



中国海南热带雨林国家公园粉孢革菌属(牛肝菌目, 粉孢革菌科)的两个新种

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摘要: 粉孢革菌属物种是一类常见于倒木上, 引起木材褐色腐朽的革状真菌。基于分子和形态证据, 本研究描述了 2 个采自海南的新种——粒状粉孢革菌和海南粉孢革菌。粒状粉孢革菌的主要区别特征是: 子实体革质, 表面具轻微小颗粒状, 呈浅橘色至灰橘色, 担孢子较大, 椭圆形, 大小为 $12.5\text{--}14.2 \times 8.2\text{--}9.5 \mu\text{m}$ 。海南粉孢革菌的主要特征是: 子实体膜质, 表面光滑, 灰橘色至褐橘色, 边缘毛缘状, 担孢子长椭圆形, 大小为 $9.8\text{--}12.2 \times 5.2\text{--}6.5 \mu\text{m}$ 。本文对两新种进行了详细描述并提供了子实体和显微结构图片。

关键词: 木腐菌; 革菌; 褐腐; 分类; 系统发育; 新种

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Two new species of *Coniophora* (Coniophoraceae, Boletales) from Hainan Province, China

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Abstract: *Coniophora* is a widely distributed genus that includes species with resupinate basidiomata

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causing brown rot on fallen trees. In this study, two new species, *Coniophora granulosa* and *Coniophora hainanensis*, are described from Hainan Province based on molecular and morphological evidence. *C. granulosa* is characterized by having coriaceous basidiomata with granulose and light orange to grayish-orange hymenophore, relatively large and ellipsoid basidiospores measuring $12.5\text{--}14.2 \times 8.2\text{--}9.5 \mu\text{m}$. *C. hainanensis* is characterized by having membranaceous basidiomata with smooth and grayish-orange to brownish orange hymenophore and fimbriate margin, and oblong-ellipsoid basidiospores measuring $9.8\text{--}12.2 \times 5.2\text{--}6.5 \mu\text{m}$. Descriptions and illustrations are provided for the two new species.

Keywords: wood-decaying fungi; corticioid fungi; brown rots; taxonomy; phylogeny; new species

INTRODUCTION

Coniophora DC. is one of the most important and widely distributed brown-rot corticioid genera. The genus is well-circumscribed in morphology, and characterized by the resupinate basidiomata usually with smooth and colored hymenophores, a monomitic hyphal system with simple-septate hyphae, usually absence of cystidia, and yellowish to yellowish-brown, thick-walled, smooth basidiospores with a dextrinoid reaction in Melzer's reagents, and growing on both angiosperm and gymnosperm wood (Bernicchia & Gorjón 2010). Phylogenetically, *Coniophora* formed a well-supported monophyletic clade in the Coniophoraceae, Boletales, and closely related to *Coniophoropsis* Hjortstam & Ryvarden. It differs from the other genera in the family in having ornamented basidiospores (Zhao *et al.* 2018). The species diversity of *Coniophora* in China is poorly known, and only limited species were reported from China (Li & He 2023; Yang *et al.* 2023).

Hainan Province is located at tropical areas and has extremely abundant plant and fungal resources in the tropical rain forests. Although many mycologists have carried out long-term studies on the species diversity of macro-fungi especially wood-inhabiting fungi in Hainan Province (Wang *et al.* 2021; Ma *et al.* 2022; Mao *et al.* 2023; Wang *et al.* 2023; Yuan *et al.* 2023; Zhang *et al.* 2023; Zhou *et al.* 2023; Liu *et al.* 2025), there are still many groups of wood-decaying fungi with inconspicuous basidiomata are under-collected and studied. During a comprehensive investigation and collection of corticioid fungi in Hainan Province in 2023, two undescribed species of *Coniophora* were found. They are described and illustrated in the present paper.

1 MATERIALS AND METHODS

1.1 Specimen collection and preservation

Field trips for specimen collection in the Hainan Tropical Rainforest National Park were carried out. Fresh specimens were dried with a portable mushroom drier (Evermat). Dried specimens were labelled and then stored in a refrigerator at minus 40 °C for at least two weeks. Voucher specimens are deposited at the fungarium of Beijing Forestry University, Beijing, China (BJFC).

1.2 Morphological studies

Microscopic examinations of thin, freehand sections were carried out with a Nikon Eclipse 80i microscope (Nikon Corporation) at magnifications up to 1 000×. Drawings were made with the aid of a drawing tube. Microscopic measurements and drawings were made from slides prepared from voucher tissues and stained with Cotton Blue (CB) and Melzer's reagent (IKI). The following abbreviations are used: KOH=2% potassium hydroxide, IKI=neither amyloid nor dextrinoid, IKI[+]=dextrinoid, CB=acyanophilous, L=mean spore length, W=mean spore width, Q=L/W ratios, n (a/b)=number of spores (a) measured from given number of specimens (b). Color codes and names follow Kornerup & Wanscher (1978).

1.3 DNA extraction and sequencing

The total genomic DNA was extracted from dried specimens by using CTAB plant genomic DNA extraction Kit (DN14, Aidlab Biotechnologies Co., Ltd). The ITS and nrLSU sequences were amplified with the primer pairs and PCR cycling procedures followed Li & He (2023). The PCR products were purified and sequenced at the Beijing Genomics Institute (BGI). All newly generated sequences were deposited in GenBank (<https://www.ncbi.nlm.nih.gov/>). BioEdit v.7.0.5.3 (Hall 1999) was used to review the chromatograms

and for contig assembly.

1.4 Phylogenetic analyses

The dataset of concatenated ITS-nrLSU sequences of *Coniophora* was analyzed, which included 40 ITS and 24 nrLSU sequences from 40 samples representing 20 ingroup taxa (Table 1). *Tapinella panuoides* (Fr.) E.-J. Gilbert was selected as the outgroup. The sequences were aligned separately using MAFFT v.7 (<http://mafft.cbrc.jp/alignment/server/>) and optimized manually in BioEdit v.7.0.5.3. Mesquite v.3.5.1 (Maddison & Maddison 2018) was used to concatenate the separate alignments. The final alignments and the topologies were deposited in TreeBase (<http://treebase.org/treebase-web/home.html>, submission ID: 32066).

Maximum parsimony (MP), maximum likelihood (ML) analyses and Bayesian inference (BI) were carried out by using PAUP* v.4.0b10 (Swofford 2002), RAxML v.8.2.10 (Stamatakis 2014) and MrBayes 3.2.6 (Ronquist *et al.* 2012), respectively. The methods and parameter setting of the phylogenetic analyses followed Li & He (2023). jModeltest v.2.17 (Darriba *et al.* 2012) was used to estimate the best-fit substitution models for BI. Four Markov chains were run for 2 000 000 for the dataset until the split deviation frequency value was lower than 0.01. Trees were sampled every 100th generation. The first quarter of the trees, which represented the burn-in phase of the analyses, were discarded, and the remaining trees were used to calculate posterior probabilities (BPP) in the majority rule consensus tree.

2 RESULTS

2.1 Phylogenetic analyses

The total aligned length of the concatenated dataset was 2 045 characters with 393 parsimony-informative. MP analysis yielded eight equally parsimonious trees (TL=933, CI=0.637, RI=0.832, RC=0.529, HI=0.363). The jModelTest suggested GTR+I+G as the best-fit model of nucleotide evolution for the dataset. The average standard deviation of split frequencies of BI was 0.007 360 at the end of the run. Only the MP tree is provided in Fig. 1 with the parsimony bootstrap values ($\geq 50\%$, first value), likelihood bootstrap values ($\geq 50\%$, second value) and Bayesian posterior probabilities (≥ 0.95 , third value) labelled along the branches. In the tree, the two undescribed species formed a strongly supported

lineage (100 100 1) sister to *Coniophora arida* (Fr.) P. Karst.

2.2 Taxonomy

Coniophora granulosa Y. Li, Q.Z. Zhu & S.H. He, sp. nov. Fig. 2

MycoBank: MB 858989

Etymology: “*Granulosa*”, refers to the granulose hymenophore due to the projecting hyphal pegs.

Diagnosis: *Coniophora granulosa* is characterized by coriaceous basidiomata with granulose hymenophore darkening in KOH, presence of hyphal pegs, the absence of cystidia, relatively large and ellipsoid basidiospores measuring $12.5\text{--}14.2 \times 8.2\text{--}9.5 \mu\text{m}$.

Holotype: China. Hainan Province, Ledong County, Jianfengling Nature Reserve, on fallen angiosperm trunk, 13 May 2023, He 7918 (BJFC 040105).

Description

Fruiting body: Basidiomata annual, resupinate, effused, closely adnate, inseparable from substrate, coriaceous, first as small patches, later confluent up to 9 cm long, 4 cm wide, $120 \mu\text{m}$ thick in section (aculei excluded). Hymenophore slightly granulose with protruding hyphal pegs, light orange (5A4) to grayish-orange (6B4) after dry, darkening in KOH, uncracked; margin determinate, indistinct, adnate, concolorous with or slightly darker than hymenophore surface. Context grayish-orange.

Hyphal structure: Hyphal system monomitic; generative hyphae simple-septate, IKI–, CB–; tissue darkening but otherwise unchanged in KOH.

Subiculum: Subiculum thin, indistinct; hyphae colorless to pale yellow, thin- to slightly thick-walled, smooth, infrequently branched, moderately septate, loosely interwoven, $2.5\text{--}4 \mu\text{m}$ in diam.

Hymenium: Subhymenium thickening, composed of collapsed hymenial elements, and basidiospores; hyphae colorless to pale yellow, thin-walled, smooth, frequently branched, rarely septate, densely interwoven, slightly agglutinated, $1.5\text{--}2 \mu\text{m}$ in diam. Hyphal pegs present, consist of pale yellow, sinuous, thick-walled hyphae. Cystidia absent. Basidia subcylindrical, slightly sinuous, colorless, thin-walled, smooth, with four sterigmata and a basal simple septum, $40\text{--}70 \times 7.5\text{--}14 \mu\text{m}$; basidioles in shape similar to basidia but slightly smaller.

Table 1 Taxa information and GenBank accession numbers of the sequences used in phylogenetic analyses

Species	Voucher No.	Locality	GenBank accession number		References
			ITS	nrLSU	
<i>Coniophora arida</i>	FP-104367	USA	GU187510	GU187573	Binder <i>et al.</i> (2010)
<i>Coniophora arida</i>	CBS 109.40	USA	MH856052	MH867547	Vu <i>et al.</i> (2018)
<i>Coniophora arida</i>	Ca30M-20Aa	Poland	MT939247	—	Pusz <i>et al.</i> (2020)
<i>Coniophora arida</i>	He 4658	China	MG763875	MH476322	Zhao <i>et al.</i> (2018)
<i>Coniophora beijingensis</i>	He 6635	China	MW192496	MW191807	Li & He (2023)
<i>Coniophora beijingensis</i>	He 6920	China	MW192497	MW191808	Li & He (2023)
<i>Coniophora beijingensis</i>	He 6926	China	MW192498	MW191809	Li & He (2023)
<i>Coniophora bimacrospora</i>	MUCL 45009	Ethiopia	MK677453	—	Dueñas <i>et al.</i> (2023)
<i>Coniophora cerebella</i>	HK '8'	USA	GU187513	GU187569	Binder <i>et al.</i> (2010)
<i>Coniophora cystidiophora</i>	CBS 153.33	Germany	MH855390	MH866840	Vu <i>et al.</i> (2018)
<i>Coniophora eremophila</i>	MA-Fungi 86371	Cape Verde	HG326617	—	Unpublished
<i>Coniophora eremophila</i>	MA-Fungi 86372	Cape Verde	HG326618	—	Unpublished
<i>Coniophora eremophila</i>	Gilbertson 10925	USA	HF921465	—	Unpublished
<i>Coniophora fusispora</i>	MA-Fungi 57734	France	HF921467	—	Unpublished
<i>Coniophora fusispora</i>	He 6777	China	MW192495	MW191806	Li & He (2023)
<i>Coniophora granulosa</i>	He 7918	China	PV261140	PV259698	Present study
<i>Coniophora hainanensis</i>	He 7931	China	PV261141	PV259699	Present study
<i>Coniophora hanoiensis</i>	He 5197	Vietnam	MG763873	—	Zhao <i>et al.</i> (2018)
<i>Coniophora hanoiensis</i>	He 5202	Vietnam	MG763874	MH476323	Zhao <i>et al.</i> (2018)
<i>Coniophora hanoiensis</i>	Ryvarden 24995	Zimbabwe	HF921468	—	Unpublished
<i>Coniophora marmorata</i>	MUCL 31667	Belgium	GU187515	GU187571	Binder <i>et al.</i> (2010)
<i>Coniophora marmorata</i>	P 307	UK	AJ518880	AJ583427	Moreth & Schmidt (2005), Schmidt <i>et al.</i> (2002)
<i>Coniophora merulioides</i>	CBS 152.35	Germany	MH855612	MH867121	Vu <i>et al.</i> (2018)
<i>Coniophora mollis</i>	Prem 36877	South Africa	HF921469	—	Unpublished
<i>Coniophora olivacea</i>	He 6100	China	OM100743	OM083975	Li & He (2023)
<i>Coniophora olivacea</i>	He 6111	China	OM100744	OM083976	Li & He (2023)
<i>Coniophora olivacea</i>	FP-104386	USA	GU187516	GU187572	Binder <i>et al.</i> (2010)
<i>Coniophora prasinoidea</i>	MA-Fungi 19417	USA	AJ419197	—	Martin & Raidl (2002)
<i>Coniophora prasinoidea</i>	Bochum 178449	Germany	HF912261	—	Unpublished
<i>Coniophora prasinoidea</i>	FP-105969	USA	GU187519	GU187576	Binder <i>et al.</i> (2010)
<i>Coniophora opuntiae</i>	AH31855	Spain	FJ790314	—	Blanco <i>et al.</i> (2009)
<i>Coniophora opuntiae</i>	MA-Fungi 6901	Spain	HF921475	—	Unpublished
<i>Coniophora puteana</i>	He 2909	China	MG763876	MH476324	Zhao <i>et al.</i> (2018)
<i>Coniophora puteana</i>	MUCL 1000	Germany	GU187521	GU187578	Binder <i>et al.</i> (2010)
<i>Coniophora puteana</i>	CBS 148.32	Germany	MH855248	MH866701	Vu <i>et al.</i> (2018)
<i>Coniophora</i> sp.	UFMGCB 1045	Brazil	FJ605253	—	Unpublished
<i>Coniophora</i> sp.	Olrim 361	Sweden	AY781253	—	Vasiliauskas <i>et al.</i> (2005)
<i>Coniophora yunnanensis</i>	CLZhao 3517	China	OP901836	—	Yang <i>et al.</i> (2023)
<i>Coniophora yunnanensis</i>	CLZhao 3577	China	MK268870	OP904195	Yang <i>et al.</i> (2023)
<i>Coniophora yunnanensis</i>	CLZhao 3594	China	OP901837	OP904196	Yang <i>et al.</i> (2023)
Outgroup					
<i>Tapinella panuoides</i>	Dai 22696	China	OL457982	OL457450	Unpublished
<i>Tapinella panuoides</i>	He 6538	China	MW192499	MW191810	Li & He (2023)

Note: New taxa are in bold.

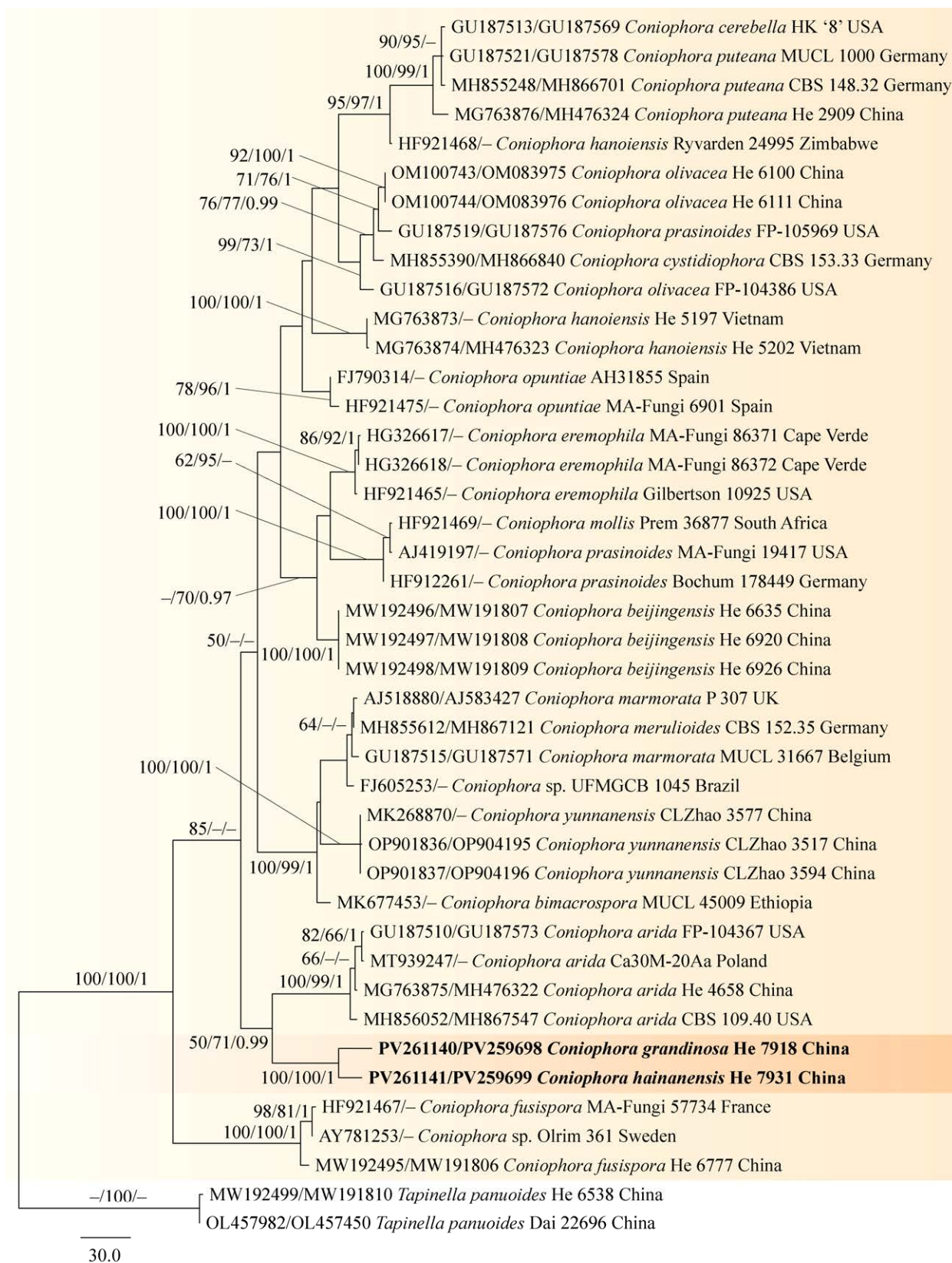


Fig. 1 Phylogenetic tree of MP analysis from the ITS-nrLSU sequences of *Coniophora*. The parsimony bootstrap values ($\geq 50\%$, first), likelihood bootstrap values ($\geq 50\%$, second) and Bayesian posterior probabilities (≥ 0.95 , third) are shown on the branches. New species are set in bold and highlighted.

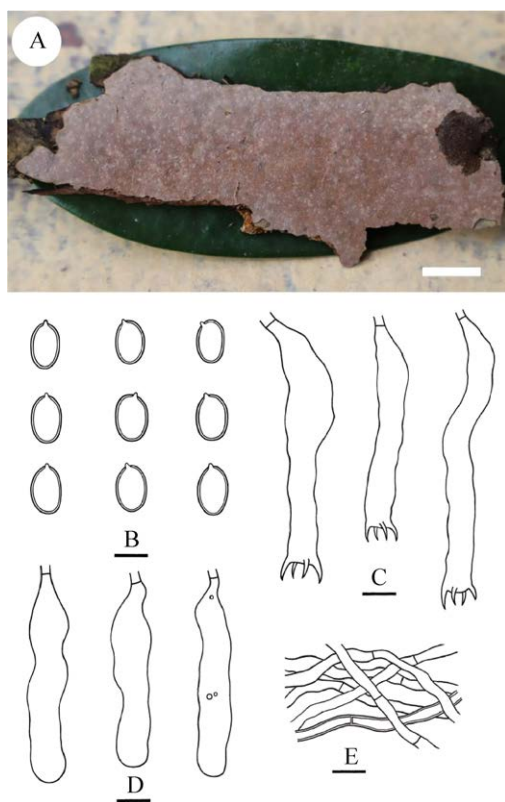


Fig. 2 *Coniophora granulosa* (the holotype, He 7918). A: Basidioma; B: Basidiospores; C: Basidia; D: Basidioles; E: Hyphae from subiculum. Bars: A=1 cm, B–E=10 μ m.

Spores: Basidiospores ellipsoid, yellowish to brownish, thick-walled, smooth, IKI[+], CB–, (12.2–)12.5–14.2(–14.8) $\times$ (8–)8.2–9.5(–9.8) μ m, L=13.6 μ m, W=8.9 μ m, Q=1.53 (n=30/1).

Coniophora hainanensis Y. Li, Q.Z. Zhu & S.H. He, *sp. nov.* Fig. 3

MycoBank: MB 858990

Etymology: “*Hainanensis*”, refers to the type locality, Hainan Province, southern China.

Diagnosis: *Coniophora hainanensis* is characterized by membranaceous basidiomata with smooth hymenophore that slightly darkening in KOH, fimbriate margin, the absence of cystidia, and oblong-ellipsoid basidiospores measuring 9.8–12.2 $\times$ 5.2–6.5 μ m.

Holotype: China. Hainan Province, Ledong County, Jianfengling Nature Reserve, on fallen angiosperm trunk, 14 May 2023, He 7931 (BJFC 040118).

Description

Fruiting body: Basidiomata annual, resupinate,

effused, closely adnate, inseparable from substrate, membranaceous, first as small patches, later confluent up to 6 cm long, 5 cm wide, 100 μ m thick in section. Hymenophore smooth, grayish-orange (5B3) to brownish-orange (5C3) after dry, slightly darkening in KOH, uncracked; margin thinning out, adnate, fimbriate, white when fresh, distinct, up to 0.5 cm wide. Context grayish-orange.

Hyphal structure: Hyphal system monomitic; generative hyphae simple-septate, IKI–, CB–; tissue slightly darkening but otherwise unchanged in KOH.

Subiculum: Subiculum distinct; hyphae colorless to pale yellow, thin- to slightly thick-walled, smooth, moderately branched and septate, interwoven, slightly agglutinated, 2–4.5 μ m in diam.

Hymenium: Subhymenium thin; hyphae colorless, thin-walled, smooth, frequently branched, moderately septate, densely interwoven, 2–3 μ m in diam. Cystidia absent. Basidia subclavate, slightly sinuous, colorless, thin-walled, smooth, with four sterigmata and a basal simple septum, 28–46 $\times$ 6–9 μ m; basidioles in shape similar to basidia but slightly smaller.

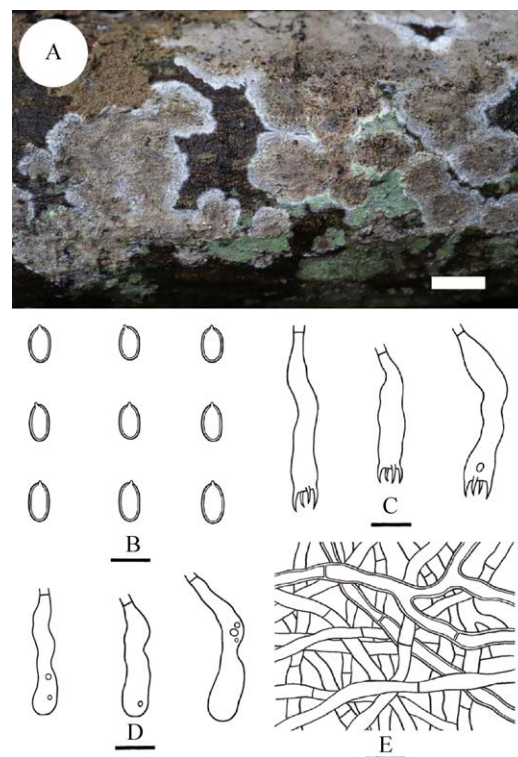


Fig. 3 *Coniophora hainanensis* (the holotype, He 7931). A: Basidiomata; B: Basidiospores; C: Basidia; D: Basidioles; E: Hyphae from subiculum. Bars: A=1 cm, B–E=10 μ m.

Spores: Basidiospores oblong-ellipsoid, pale yellowish, thick-walled, smooth, IKI[+], CB–, (9–)9.8–12.2(–12.5) × (5–)5.2–6.5 µm, L=11 µm, W=5.9 µm, Q=1.86 (n=30/1).

3 DISCUSSION

Coniophora granulosa is characterized by having coriaceous basidiomata, light orange to grayish-orange and granulose hymenophores, relatively large and yellowish to brownish basidiospores. Phylogenetically, *C. granulosa* is closely related to *C. arida* (Fr.) P. Karst. Both species share simple-septate generative hyphae and similar sized basidia and basidiospores. However, *C. arida* can be easily distinguished from *C. granulosa* by having smooth and pale yellowish to brown hymenophores, and fimbriate margin (Bernicchia & Gorjón 2010). *Coniophora yunnanensis* Y. Yang & C.L. Zhao, recently reported from southern China, is similar to *C. granulosa* by having odontoid hymenophores and simple-septate generative hyphae, but differs by having ceraceous and olivaceous buff basidiomata when fresh, smaller ovoid to broadly ellipsoid basidiospores (8.5–12.5 × 6.5–8.5 µm, Yang *et al.* 2023).

Coniophora hainanensis is characterized by having membranaceous basidiomata, grayish-orange to brownish-orange and smooth hymenophores, fimbriate margin, oblong-ellipsoid and pale yellowish basidiospores. In the phylogenetic tree, *C. hainanensis* clustered together with *C. granulosa*, which can be easily distinguished by having coriaceous basidiomata, granulose hymenophores, larger basidia and basidiospores. *Coniophora olivacea* (Fr.) P. Karst. resembles *C. hainanensis* by having membranaceous basidiomata, white and fimbriate margin, similar sized basidia and basidiospores, but differs by having gray-brownish to brown-olivaceous basidiomata, cylindrical and long cystidia (Bernicchia & Gorjón 2010).

Author contributions

LI Yue and ZHU Qizhi performed the experiment, and wrote the original draft; HE Shuanghui designed the project, collected samples, reviewed and edited the manuscript; HE Shuanghui and ZHU Anhong supervised the project.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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