



Taxonomy, phylogeny and ecology of a new bambusicolous *Resupinatus* species (Agaricales, Resupinataceae) from Northern Thailand

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Abstract

The exploration of the fungal diversity associated with bamboos in Northern Thailand has yielded a hitherto undescribed species, *Resupinatus reviviscens* sp. nov. It is characterized by brownish grey to dark grey basidiomata, basal hairs forming an off-white to yellowish grey subiculum-like felt and composed of hyphae that are thin-walled near the apex and thick-walled near the base, broadly ellipsoid to ellipsoid basidiospores, lack of cheilocystidia and presence of clavate pleurocystidia, and habitat on bamboo culms. Additionally, it has distinct ITS sequences and forms a supported species-level clade separated from other *Resupinatus* species as revealed by the ML phylogenetic analysis combining ITS and LSU sequences.

Key words: 1 new species, Bamboo, Basidiomycota, cyphelloid mushrooms, Pleurotineae, tropical Asia

Introduction

Resupinatus Nees ex Gray (1821:617) are characterized by their small and resupinate morphology, with partially gelatinized context and clamped hyphae (Singer 1962; Thorn & Barron 1986). These saprotrophic, usually lignicolous fungi are typically found on the underside of decaying woody material and herbaceous debris (Thorn *et al.* 2005). Forty-eight species of *Resupinatus* have been recorded (He *et al.* 2019; *Species Fungorum* 2024).

Morphologically *Resupinatus* resembles *Hohenbuehelia* Schulzer (1866); both share characteristics including a gelatinized trama and inamyloid basidiospores (McDonald 2015; Thorn *et al.* 2005). Conversely to *Hohenbuehelia*, the pileipellis and assimilative (as observed from cultures) hyphae of *Resupinatus* are diverticulate and possess tapering pegs. The genus also lacks a nematophagous asexual morph (Consiglio *et al.* 2018; Thorn *et al.* 2005). Until recently, the phylogenetic placement of *Resupinatus* was uncertain. The genus had been classified within various families without significant phylogenetic support or designated as incertae sedis within the Agaricales (Vizzini *et al.* 2024). Numerous phylogenetic studies have supported a close relationship between *Resupinatus*, *Hohenbuehelia*, and *Pleurotus* (Fr.) P. Kumm. (1871) within Pleurotaceae, consistent with morphological observations (Justo *et al.* 2011; Matheny *et al.* 2006). However, *Resupinatus* also exhibits distinct differences from the latter two genera, suggesting its placement close to but not within Pleurotaceae, as indicated by Consiglio *et al.* (2018) and McDonald (2015). Correspondingly, some scholars (Jülich 1981; Kalichman *et al.* 2020) have proposed placing *Resupinatus* in a standalone family, the Resupinataceae. It is only recently that a comprehensive study of Agaricales (Vizzini *et al.* 2024) provided significant phylogenetic evidence supporting the resurrection of Resupinataceae. This family clusters with Fistulinaceae, Pleurotaceae, and Schizophyllaceae, forming the Pleurotineae.

The genus has been the subject of extensive taxonomic scrutiny globally. However, published data on *Resupinatus* in Thailand (Harms *et al.* 2023) only include identification to genus level. Data about this genus in Thailand is scarce despite the rich diversity of mushrooms in the country (e.g., Thongbai *et al.* 2018). This study reveals a new species

of *Resupinatus* from Thailand. Our analysis includes morphological descriptions, ecological considerations, and molecular investigations to ascertain its taxonomic position within *Resupinatus*.

Materials and methods

Specimens were collected during the rainy season (June to October) of 2022 in Chiang Rai and Chiang Mai Provinces, Northern Thailand. For each collection, photographs of fresh basidiomata were taken in the field or in the lab, and notes such as location, forest type, habit, habitat and substrate were recorded. Macromorphology was described based on the fresh materials and colours were coded following Kornerup & Wanscher (1963). Specimens were dried in a hot air dryer with temperature from 40 to 60 °C for ca. 24 hours or until specimens were completely dried and then preserved in ziplocked plastic bags. Dried specimens were later deposited in the Mae Fah Luang University Herbarium (MFLU). The micromorphology was examined from dry specimens. Thin sections were made by free hand with a razor blade using a stereo microscope Zeiss Stemi 305, and mounted in water, 5% KOH and 1% Congo red. Microscopic structures were observed, photographed and measured using a compound microscope Olympus BX53. The measurements of 15–70 basidiospores, 10–30 basidia, and 10 pleurocystidia were taken from each specimen using cellSens version 4. The notation [x, y, z] indicates that measurements were made on x basidiospores from y basidiomes in z collections. The dimensions of microscopic structures are given as follows: (a–)b–c–d(–e), in which c represents the average, b the 5th percentile, d the 95th percentile and minimum and maximum values a and e are shown in parentheses. Q, the length/width ratio of the spores is given in the same format.

DNA extraction, PCR, sequencing and sequence analyses

DNA was extracted by using a CTAB extraction protocol slightly modified from Doyle & Doyle (1990). The ITS region of rDNA, including ITS1–5.8S–ITS2, was amplified using the primers ITS1-F (Gardes & Bruns 1993) and ITS4 (White *et al.* 1990). Part of the nuclear rDNA large subunit was amplified using the primers LR0R and LR5 (Vilgalys & Hester 1990). The PCR cycling conditions for ITS and nrLSU were as follows: 3 min at 94 °C; 35 cycles of 30 s at 94 °C, 30 s at 52 °C, 1 min at 72 °C; 10 min at 72 °C. Sequences were edited and contigs assembled using SeqMan (DNASTAR, Madison, WI, USA), visually checked for quality, then blasted against the GenBank database.

Sequence alignment and phylogenetic analyses

Sequences from 45 specimens were retrieved from GenBank and included in the ingroup along with the fourteen newly generated sequences. Sequences from *Hohenbuehelia flabelliformis* Phonemany & Raspé (2023:115), *H. lageniformis* Phonemany & Raspé (2023:118), and *H. thornii* Consiglio & Setti (2017a:1) were used as outgroup. The sequences were aligned separately for each gene region with MAFFT version 7 (Kato *et al.* 2018) then checked and edited where necessary in Bioedit version 7.0.5 (Hall 1999). Ambiguously aligned positions were removed with TrimAl (Capella-Gutiérrez *et al.* 2009), with the strict automatic run parameter. Because 5.8S was highly conserved and showed only one parsimony-informative site in the ingroup, this gene was removed from the alignment.

Phylogenies and node support were first inferred by maximum likelihood (ML) from the two single-gene alignments separately, using RAxML-HPC2 version 8.2.12 (Stamatakis 2014) with 1,000 rapid bootstraps, as implemented on the CIPRES portal (Miller *et al.* 2010). Since there was no supported conflict (MLBS \geq 70%), the two single-gene alignments were concatenated with SequenceMatrix (Vaidya *et al.* 2011). This alignment was deposited in Zenodo (doi: 10.5281/zenodo.14046659). A second, partitioned ML analysis was performed on the concatenated data set, with two character sets, ITS1+ITS2 and LSU. For Bayesian Inference (BI), the best substitution model for each character set was determined with jModeltest 2.1 (Darriba *et al.* 2012) on CIPRES, using the Akaike information criterion and limiting the search to models that are implementable in MrBayes. The inferred best-fit models were GTR+G for ITS1+ITS2 and GTR+I+G for LSU. Partitioned Bayesian analysis was performed using MrBayes version 3.2.7a (Ronquist 2012) as implemented on the CIPRES portal (Miller *et al.* 2010). Two runs of four chains each were conducted for 2,000,000 generations and sampled every 200 generations. At the end of the run, the average standard deviation of split frequencies was checked to be lower than 0.01, and convergence was further assessed by checking that ESS values exceeded 200 for all parameters and that the PSRF values were close to 1. The log-likelihood scores for all sampling points were analysed using Tracer (Rambaut *et al.* 2018) to determine the appropriate burn-in phase. A

50% majority consensus tree and associated posterior probabilities were then computed after excluding the first 40% of samples as burn-in phase. A clade was considered to be supported if showing a BS \geq 70% and a posterior probability (PP) \geq 0.90.

TABLE 1. GenBank accession numbers of sequences used in the phylogenetic analyses. The newly-generated sequences in this study are presented in bold, “-” refers to the unavailability of sequence.

Species	Country	Voucher code	ITS	nrLSU	Reference
<i>Hohenbuehelia flabelliformis</i>	Thailand	MFLU22 0008 TYPE	OP236779	OM521957	Phonemany <i>et al.</i> (2023)
<i>Hohenbuehelia lageniformis</i>	Thailand	MFLU22 0010 TYPE	OP236781	OM521958	Phonemany <i>et al.</i> (2023)
<i>Hohenbuehelia thornii</i>	Italy	AMB 18086 TYPE	NR_166381	KU355400	Consiglio & Setti (2018)
<i>Resupinatus alboniger</i>	USA	iNaturalist 146929499	OR081334	-	Unpublished
<i>Resupinatus americanus</i>	USA	RC19101201	OM397444	-	Unpublished
<i>Resupinatus applicatus</i>	Italy	AMB 18075 Epitype	KU355368	KU355411	Consiglio & Setti (2018)
<i>Resupinatus applicatus</i>	France	PB335	AY571059		Bodensteiner <i>et al.</i> (2004)
<i>Resupinatus “applicatus”</i>	New Zealand	PDD:95777	HQ533025		Unpublished
<i>Resupinatus cinerascens</i>	Australia	G1711	-	MK278551	Varga <i>et al.</i> (2019)
<i>Resupinatus conspersus</i>	Ecuador	C61852	AY571061	AY571024	Bodensteiner <i>et al.</i> (2004)
<i>Resupinatus dealbatus</i>	USA	iNaturalist 14815677	ON416908	-	Unpublished
<i>Resupinatus europaeus</i>	Italy	AMB 18077 Neotype	KU355366	KU355410	Consiglio & Setti (2018)
<i>Resupinatus griseopallidus</i>	Spain	Blasco	MG553642	MG553649	Consiglio & Setti (2017b)
<i>Resupinatus hausknechtii</i>	Austria	WU 7659 TYPE	KU355370	KU355412	Consiglio & Setti (2018)
<i>Resupinatus kavinae</i>	Spain	AVM 3128	MG553643	MG553650	Consiglio & Setti (2017b)
<i>Resupinatus niger</i>	Italy	MCVE 10781 Holotype	KU355331	KU355395	Consiglio & Setti (2018)
<i>Resupinatus niger</i>	Italy	AMB 18095 Neotype	KU355371	KU355413	Consiglio & Setti (2018)
<i>Resupinatus niger</i>		Roux 3740	KU355372	KU355414	Consiglio & Setti (2018)
<i>Resupinatus niger</i>	Turkey	oka263	OL693686		Demirak Sengul & Kaygusuz (2021)
<i>Resupinatus odoratus</i>	India	TBGT17789	MT452498	-	Bijeesh <i>et al.</i> (2020)
<i>Resupinatus poriiformis</i>	Canada	CBS 327 91	AY571062	AY571025	Bodensteiner <i>et al.</i> (2004)
<i>Resupinatus poriiformis</i>	UK	K(M):180118	MZ159469	-	Unpublished
<i>Resupinatus porosus</i>	USA	CFMR PR-5832 Paratype	NR_119556	-	Schoch <i>et al.</i> (2014)
<i>Resupinatus reviviscens</i>	Thailand	MFLU24-0230	PQ036933	PQ036939	This study
<i>Resupinatus reviviscens</i>	Thailand	MFLU24-0231	PQ036934	PQ036940	This study
<i>Resupinatus reviviscens</i>	Thailand	MFLU24-0232	PQ036935	PQ036941	This study
<i>Resupinatus reviviscens</i>	Thailand	MFLU24-0233	PQ036937	PQ036942¹ PQ570401²	This study
<i>Resupinatus reviviscens</i>	Thailand	MFLU24-0234	PQ036938	PQ036943¹ PQ570402²	This study
<i>Resupinatus rouxii</i>	Spain	ERD 9463	OP289290	-	Unpublished

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TABLE 1 (Continued)

Species	Country	Voucher code	ITS	nrLSU	Reference
<i>Resupinatus rouxii</i>	Switzerland	Z ZT 971	MH168326	MH190787	Consiglio & Setti (2018)
<i>Resupinatus</i> sp.	USA	TENN F 63042	KP026232	-	Unpublished
<i>Resupinatus</i> sp.	Germany	TENN F 67920	KP026233	-	Unpublished
<i>Resupinatus</i> sp.	Thailand	RSPG00698	OL672739	-	Unpublished
<i>Resupinatus</i> sp.	China	HMJAU7036	GQ142021	-	Unpublished
<i>Resupinatus</i> sp.	USA	TENN F 60481	KP026230	-	Petersen <i>et al.</i> (2015)
<i>Resupinatus</i> sp.	USA	TENN F 62209	KP026229	-	Petersen <i>et al.</i> (2015)
<i>Resupinatus</i> aff. <i>trichotis</i>	USA	TENN F 63042	KP026231	-	Unpublished
<i>Resupinatus</i> sp. PA-2015b	Italy	Thorn 870601/19 ALV5614	KU355376	-KU355415	Consiglio & Setti (2018)
<i>Resupinatus</i> sp. ‘trichotis-IN01’	USA	iNaturalist 129942182	OP549157	-	Unpublished
<i>Resupinatus</i> sp. ‘trichotis-IN01’	USA	iNaturalist 39114228	ON561766	-	Unpublished
<i>Resupinatus</i> sp. ‘trichotis-IN01’	USA	iNaturalist 57471425	ON059263	-	Unpublished
<i>Resupinatus</i> sp.	Thailand	OR1781	PQ475810	PQ036943	This study
<i>Resupinatus</i> sp.	USA	iNaturalist 146745663	OQ540553	-	Unpublished
<i>Resupinatus</i> sp.	USA	iNaturalist 91751864	OQ389423	-	Unpublished
<i>Resupinatus</i> sp.	USA	Mushroom Observer 488179	OP327381	-	Unpublished
<i>Resupinatus</i> sp.	Singapore	SL1552	OR636177	-	Unpublished
<i>Resupinatus striatulus</i>	France	Wilhelm 1504 Neotype	KU355374	-	Consiglio & Setti (2018)
<i>Resupinatus striatulus</i>	France	Wilhelm 5316	MH137831	MH169342	Consiglio & Setti (2018)
<i>Resupinatus striatulus</i>	Germany	KR M 053702	MW035051	-	Lotz-Winter <i>et al.</i> (2021)
<i>Resupinatus striatulus</i>	USA: Arizona	MO527419	PP047668	-	Unpublished
<i>Resupinatus taxi</i>	USA	TENN 074428	MH558280	-	Unpublished
<i>Resupinatus trichotis</i>	Italy	AMB 18074 Epitype	KU355378	KU355416	Consiglio & Setti (2018)
<i>Resupinatus vinosolidus</i>	New Zealand	ICMP:16568	MZ325958	-	Unpublished
<i>Resupinatus yunnanensis</i>	China	CLZhao 8651 Holotype	OP901839	OP904197	Yang <i>et al.</i> (2023)
<i>Resupinatus yunnanensis</i>	China	CLZhao 7168	OP901838	-	Yang <i>et al.</i> (2023)

¹ Haplotype 1 (longer haplotype)

² Haplotype 2 (shorter haplotype)

Results

Phylogenetic analyses

The combined matrix contained 1,193 nucleotide sites (ITS1+ITS2: 1–300; LSU: 301–1,193) and had 190 distinct patterns for ITS1+ITS2, and 201 distinct patterns for LSU. ML and BI analyses generated nearly identical tree topologies. Thus, only the BI tree is displayed (Figure 1). All collections of the novel species formed a clade with high BIPP (0.90) but no significant MLBS support. A larger clade encompassing *R. reviviscens*, *Resupinatus* sp. “*trichotis*” (iNaturalist numbers 39114228, 57471425, and 129942182) and *R. aff. trichotis* (TENN-F-63042) was strongly

supported by both MLBS (93%) and BIPP (1.0). All the sequences within this clade could thus represent a single species with intraspecific variation or distinct, closely related species. Further molecular and morphological analyses are required to help clarify species boundaries.

Another of our collections (OR1781) was phylogenetically isolated from all others and potentially represents yet another novel species. However, more specimens are needed to properly describe that species.

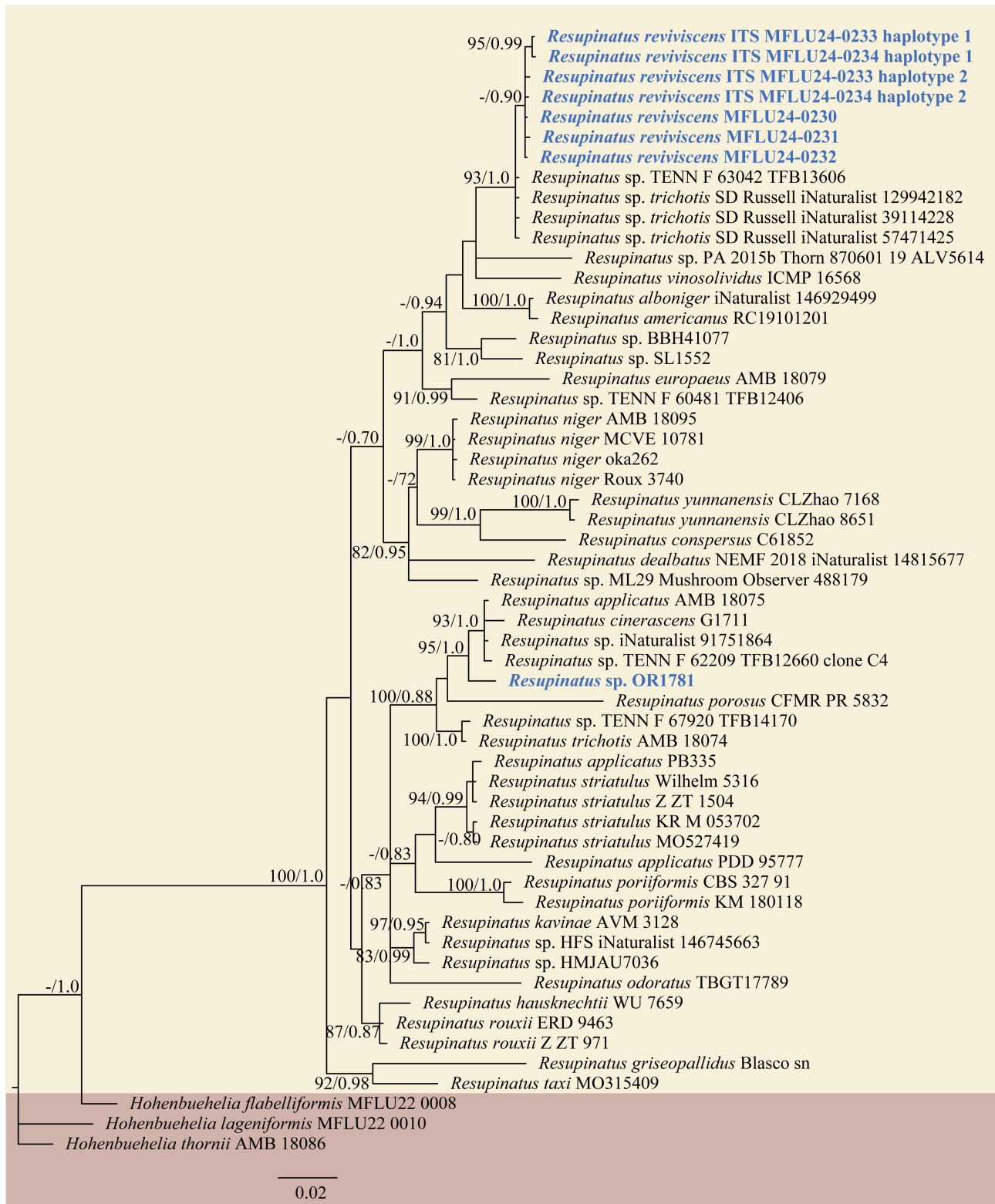


FIGURE 1. Fifty percent majority rule consensus tree generated by Bayesian analysis from combined ITS and LSU sequence data. Maximum likelihood bootstrap support values $\geq 70\%$ and Bayesian posterior probabilities ≥ 0.90 are indicated at the nodes. Lower values are indicated by a dash (-). The new species are in bold blue font.

Taxonomy

Resupinatus reviviscens Carpouren & Raspé, *sp. nov.* Figure 2

Etymology:—The specific epithet “*reviviscens*”, from Latin, refers to the ability of basidiomes to withstand drying.

Holotype:—THAILAND. Chiang Mai Province, Mae On District, Huay Kaew, 3 July 2022, *Olivier Raspé 1769* (MFLU24-0233).

Diagnosis:—*Resupinatus reviviscens* most resembles *R. applicatus* and *R. trichotis* but differs in having hyaline to yellowish basal hairs forming an off-white to yellowish grey subiculum-like felt, broadly ellipsoid to ellipsoid basidiospores, and clavate pleurocystidia.

Mycobank:—856548

Basidiomata astipitate, small, gregarious, attached dorsally, laterally or eccentrically, fleshy, leathery, hard when dry; base covered with coarse surface hairs forming a dense, off-white to yellowish grey mat near the point of attachment. *Pileus* 3–7 mm diameter, cupuliform when young, convex to plano-convex, and subcircular to rounded-flabelliform or flabelliform when mature; surface even and entirely covered with whitish minute pubescence when young, becoming radially rugulose-veined, sparsely mechulose and moist-hygrophanous except near the point of attachment, where it is densely covered by an off-white to greyish yellow strigose felt, brownish-grey to dark grey, light yellowish grey towards the margin; margin straight to slightly involute, striate; context greyish, gelatinous. *Lamellae* yellowish grey to brownish grey, moderately close to sub-distant, thick, with 1–3 unequal lamellulae. Stipe absent. *Odor and taste* not recorded.

Basidiospores (3.8–)4.4–5.7–6.8(–7.6) × (2.8–)3.2–3.9–5(–5.8) μm {N=204,5,5}, broadly ellipsoid to ellipsoid, smooth, inamyloid, thin-walled, guttulate, hyaline. *Basidia* (17.4–)18.2–23.3–28.8(–30.4) × (4.1–)4.5–5.8–7(–7.4) μm {N=105,5,5}, 4-sterigmate, clavate to cylindrico-clavate, hyaline in KOH. *Pleurocystidia* (29.5–)30.1–34.8–40.1(–42.9) × (5.3–)5.6–6.9–8.9(–11.4) μm {N=47,4,4}, clavate, slightly thick-walled. *Subhymenium* compact and light brown. *Hymenophoral trama* subregular, with hyphae imbedded in a gelatinous matrix. *Pileal trama* monomitic, gelatinized, composed of branched, loosely interwoven hyphae, 3.3–4.1 μm broad, thin-walled, hyaline. *Pileipellis* a cutis composed of compact, interwoven layer of 2.3–5.5 μm broad hyphae with thin walls that are lightly encrusted with brownish and highly refractive materials. *Clamp connections* present in all tissues. *Basal hairs* composed of hyaline, frequently clamped hyphae that are thick-walled, dense and compacted near the base, loosely interwoven, thin-walled near the end, hyaline in isolation to greyish yellow in the mass, 3.0–4.2 μm in diam.

Habitat and distribution:—Gregarious on dead bamboo branches suspended or still attached to bamboo culms, in dry dipterocarp forests in Northern Thailand.

Ecology:—All collections of the new species were made on dead bamboo branches suspended or still attached to bamboo culms. In this environment, solar radiation and wind exposure is high and humidity level is low relative to other bamboo parts or debris fallen on the ground. Moreover, all specimens occurred in dry dipterocarp forests at the beginning of the rainy season, where and when temperature and humidity can reach challenging levels. Correspondingly, the basidiomes of *Resupinatus reviviscens* display a remarkable resistance to desiccation, capable of surviving dry conditions and fully recovering upon rehydration. This ability to revive after receiving moisture classifies them as truly reviviscent.

Additional materials examined (paratypes):—THAILAND. Chiang Mai Province, Mae Taeng District, Pa Pae, Baan Tha Pha, 4 August 2022, *Olivier Raspé 1833* (MFLU-0234); Chiang Rai Province, Mueang Chiang Rai, Doi Pui community forest, 22 June 2022, *Olivier Raspé 1764* (MFLU-0230); *ibid.*, 22 June 2022, *Olivier Raspé 1766* (MFLU-0231); *ibid.*, 22 June 2022, *Olivier Raspé 1767* (MFLU-0232).

Notes:—*R. reviviscens* mostly resembles *R. applicatus* (Batsch) Gray (1821: 617), *R. striatulus* (Pers.) Murrill (1915: 242) and *R. trichotis* (Pers.) Singer (1961: 48) in terms of basidiome color, size, and shape. In fact, the latter three species have long been considered as a single species owing to their numerous morphological similarities (Consiglio & Setti 2018). The basidiome shapes of all four species are similar and their sizes fall more or less within the same range (Consiglio & Setti 2018; McDonald 2015; Thorn & Barron 1986). Moreover, the basidiome colour of *R. reviviscens* is similar to *R. applicatus* and *R. trichotis* but differs at the margin where it is lighter in colour (Table 2).

The hairs forming a subiculum-like felt at the base of the basidiomes is an important distinguishing feature in *Resupinatus* (Consiglio & Setti 2018; McDonald 2015). The off-white to greyish yellow hairs near the zone attached to the substratum is a characteristic macroscopic feature in *Resupinatus reviviscens* and a marked distinction from *R. trichotis*, which features black basal hairs (Consiglio & Setti 2018; McDonald 2015). Correspondingly, these basal

hairs possess dark brown parietal and/or intracellular pigments in *R. trichotis* (Consiglio & Setti 2018) whereas they are mostly hyaline to greyish yellow in *R. reviviscens*. *R. reviviscens* also differs from *R. applicatus* and *R. trichotis* in its spore shape and size. Its spores resemble mostly those of *R. cyathae* Corner (1996: 125) which are ellipsoid and $4.5\text{--}6 \times 3.5\text{--}4 \mu\text{m}$ (Corner 1996). A morphological comparison between *R. reviviscens* and its closely related species is given in Table 2.

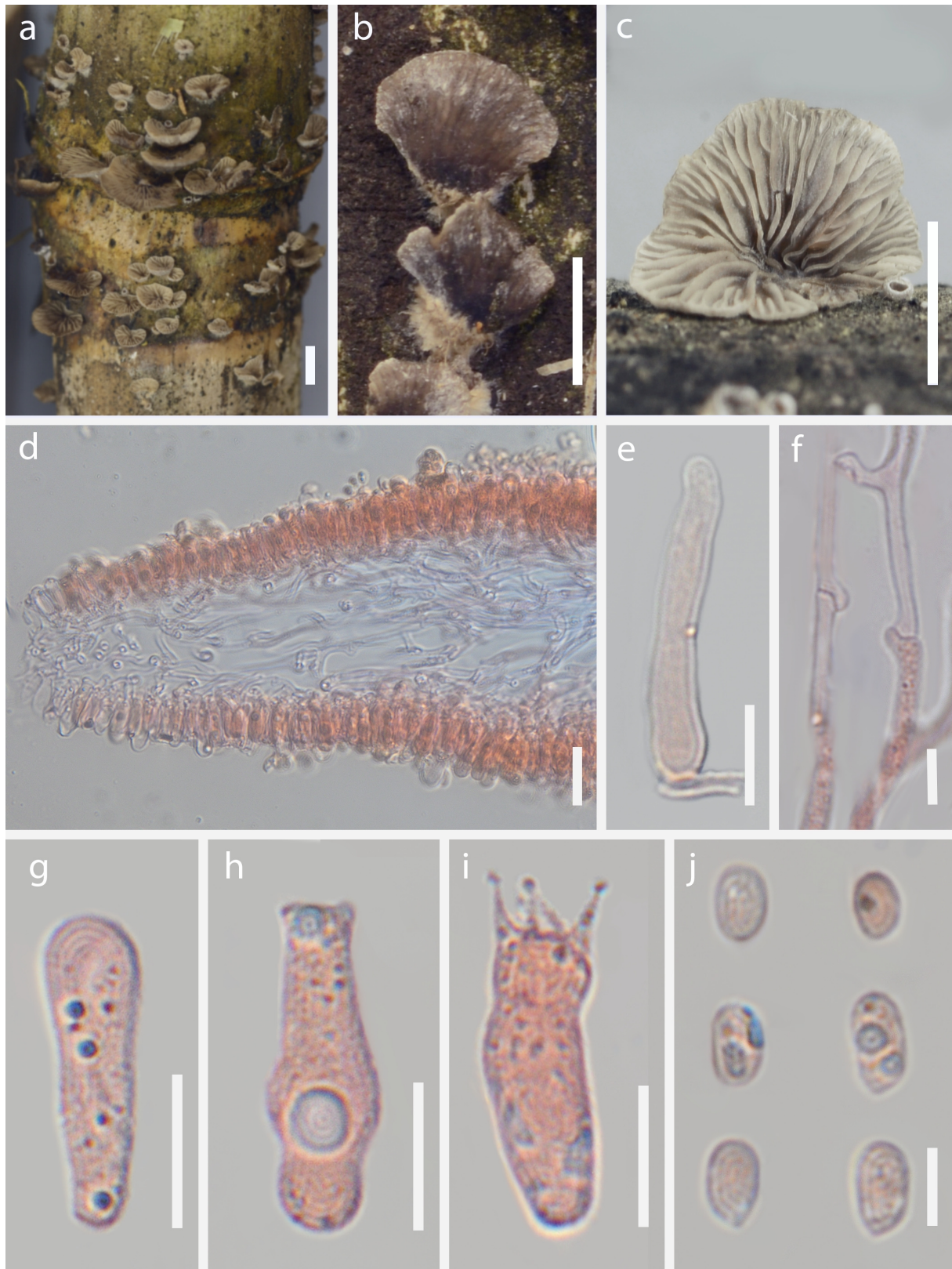


FIGURE 2. *Resupinatus reviviscens*: holotype, MFLU-0233 (OR1769). a–c) Basidiomata, d) Cross section of lamella, e) Pleurocystidia, f) Hyphae of hymenophore trama showing clamp connections, g) Basidiolae, h–i) Basidia, j) Basidiospores. Scale bars: a–c = 5 mm, d = 30 μm , e–i = 10 μm , j = 5 μm .

TABLE 2. Comparison of *Resupinatus reviviscens* and closely related species.

Species name	Stipe	Basidiome colour	Subiculum-like structure	Basidiome width (mm)	Lamellae colour	Spores shape	Spores width (µm)	Cheilo-cystidia	Pleuro-cystidia	Substrate	Reference
<i>R. applicatus</i>	+	light grey, pale brownish grey then darker	coarse greyish or brownish-grey felt; never black	2–8	greyish	globose to subglobose	4.8–5.5 × 4.3–5.1	+	+	hard and soft wood	Consiglio & Setti (2018)
<i>R. applicatus</i>	+	chocolate brown to black when wet; not striate or translucent	dense coarse tomentum, pale greyish buff to brownish grey	2–5	dark brown	globose to subglobose	(4.0) 4.4–6.0 × 4.0–4.8	+	N.A	dead woody dicots	Thorn & Barron, (1986)
<i>R. reviviscens</i>	–	brownish-grey to dark grey, light yellowish grey towards the margin	off-white to greyish yellow felt	3–7	yellowish grey to brownish grey	broadly ellipsoid to ellipsoid	(3.8–)4.2–5.1–6(–6) × (2.8–)3.1–3.7–4.2(–4.7)	–	+	bamboo	This Study
<i>R. sp. "trichotis"</i>	+	mouse grey or cloud grey with paler margin	N.A	N.A	N.A	subglobose	N.A	N.A	N.A	<i>Juglans</i> bark	Miller & Bates (2017)
<i>R. striatulus</i>	–	brown-grey, pinkish-brown or blackish	–	9.5–3	greyish white, dark grey or brown grey	globose to subglobose	4.8–5.6 × 4.2 × 5	+	–	hardwood	Consiglio & Setti (2018)
<i>R. trichotis</i>	–	greyish, brownish-grey or beige, then blackish-grey, glabrous on the rim	with a blackish tomentum (woolly hairs)	2–10	dark-grey when fresh, black when dry, edge white	globose to subglobose	4.7–5.5 × 4.3–5.1	+	+	hard and soft wood	Consiglio & Setti (2018)
<i>R. trichotis</i>	–	grey to blackish brown or black	black shaggy hairs	1.5	At first greyish brown to brownish grey to nearly black	globose smooth	4.8–6.5 × 4.5–5.0	+	N.A	rotting hard wood	Thorn & Barron, (1986)

Note: The new species described is in bold. Key: + = present ; – = absent; N.A = data not available.

Discussion

The placement of *Resupinatus reviviscens* in *Resupinatus* is supported by its morphological characteristics including: sessile, small, cupuliform then convex to plano-convex, and subcircular to rounded-flabelliform or flabelliform basidiomes, lamellate hymenophore, inamyloid spores, clamped generative hyphae, and gelatinized hymenophoral trama. Yet, the species is distinct in its genus due to the unique combination of the following features: basidiome and lamellae colour, spore shape, absence of cheilocystidia, presence of pleurocystidia and distinct subiculum-like structure. The hyphae of the felt at the base is thoroughly described and is a crucial distinguishing characteristic in the new species introduced. A remarkable biological feature of *Resupinatus reviviscens* is the ability of its basidiomes to withstand desiccation. This characteristic has not been reported in any other *Resupinatus* species and might be considered as an adaptation to the environment and substrate in which the species grows.

The taxonomic status of the American specimens TENN-F-63042, IN01-57471425, IN01-39114228, and IN01-129942182, is unclear. They formed a well-supported clade with all *Resupinatus reviviscens* sequences (MLBS = 93; BIPP = 1.0) but showed only a small genetic distance from them. Differences in morphology, geographic distribution, and host substrate (Table 2) indicate that despite little genetic differentiation, the American specimens may represent a distinct species. They were found growing on decorticated wood in Indiana and Tennessee (Miller & Bates 2017), whereas *R. reviviscens* is found on bamboo in tropical Thailand. Additionally, the macromorphological features of *R. aff. trichotis* (TENN-F-63042) do not align with those of *R. reviviscens* (Table 2). The American materials, labeled as *R. aff. trichotis* and *R. sp. "trichotis,"* suggest a similarity to *R. trichotis*; however, their phylogenetic placement is distant from that of the epitype sequence for *R. trichotis* (AMB 18074, designated by Consiglio & Setti, 2018). Clarifying the identity of the American specimens would require sequencing additional gene regions and a comprehensive morphological assessment.

In conclusion, *R. reviviscens* clearly belongs in *Resupinatus*, yet it can be easily distinguished from other *Resupinatus* species by its morphology, DNA sequences, phylogenetic position, as well as its biological and ecological characteristics. Further study is needed to confirm or reject its presence in North America.

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