilleminia* based on the ITS+nLSU dataset, in which *V. ellipsoidea* is closely related to *V. bambusicola* and *V. punctata* (Fig. 1). Morphologically, *Vuilleminia ellipsoidea* resembles *V. bambusicola* in having cylindrical cystidia and cylindrical to tubulate, long clavate basidia, but *V. bambusicola* has smaller basidiospores (8–10 × 5.5–7 µm vs. 10.7–13 × 6.3–7.8 µm, Wijesinghe *et al.* 2025). *V. punctata* differs from *V. ellipsoidea* in having two types of cystidia (with tapering to apex, or capitate), smaller basidia (22–32 × 5.5–8 µm vs. 34.5–92.7 × 6.5–10.5 µm) and smaller basidiospores (7–8.5 × 4–5 µm vs. 10.7–13 × 6.3–7.8 µm, Wijesinghe *et al.* 2025).

Morphologically, *Vuilleminia ellipsoidea* is closely related to *V. beltraniae* M. Dueñas, Tellería & M.P. Martín, sharing the characteristics of clavate to long-clavate, sinuous basidia. However, *V. beltraniae* differs in its crustaceous to coriaceous basidiomata, cylindrical to fusiform or tubular to capitate cystidia, and larger basidiospores (14–23 × 5–7 µm vs. 10.7–13 × 6.3–7.8 µm, Crous *et al.* 2023). *V. ellipsoidea* is similar to *V. tropica* Hembrom, A. Ghosh, A. Parihar & K. Das in having frequently branched dendrohyphidia and cylindrical basidia, but *V. tropica* differs in its lemon yellow hymenophore and larger cylindrical to narrowly ellipsoid basidiospores (13.6–16 × 6.35–8 µm vs. 10.7–13 × 6.3–7.8 µm, Buyck *et al.* 2022).

Wood-decaying fungi are very rich in Yunnan Province of China, and many new taxa have been recently described from this area (Dai *et al.* 2021; Wang *et al.* 2021; Wu *et al.* 2022; Deng *et al.* 2024; Zhao *et al.* 2025; Li *et al.* 2026; Su *et al.* 2026; Zhou *et al.* 2026). The coriaceous fungi represent a frequently overlooked resupinate group of wood-decaying basidiomycetes. However, many species are widely distributed across diverse habitats due to their remarkable adaptability, and these fungi possess a strong capacity to degrade fallen branches in broad-leaved forests (Ghobad-Nejhad *et al.* 2012; Buyck *et al.* 2022; Crous *et al.* 2023; Wang *et al.* 2025; Yang *et al.* 2025b). Our findings will enhance the understanding of fungal diversity in these ecosystems. Further studies should focus on the relationships between *Vuilleminia* species and their hosts, as well as on the evolutionary trajectories of hosts and *Vuilleminia* species.

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