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Pseudobaeospora taluna (Fungi: Agaricales) newly described from southern Australia

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Abstract

Pseudobaeospora taluna is formally described from southern Australia, representing the first report of the genus from Australia given that *P. lamingtonensis* is excluded from the genus. Analysis of sequences of the internal transcribed spacer (ITS) shows that *P. taluna* is a distinct phylogenetic species. The distinctive morphological characteristics of the species are the combination of a pinkish grey to dull grey pileus, pale rhizomorphs at the base of the stipe extending into soil, thick-walled dextrinoid spores, presence of cheilo- and pleurocystidia, and a trichoderm pileipellis that stains bluish green in KOH. Three of the examined collections, from Tasmania, were 4-spored but a single collection from Victoria produced 2-spored basidia. Apart from the 2-spored basidia and larger spores, this 2-spored collection was similar in morphological and sequence characters to the 4-spored collections and is placed under *P. taluna*. The specific epithet was chosen in collaboration with the Tasmanian Aboriginal Centre and the *palawa kani* Language Program. In *palawa kani,* the language of Tasmanian Aborigines, *taluna* is the name of the Huon River area, where the holotype was collected.

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Introduction

The genus *Pseudobaeospora* Singer was etablished to accommodate a species from the Altai region of central Asia originally described as *Baeospora oligophylla* Singer (Singer 1938, 1942). *Pseudobaeospora* was differentiated from the amyloid-spored genus *Baeospora* Singer by its small, thick-walled and dextrinoid mature spores (Singer 1951). In subsequent decades four species of the genus were described from South America by Singer (1963, 1969) and Horak (1964) including *P. defibulata* Singer and *P. chilensis* E.Horak. At this time, *P. oligophylla* (Singer) Singer and *P. pillodii* (Quél.) Wasser were the only known species of the genus with European distributions. The former is now regarded as a synonym of the latter (Ronikier & Moreau 2007; Voto 2021). *Pseudobaeospora* was subject to an extensive taxonomic treatment by Bas (1995, 2002, 2003) resulting in the for-

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mal description of eleven novel species from Europe. Renewed interest in the genus following the publications by Bas prompted the description of further novel species from North American, Europe, India, China and New Zealand, resulting in 33 species currently accepted in the genus (see Voto 2021 for details of all species).

Only one species of *Psuedobaespora* has previously been recorded from Australia (May & Wood 1997). *Pseudobaeospora lamingtonensis* Aberdeen was described from Queensland in a treatment of lepiotoid fungi (Aberdeen 1992). The presence of an annulus indicates that this species does not belong in *Pseudobaeospora* as currently circumscribed, but likely belongs in *Agaricaceae* in a genus such as *Leucoagaricus* Locq. ex Singer, as suggested by Voto (2009), who indicated a placement in *Sericeomyces* Heinem. [a genus now placed under *Leucoagaricus*, see for example Vellinga (2001)].

We examined morphologically and sequenced a series of collections from southern Australia that are attributable to *Pseudobaeospora*. From among these, we describe a novel species, *P. taluna.*

Methods

Morphological observations:

Macromorphological characters are described from field notes and photographs made at the time of collection. Colours are described from fresh collections in daylight conditions in field notes, and where possible according to the Methuen Handbook of Colour (Kornerup & Wanscher 1978).

Micromorphological characters are from examination of dried fungarium specimens, from which hand-cut sections were rehydrated in 5% KOH to observe and measure pellis, trama and hymenium tissues. Sections were stained with Congo Red to view hyaline elements and mounted in Melzer's reagent to observe spore size, shape, ornamentation and presence or absence of amyloid reaction. Microscopic features were observed and photographed using an Olympus BX-52 light field microscope and measurements were taken at ×400 or ×1000 using measurement tools on Olympus CellSens standard (v. 1.16).

Spore measurements are shown as a raw range followed by the range of collection means including the mean of the collection means in italics. Each collection mean is from measurements of at least 20 randomly selected mature spores observed on the pileipellis. The quotient 'Q' is the ratio of spore length to spore width and is given as a raw range, followed by the range of collection means including the mean of the collection means in italics. Where only one collection was examined, measurements are given as raw ranges with the mean in italics. All other measurements are given as observed ranges to the nearest half-micron for microscopic features and to the nearest half-millimetre for macroscopic features.

Molecular methods and analysis:

Approximately 20-50 mg of dried tissue from selected fungarium specimens was disrupted in 2 ml microcentrifuge tubes using a TissueLyser II bead mill (Qiagen, Germany). DNA was isolated from the tissue using a protocol based on that of Gardes and Bruns (1993). Briefly, 500 µl of 2% CTAB lysis buffer with 1% (v/v) β-mercaptoethanol, 0.01 mg BSA and 0.1 mg RNase was added to each tube and incubated at 65°C for 60 mins. 500 µl of 24:1 chloroform: isoamyl alcohol was added to each tube, the tube briefly vortexed and then centrifuged for 10 mins at 21000 g. DNA in the resultant aqueous phase was then precipitated in a new tube by adding 0.15x volume 2.4M sodium acetate and an equal volume of cold isopropanol. Tubes were left at -20°C overnight and then centrifuged for 10 mins at 21000 g. The resultant DNA pellet was washed twice with 80% ethanol before being resuspended in 100 µl of 10 mM Tris-HCl, ph 8.

The internal transcribed spacer (ITS) region was PCR amplified in 20 µl reactions using MyTaq Red Mix (Bioline, UK), 1 µl of DNA template and the primer pair ITS1f/ITS4 (Gardes and Bruns 1993; White et al. 1990). PCRs were performed on a Master Cycler (Eppendorf, Hamburg, Germany) with the following protocol: 95°C for 5 min; 38 cycles of 94°C for 35 s, 50°C for 60 s, and 72°C for 60 s;a final extension at 72°C for 60 s (Davoodian et al. 2020). Amplicons were assessed by gel electrophoresis. In cases where initial amplification was poor, PCRs were repeated with either 1:40 diluted DNA template or 2 µl of template. Collection MEL 2367169 was sequenced twice from repeat extractions (extractions FT0031 and FT0060). Sequencing was undertaken by AGRF (Melbourne, Australia) and resultant chromatograms aligned and edited manually using Geneious Prime (Version 2021.0.3, https://www.geneious.com) to generate consensus sequences.

ITS sequences in GenBank identified as *Pseudobaeospora* were assembled along with the sequences generated from MEL specimens and any additional sequences from GenBank that had a percentage identity of greater than 80% in a BLAST search to *P. wipapatiae* Desjardin, Hemmes & B.A.Perry (KF271798) (Altschul et al. 1990; Morgulis et al. 2008). Additional sequences in the UNITE database (Version 9.0, https://unite.ut.ee/repository.php) were downloaded from PLUTOF to cover lineages not represented in GenBank to a maximum of five sequences per 3% species hypothesis (SH) (Abarenkovet al. 2010; Nilsson et al. 2018). UNITE 3% SHs were examined by search of UNITE Fungal Species Hypotheses index (https://unite.ut.ee/index.php).

Sequences (Table 1) were processed with MUSCLE Alignment (Version 3.8.425) implemented in Geneious Prime, and the resultant alignment manually checked and edit-

Table 1. ITS sequences from NCBI, UNITE and newly generated for this study (in bold). Sequences in grey highlight represent the newly described species. Type status: H=holotype, I=isotype.

Herbarium/observation*	Collector	Taxon as in DNA repository	Country	ITS GenBank / UNITE accession	TYPE status
SFSU F033184	K.M.Shanks 249	*Tricholoma inamoenum*	USA	AF377246	
PUL F27632/iNat:30847449	G.Taylor	*Pseudobaeospora sp.*	USA	MZ269236	
MO:268227	A.Rockefeller	*Pseudobaeospora aphana*	USA	MH298912	
**	AB122	*Tricholoma sp.*	Cameroon	KR819126	
MEL 2363200	**T.W.May 2042**	***Pseudobaeospora taluna***	**Australia**	**OQ457539**	
MEL 2525019	**G.M.Gates & D.A.Ratkowsky 4130**	***Pseudobaeospora taluna***	**Australia**	**OQ457538**	
MEL 2446695	**N.Siegel 2844 & G.M.Gates**	***Pseudobaeospora taluna***	**Australia**	**OQ457537**	**H**
MEL 2367169 (FT0031)	**G.M.Gates & D.A.Ratkowsky 2047**	***Pseudobaeospora taluna***	**Australia**	**OQ552854**	
MEL 2367169 (FT0060)	**G.M.Gates & D.A.Ratkowsky 2047**	***Pseudobaeospora taluna***	**Australia**	**OQ535387**	
MEL 2525020	**G.M.Gates & D.A.Ratkowsky 4129**	***Pseudobaeospora sp.***	**Australia**	**OQ535390**	
MEL 2363205	**J.Weller 6/R7/11**	***Pseudobaeospora sp.***	**Australia**	**OQ535391**	
MEL 2525018	**G.M.Gates & D.A.Ratkowsky 4131**	***Pseudobaeospora sp.***	**Australia**	**OQ535389**	
MEL 2363203	**T.W.May 2057**	***Pseudobaeospora sp.***	**Australia**	**OQ457540**	
MEL 2300736	**S.J.M.McMullan-Fisher 1480**	***Pseudobaeospora sp.***	**Australia**	**OQ535386**	
MEL 2524974	**G.M.Gates & D.A.Ratkowsky 4134**	***Pseudobaeospora sp.***	**Australia**	**OQ535388**	
TUF 110801	G.M.Gates	*Pseudobaeospora sp.*	Australia	UDB013451	
TENN 067659	E.C.Vellinga 5550	*Pseudobaeospora celluloderma*	USA	KU058501	
TENN 070699	C.C.Braaten 143666	*Pseudobaeospora sp.*	USA	KU058500	
O F21860	A.Molia 242w-2013 & T.Læssøe	*Pseudobaeospora calcarea*	Norway	UDB036674	
O F22037	T.Læssøe & A.Molia 263f-2013	*Pseudobaeospora calcarea*	Norway	UDB036661	
TUE 000405 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Portugal	UDB05320713	
TUE 000405 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Portugal	UDB05320715	
TUE 000405 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Portugal	UDB05320714	
TUE 000405 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Portugal	UDB05320708	
SFSU F000719	D.E.Desjardin 8605	*Pseudobaeospora wipapatiae*	Hawaii	KF271798	H
iNat:34223688	J.K.Stallman 236	*Pseudobaeospora wipapatiae*	Hawaii	MW018883	
UCSC 7451	C.Schwarz 12Jan2010-1	*Pseudobaeospora deckeri*	USA	JF898319	H
iNat:10021818	jdiggity22	*Pseudobaeospora sp.*	USA	MH020190	
MO:270813	A.Rockefeller	*Pseudobaeospora deckeri*	USA	MF144428	
MO:335838	A.Rockefeller	*Pseudobaeospora sp.*	Mexico	OM655256	
REG**	L.Krieglsteiner	*Pseudobaeospora pyrifera*	Germany	AF391034	I
O F245759	T.Læssøe	*Pseudobaeospora pyrifera*	Norway	UDB037347	
TUF 132017	T.Ploompuu	*Pseudobaeospora pyrifera*	Estonia	UDB0799048	
TUF 111505	T.Ploompuu	*Pseudobaeospora pyrifera*	Estonia	UDB034593	
GDGM 25609	T.H.Li, X.L.Chen & Y.Li	*Pseudobaeospora lilacina*	China	KX266951	
SYAU FUNGI-009	M.Zhang 3459	*Pseudobaeospora lilacina*	China	KU528840	H
SYAU-FUNGI-010	X.D.Yu 3450	*Pseudobaeospora lilacina*	China	KU528842	
TUF 123953	U.Kõljalg	*Pseudobaeospora sp.*	Seychelles	UDB039729	
GDOR M3986	D.Gisotti & F.Boccardo	*Pseudobaeospora cyanea*	Italy	MT271829	
G4422 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora*	Estonia	UDB0618517	
FLAS F68471	J.Kalichman	*Pseudobaeospora sp.*	USA	OM672808	
TUE002760 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Papua New Guinea	UDB05320730	

Herbarium/observation*	Collector	Taxon as in DNA repository	Country	ITS GenBank / UNITE accession	TYPE status
SFSU F033184	K.M.Shanks 249	*Tricholoma inamoenum*	USA	AF377246	
PUL F27632/iNat:30847449	G.Taylor	*Pseudobaeospora sp.*	USA	MZ269236	
G4779 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Estonia	UDB0519248	
O F22005	A.Molia	*Pseudobaeospora sp.*	Norway	UDB036654	
NYBG**	R.E.Halling, REH1979	*Pseudobaeospora sp.*	USA	UDB023460	
TUE 003102 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	USA	UDB05320737	
TENN F061545	E.Lickey	*Pseudobaeospora sp.*	USA	MK268233	
TUE 002388 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Georgia	UDB05320721	
TUE 003102 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	USA	UDB05320752	
TENN 067672	E.C.Vellinga 5553	*Pseudobaeospora sp.*	USA	KU058502	
TUE000894 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	USA	UDB05320718	
TUE000894 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	USA	UDB05320717	
TUE000894 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	USA	UDB05320716	
MO:265707	A.Rockefeller	*Pseudobaeospora sp.*	USA	MH304401	
AH 49303	A.Banares & O.Bermudez	*Pseudobaeospora brunnea*	ES, Canary Islands	OP375152	
TUE 000265 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Estonia	UDB05320705	
TUE 000265 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Estonia	UDB05320706	
TUE 002425 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Georgia	UDB05320724	
TUE 002425 (Soil Sample)	L.Tedersoo et al.	*Pseudobaeospora sp.*	Georgia	UDB05320725	

* Observational records include MO (Mushroom Observer, mushroomobserver.org) and iNat (iNaturalist, inaturalist.org)

** Catalogue number of specimen not recorded in GenBank record

ed with ends masked (Edgar 2004). A phylogenetic tree was generated using RAxML as implemented in Geneious Prime with default settings including a GTR-CAT substitution model and with 1000 bootstrap (BS) replicates (Lartillot & Philippe 2004; Stamatakis 2014). *Tricholoma inamoenum* (Fr.) Gillet (AF377246) was chosen as the outgroup (Desjardin et al. 2014; Wu et al. 2017).

Results

In the phylogenetic tree based on ITS sequences (Fig. 1), named species with more than one sequence available show a relatively small amount of variation, as shown by the well-supported (100% BS support) clades representing *Pseudobaeospora pyrifera* Bas & L.G. Krieglst., *P. wipapatiae*, *P. deckeri* C.F. Schwarz, *P. lilacina* X.D.Yu, Ming Zhang & S.Y.Wu and *P. calcarea* Clémençon & Ayer. The corresponding UNITE SHs for these five species are all formed at the 3% level (although in some species there is less variation than this). There are five additional clades of un-named species that correspond to UNITE species hypotheses at the 3% threshold. SH0004636.09FU contains four sequences from soil samples from Portugal including UDB05320708; SH0126028.09FU contains three sequences from soil samples from the USA including UDB05320716; SH0253439.09FU contains two sequences from Norway (from a specimen) and Estonia (from soil sample) including UDB036654; SH0126026.09FU includes 22 soil-derived sequences mainly from the USA (e.g. UDB05320737) but also three soil-derived sequences from Georgia, along with four sequences from specimens from the USA (e.g. MK268233); and SH1111686.09FU (labelled in UNITE as *Tricholomataceae*) containing 14 soil-derived sequences from Estonia and Georgia including UDB05320706. This last clade is very close to the sequence of *P. brunnea* Arauzo, P.Iglesias & J.Fernández (OP375152) but this sequence is too recent to be included in the current version of UNITE. Three of the five un-named clades are known only from soil samples.

The Australian sequences fall in two main clades. One, comprising five sequences (from four collections) is sister to the sole sequence of *P. cyanea* Arnolds, Tabarés & Rocabruna. Within this clade, which has 100 BS support, pairwise comparisons vary between 98.4% and 99.9%. This is the clade we name as *P. taluna*. The other clade containing seven Australian sequences is sister to the clade containing *P. lilacina*. In this second clade, there are two well-supported subclades containing sequences from Tasmania (Aus-1 and Aus-2) that are at same level of variation as shown by named species. In addition, there is a well-separated singleton (OQ535386 from Tasmania). A sequence from Victoria (OQ457540) is sister to Aus-1 with pairwise comparisons with sequences in Aus-1 ranging from 87.3% to 89.0%. The two sequences from separate extractions of MEL 2367169 were iden-

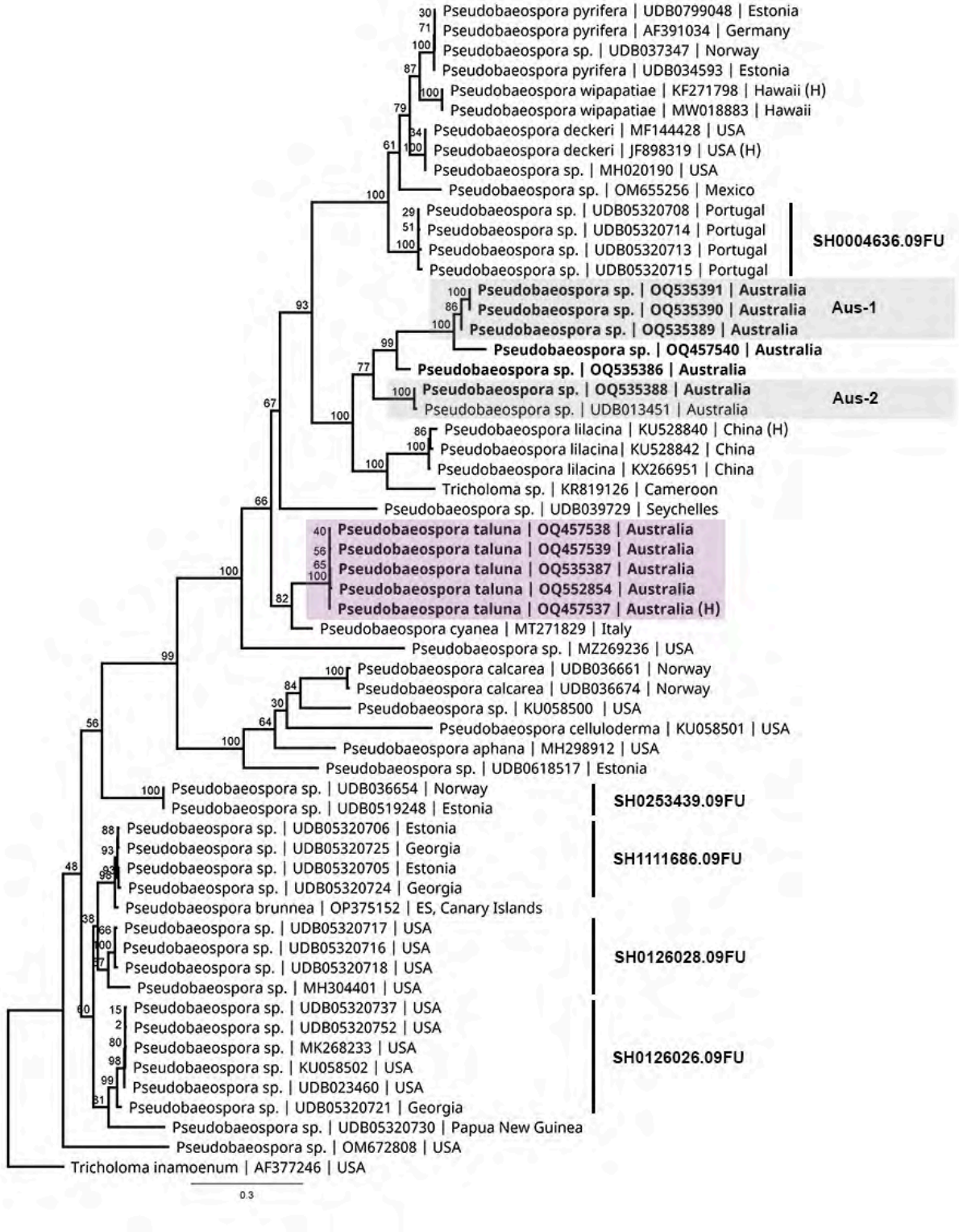

Figure 1. RAxML tree based on ITS sequences of *Pseudobaeospora* from NCBI, UNITE and generated from MEL specimens for this study. Phylogeny created in Geneious Prime (Version 2021.0.3) using RAxML 8.2.11 and GTR-CAT substitution model with 1000 bootstrap replicates. Branch support is indicated by bootstrap support percentage. *Tricholoma inamoenum* was used as outgroup. The names of species in this tree are as they appear in the DNA repositories. Sequences in bold type were generated through this project. Sequences highlighted in purplish grey represent the newly described species. UNITE 3% species hypotheses (SH) are shown for clades that do not contain sequences corresponding to named species. Two clades comprising sequences from Australian collections that are not formally named are shown in light grey highlight. (H)=holotype.

tical (extraction FT0031, OQ552854 and FT0060, OQ535387).

The two main clades, as far as named species, are the clade consisting of *P. calcarea*, *P. celluloderma* Bas and *P. aphana* Vellinga (which we designate the *P. calcarea* clade), with 100% BS support, and the clade consisting of the other named species: *P. pyrifera*, *P. wipapatiae*, *P. deckeri*, *P. lilacina*, *P. taluna* and *P. cyanea* (which we designate the *P. pyrifera* clade), also with 100% BS support.

Discussion

Given that *P. lamingtonensis* does not belong in *Pseudobaeospora*, *P. taluna* is the first species in the genus confirmed from Australia. It is distinct on DNA sequence data but, as with many species in the genus, does not have particularly distinctive macroscopic characters and detection of diagnostic microscopic features required close examination.

Overall, the molecular phylogeny of *Pseudobaeospora* worldwide contains as many un-named clades as clades comprising named species. It is possible that some of the un-named clades will end up being matched to known species, once sequences are available for other species in the genus. However, for Australia, in addition to *P. taluna*, the molecular phylogeny indicates at least three further un-named species of *Pseudobaeospora* among fungarium collections. The variation among observational records from Australia on citizen-science platforms such as iNaturalist also indicates the presence of further species. Further examination of fungarium collections is necessary to determine diagnostic characters of these other putative species.

We consider a 2-spored collection from Victoria to be conspecific with 4-spored collections of *P. taluna* from Tasmania. In *Pseudobaeospora*, most previously described species have 4-spored basidia but the there are a number of exceptions. *Pseudobaeospora wipapatiae* Desjardin, Hemmes & B.A.Perry has consistently 2-spored basidia and *P. pillodii* and *P. brunnea* have a mixture of 2- and 4-spored basidia (Bas 2003; Desjardin et al. 2014; Voto 2021). In many agaric lineages, the number of sterigmata on basidia is a specific character, but it can also vary within species (Singer 1986: p. 115).

Gisotti et al. (2021) pointed out that the morphology-based infrageneric classification of the genus as elaborated by Voto (2009, 2015, 2021) is not consistent with the molecular phylogeny, in particular the separation of species with a hymeniform pilepellis in section *Anistoderma* from those with a trichoderm or cutis in section *Pseudobaeospora*. Our molecular phylogeny, now including *P. taluna* as a sixth species of the *P. pyrifera* clade, leads to the same conclusion. In particular, both *P. wipapatiae* (of the *P. pyrifera* clade) and *P. celluloderma* (of the *P. calcearea* clade), which were placed by Voto (2021) in section *Anistoderma,* do not form a separate clade but are each intermingled with species of section *Pseudobaeospora.* Assessing the tabulation by Voto (2021) of morphological characters (and taking into account the characters of *P. taluna*), only two characters map closely to the two main clades in our molecular phylogeny. Firstly, the three species of the *P. calcarea* clade all lack cheilocystidia, whereas among the species of the *P. pyrifera* clade, cheilocystidia are usually present, albeit often not well-differentiated. Secondly, in the *P. calcarea* clade, there is no reaction to KOH (or at most a pale brownish reaction in *P. celluloderma*), while in the *P. pyrifera* clade, five of the six species have a strong reaction in KOH, becoming either blue-green, green or ruby red.

Taxonomy

Pseudobaeospora taluna S.Craig, L.J.Vaughan & T.W.May, *sp. nov.*

Registration identifier: MB 847844

Type: AUSTRALIA, Tasmania, Oigles Road, near Kermandie Falls track, 31 May 2018, *N. Siegel 2488 & G.M. Gates* (holotype: MEL 2446695) (ITS: OQ457537).

Figs 2–5.

Diagnostic characters: the combination of a pinkish grey to dull grey pileus, pale rhizomorphs at the base of the stipe extending into soil, thick-walled dextrinoid spores, presence of cheilo- and pleurocystidia, and a trichoderm pileipellis that stains bluish green in KOH.

Basidiomes collybioid. *Pileus* 5–15(–22) mm diameter, convex to plane or uplifted, faintly umbonate; colour pinkish grey to dull grey, often with darker patch of purplish grey (15D2) around apex, becoming unevenly blotched and pale toward margin; surface dry, suede-like; margin narrowly incurved, persisting as pileus becomes uplifted, occasionally becoming finely crenulate, splitting with age. *Lamellae* to 2 mm deep, adnate, adnexed, or sinuate, moderately thick, subdistant to close, in 2–3 series, face and margin smooth, edge eroding slightly with damage or age; colour pale citrine yellow to olive green, darkening close to colour of stipe apex when damaged. *Stipe* 25–42 × 1–2 mm, central, cylindrical; colour reddish brown (9E8), darkest at apex and base, sometimes paler middle to greyish orange (5B6); surface smooth, dry, pruinose or finely pulverulent at stipe apex, bare in middle, strongly strigose at base with off-white rhizomorphs extending into soil. *Macrochemical reactions* KOH on pileus teal green. *Odour* not distinctive. *Spore print* white.

Basidiospores 3.5–5.5 × 3.0–5.0 µm (72/3), means 4.24–*4.29*–4.42 × 3.72–*3.79*–3.92 µm, globose to ellipsoid, Q: (0.92–)1.00–1.35, means 1.13–*1.14*–1.14, hyaline, thick-walled, dextrinoid, hilar appendage up to 1 µm long. *Basidia* 20–30.5 × 6–8 µm, 4-spored, clavate, with sterigmata 2–4 × 1–1.5 µm. *Basidioles* 16–25 × 4–6 µm, clavate with widely rounded apex. *Cheilocystidia* present at lamellae edge, often extending beyond basidia and basidioles, 21–44 × 3.5–6.5 µm, irregularly

cylindrical, occasionally with asymmetric constrictions, often flexuose, sometimes bent or branched or narrowed toward apex, apex rounded. *Pleurocystidia* present on lamellae face, 20–30.5 × 2.5–6 µm, similar in shape to cheilocystidia, also often narrow-cylindrical. *Hymenophoral trama* consisting of cylindrical elements 7–40 × (2–)4–14 µm, walls to 1 µm thick, hyaline. *Pileipellis* a loose disrupted trichoderm staining bluish green in KOH, roughly vertically arranged toward centre, often more repent at margin, consisting of pluriseptate elements terminating in pileocystidia; *pileocystidia* 23–55 × 5–13(–18) µm, cylindrical to fusiform or clavate, apex rounded, often slightly flexuose, thin-walled, with basal clamp; *subterminal cells* cylindrical to globose, 20–59 × 5–23 µm, occasionally branching, segments becoming more cylindrical towards pileocystidia, more globose and inflated near pileus trama. *Pileus trama* consisting of interwoven hyphae, often in short segments, cylindrical to inflated-cylindrical to globose, 10–52 × 5–21¸ hyaline. *Stipitipellis* a cutis of repent cylindrical hyphae, 4–11 µm diameter, walls to 1.5 µm thick, hyaline or slightly encrusted, on upper stipe, clusters of terminal elements staining bluish green in KOH. *Caulocystidia* present, 10–50 × 4–8 µm, cylindrical, straight or flexuose, apex rounded, often forming tangled clusters, or, rarely, arising singly in stipitipellis, perpendicular to almost parallel to stipe surface. *Stipe trama* consisting of cylindrical hyphae 4–16 µm diameter. *Clamp connections* detected in all tissues, conspicuous.

Other specimens examined: AUSTRALIA, TASMANIA: Huon Valley; Warra Long Term Ecological Research site, coupe WR008J, 27 April 2004, *G.M. Gates & D.A. Ratkowsky 2047* (MEL 2367169); Mt Mangana, Bruny Island, 7 April 2001, *G.M. Gates & D.A. Ratkowsky 4130* (MEL 2525019).

Distribution & habitat. Wet sclerophyll forest with *Eucalyptus* species dominant.

Conservation status. Insufficient information to assess. Apparently rare, but easily overlooked due to the small and dull-coloured sporing bodies.

Etymology. In *palawa kani,* the language of Tasmanian Aborigines¸ *taluna* is the name of the Huon River area from which the holotype of the species was collected. This specific epithet was chosen in collaboration with the Tasmanian Aboriginal Centre and the *palawa kani* Language Program. The epithet is a noun in apposition.

Notes. The pileipellis stains bluish green in KOH. The strength of this reaction varied among the collections. It was not particularly strong in the holotype (Fig. 4a) but was very evident in MEL 2525019 and also in the 2-spored collection (Fig. 8a, 8b).

Pseudobaeospora aciculifera Voto & Soop, recently described from New Zealand (Voto & Soop 2018), has similar macro-morphology to *P. taluna*, with greyish pink pilei and a slightly strigose stipe base. It was the first species in the genus to be described with pleurocystidia. These are also present in *P. taluna* but are less consistently needle-like than those seen in *P. aciculifera*, which also differs by the presence of conspicuous encrusting pigment on cheilocystidia. Cooper (2018) describes and illustrates characters of several putative novel species from Australasia. Of these, *P. sp. 'JAC14558'* from New Zealand is most similar to *P. taluna*, including a similar macromorphology and a trichoderm pileipellis, but it appears to lack pleurocystidia.

Voto (2021) provided a synoptic key based on morphological characters of all described species of *Pseudobaeospora* worldwide known at that time. Using this key, *P. taluna* is placed in section *Pseudobaeospora* due to the trichoderm pileipellis. It shares a bluish green KOH reaction with a number of other species. Among these, only *P. cyanea*, *P. euganea* Voto and *P. lavendulamellata* Arnolds, Leelav. & Manim. also have a trichoderm pileipellis, and only *P. cyanea* also has a strigose stipe base. Other species share the strigose stipe base character, but only *P. cyanea* and *P. deckeri* also have a trichoderm pileipellis and cheilocystidia. *Pseudobaeospora deckeri* has very similar morphology to *P. taluna*, including a very similar mean Q ratio, but differs in having a green KOH reaction and a deeper purple pileus. *Pseudobaeospora cyanea* has the most similar morphology to *P. taluna*, particularly in the pluriseptate pileipellis elements and irregular cheilocystidia. However, *Pseudobaeospora cyanea* has larger spores with higher mean Q and a more boldly coloured pileus. In addition, the DNA sequence data separate *P. taluna* from *P. cyanea* and *P. deckeri*. There are no sequences available for the New Zealand species *P. aciculifera.*

One collection of *P. taluna* (MEL 2525019) was identified by the field name "*Pseudobaeospora* sp. 'pink, peach, lemon, grey'" but at least some of the other collections under this field name (such as MEL 2524974) are not *P. taluna*, according to the sequence data. Another collection of *P. taluna* (MEL2367169) was identified by the field name "*Pseuobaeospora* sp. 'bloomers'. Gates & Ratkowsky (2014) introduced the name "*Pseudobaeospora* sp. 'pink, peach, lemon, grey'", noting that sporing bodies "are variable in colour with pale lemon, peach, pink and grey forms recorded". Two separate sporing bodies are depicted by Gates & Ratkowsky (2014), one grey and one with much richer reddish tones. Without being able to link these images to voucher collections, it is not possible to provide an identification. Field names are useful in alerting to the presence of novel taxa among fungarium material and for communicating about undescribed taxa, but in this case, there is not a one to one match between field names and the species as delimited by molecular data.

Two-spored collection of *Pseudobaeospora taluna*

Figs 6–9.

Basidiomes collybioid. *Pileus* 8–23 mm diameter, convex to plane or uplifted; colour purplish grey (14D2), becoming unevenly blotched toward margin; surface dry, matt. *Lamellae* to 2 mm deep, adnexed, in 2-3 series, edge concolourous. *Stipe* 20–40 × 1.5–2.2 mm, central, at base with off-white rhizomorphs in soil. *Macrochemical Reactions.* KOH on pileus bluish green (25A8).

Basidiospores 3.5–*5.60*–6.5 × 3.9–*4.59*–5.5 µm (49/1), globose to ellipsoid, Q: 0.78–*1.22*–1.52, hyaline, thick-walled, dextrinoid, hilar appendage up to 1 µm long. *Basidia* 20–27 × 6–10 µm, 2-spored, clavate, with sterigmata 2–3 × 1–1.5 µm. *Basidioles* 16–25 × 4–8 µm, clavate with widely rounded apex. *Cheilocystidia* present at lamellae edge, 15–40 × 3–7 µm, irregularly cylindrical, occasionally with asymmetric constrictions, sometimes flexuose, occasionally bent or branched or narrowed toward apex, apex rounded. *Pleurocystidia* present on lamellae face, 20–35 × 3–7 µm, similar in shape to cheilocystidia. *Hymenophoral trama* consisting of cylindrical elements 3–10 µm diameter, walls to 1 µm thick, hyaline. *Pileipellis* a loose disrupted trichoderm strongly staining bluish green in KOH, roughly vertically arranged toward centre, often more repent at margin, consisting of pluriseptate elements terminating in pileocystidia; *pileocystidia* 20–40 × 2.5–12 µm, cylindrical to fusiform or clavate, apex rounded, often slightly flexuose, thin-walled, with basal clamp; *subterminal cells* cylindrical to globose, 20–40 × 5–15 µm, occasionally branching, segments becoming more cylindrical towards pileocystidia, more globose and inflated near pileus trama. *Pileus trama* consisting of interwoven hyphae, often in short segments, cylindrical to inflated-cylindrical to globose, 10–55 × 5–15 µm, hyaline. *Stipitipellis* a cutis of repent cylindrical hyphae, 38–92 × 4–15 µm, walls to 1.5 µm thick, hyaline or slightly encrusted. *Caulocystidia* 15–40 × 4–8 µm, cylindrical, apex rounded, arising individually or in tangled clusters. *Stipe trama* consisting of cylindrical hyphae 4–20 µm diameter. *Clamp connections* detected in all tissues.

Specimens examined: AUSTRALIA, VICTORIA, Tarwin Lower Road, Drumdlemara H8 Bushland Reserve, 2 July 2016, *T.W. May 2042* (MEL 2363200).

This collection from Victoria differs from the Tasmanian specimens of *P. taluna* by the 2-spored basidia and larger, more strongly dextrinoid spores. The staining reaction of the pileipellis is particularly strong in this collection, but the blue-green staining is also shown in the Tasmanian collections. Given that the DNA sequence data indicates conspecificity, and that there are no other morphological differences, we place the collection under *P. taluna.* The habitat for the Victorian collection is heathy woodland dominated by *Melaleuca squarrosa* with a relatively open ground layer of moss and litter, contrasting to the wet sclerophyll forest where the Tasmanian collections were made.

Disclosures

There are no conflicts of interest to disclose.

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Figure 2. Sporing bodies of *Pseudobaeospora taluna* (MEL 2446695). Photograph by Noah Siegel.

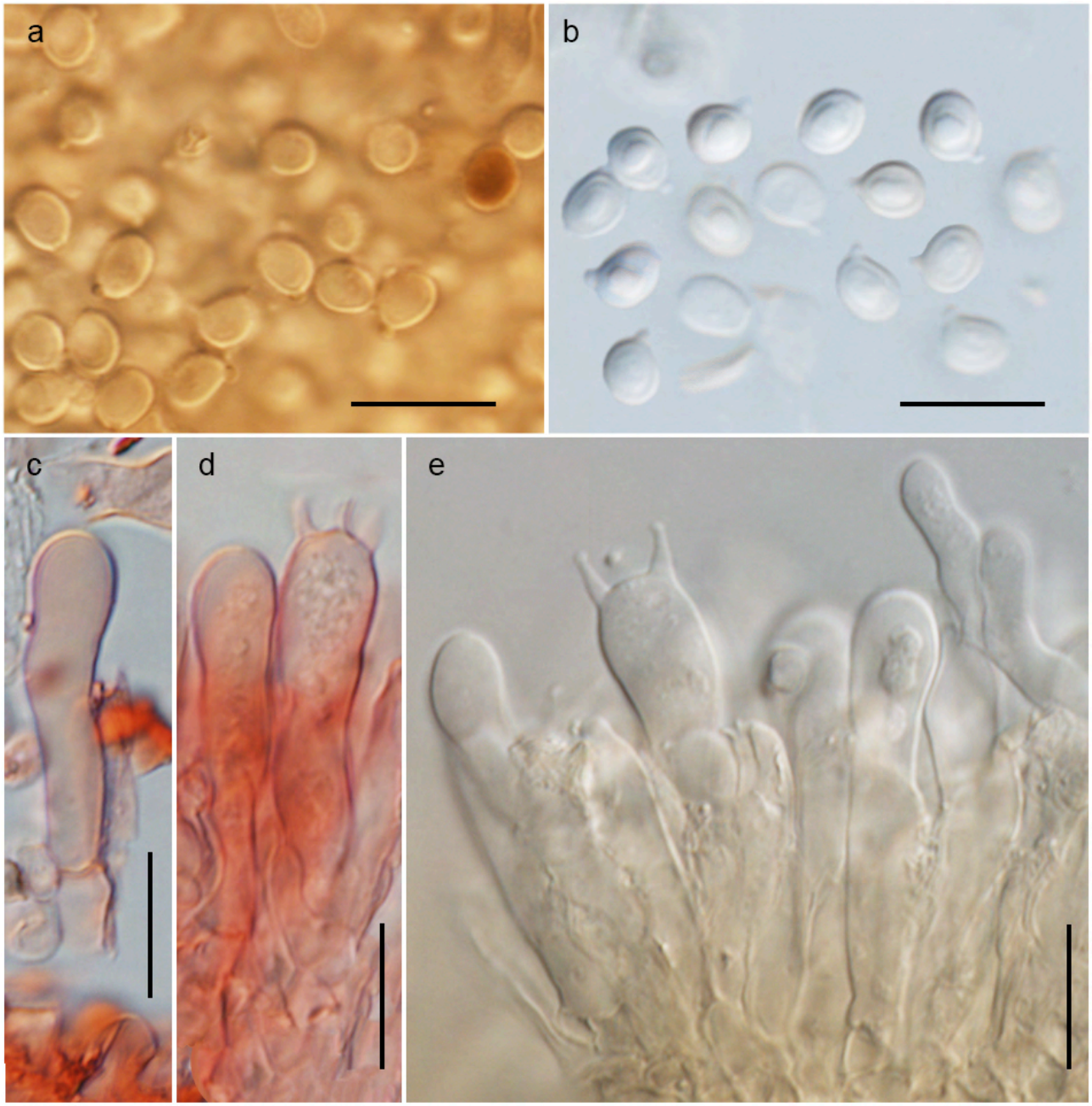

Figure 3. Microscopic features of *Pseudobaeospora taluna* (MEL 2446695). Basidiospores **a** dextrinoid in Melzer's reagent and **b** hyaline in 5% KOH, **c** basidiole in 5% KOH and Congo Red, **d** basidole and basidium in 5% KOH and Congo Red, **e** hymenium in 5% KOH with basidium, basidioles and pleurocystidia. Scale **a**–**e**=10 µm.

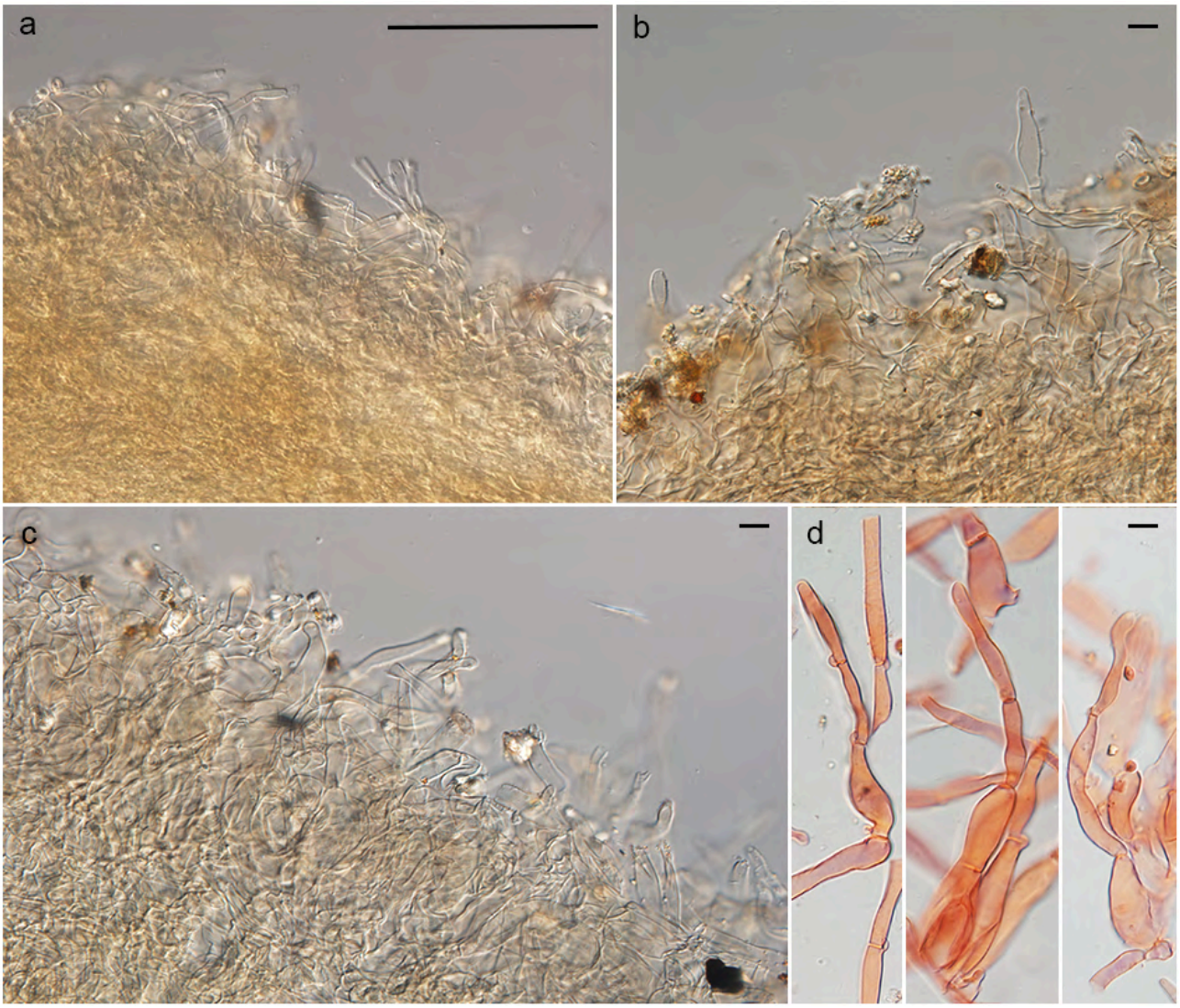

Figure 4. Pileipellis features of *Pseudobaeospora taluna* (MEL 2446695). **a** disrupted trichoderm showing bluish green staining, **b** closer detail with fusiform pileocystidium, **c** closer detail with flexuose hyphae, **d** pluriseptate elements with inflated subterminal hyphae, terminating in pileocystidia. All in in 5% KOH except for **d** which is in 5% KOH with Congo Red. Scale **a**=100 µm, **b**–**d**=10 µm.

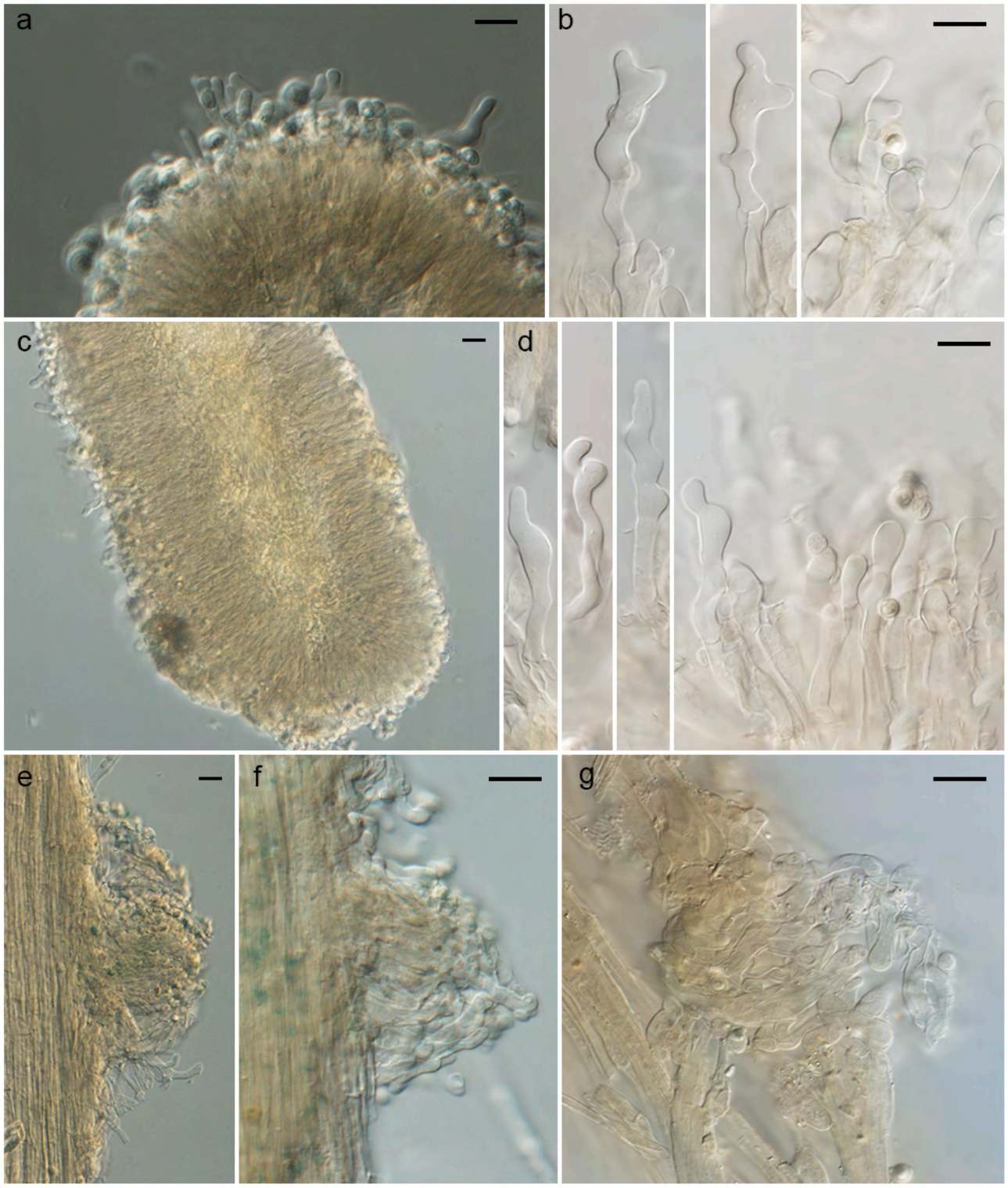

Figure 5. Cystidia of *Pseudobaeospora taluna* (MEL 2446695) in 5% KOH. **a** cheilocystidia emerging at lamellar edge, **b** detail of cheilocystidia **c** pleurocystidia emerging from lamellar face, **d** detail of pleurocystidia, **e**, **f**, **g** clustered caulocystidia on stipitipellis. Scale **a**–**g**=10 µm.

Figure 6. Illustration of sporing body of 2-spored collection of *Pseudobaeospora taluna* (MEL 2363200), scale=10 mm.

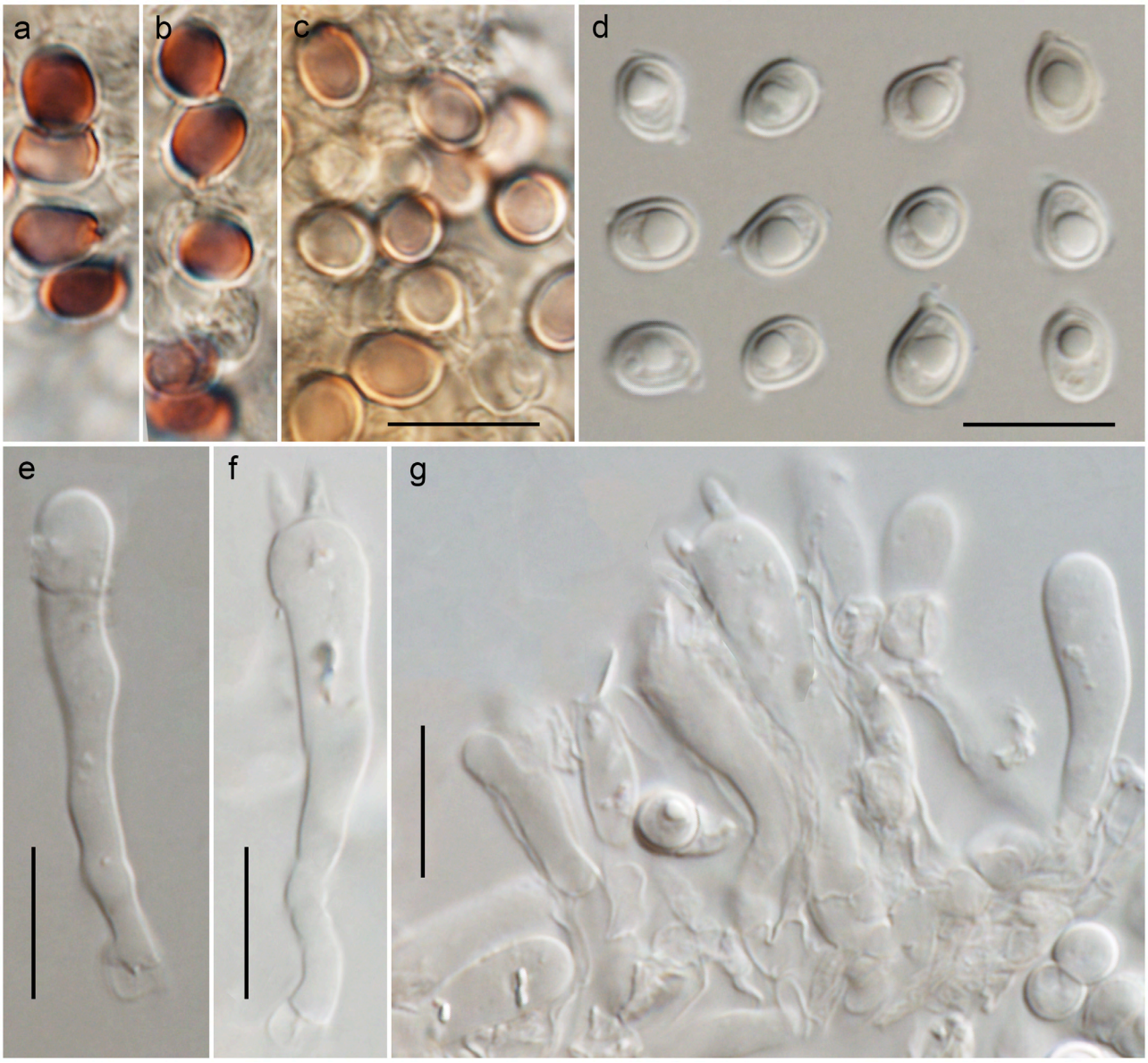

Figure 7. Microscopic features of 2-spored collection of *Pseudobaeospora taluna* (MEL 2363200). Basidiospores **a**, **b**, **c** dextrinoid in Melzer's reagent and **d** hyaline in 5% KOH, **e** basidiole in 5% KOH, **f** 2-spored basidium 5% KOH, **g** hymenium in 5% KOH with 2-spored basidium and basidioles. Scale **a**–**g**=10 µm.

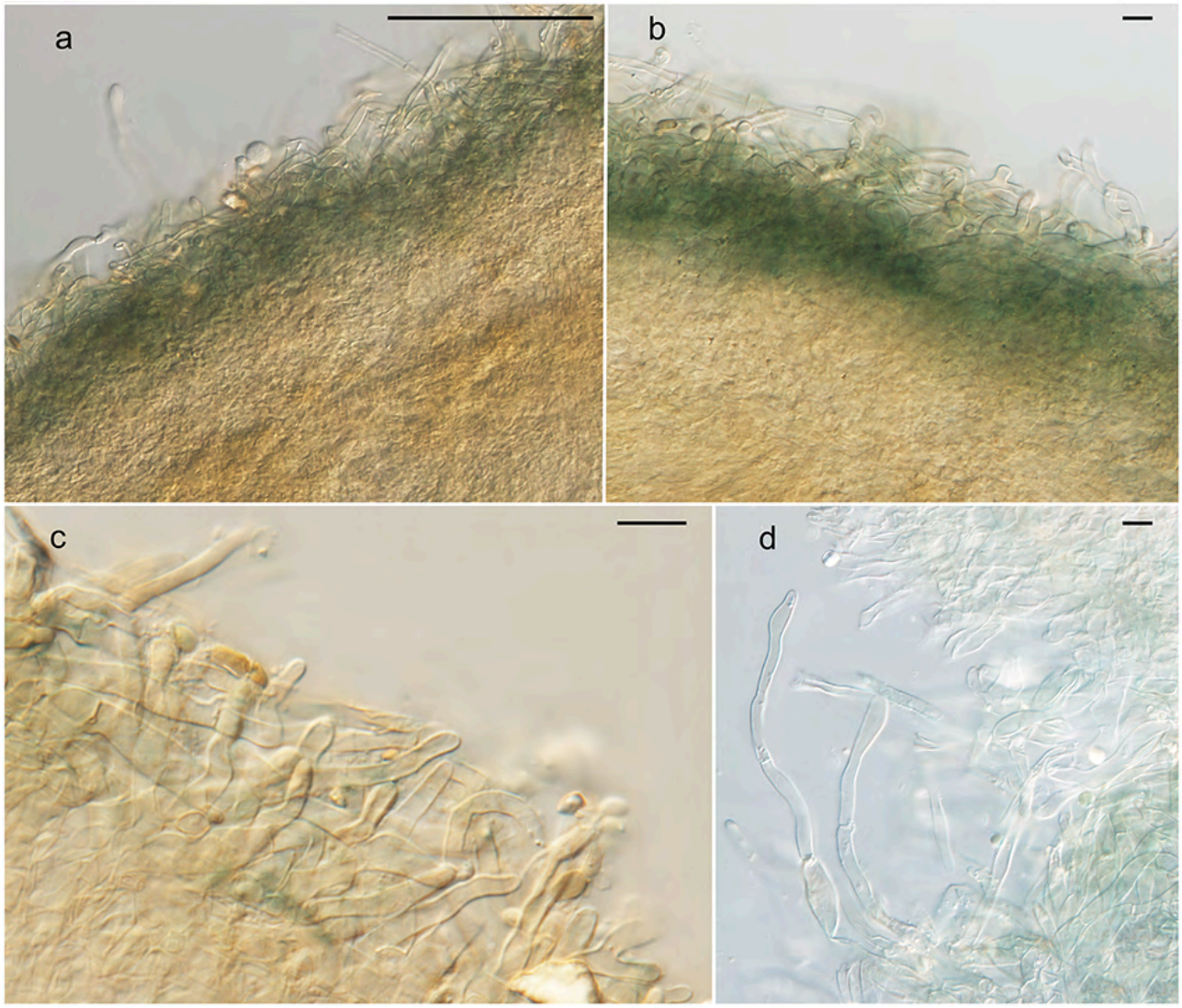

Figure 8. Pileipellis features of 2-spored collection of *Pseudobaeospora taluna* (MEL 2363200) in 5% KOH. **a** disrupted trichoderm showing strong bluish green staining, **b** closer detail, **c** closer detail with pileocystidia, **d** pluriseptate elements with inflated subterminal hyphae, terminating in pileocystidia. Scale **a**=100 µm, **b**–**d**=10 µm.

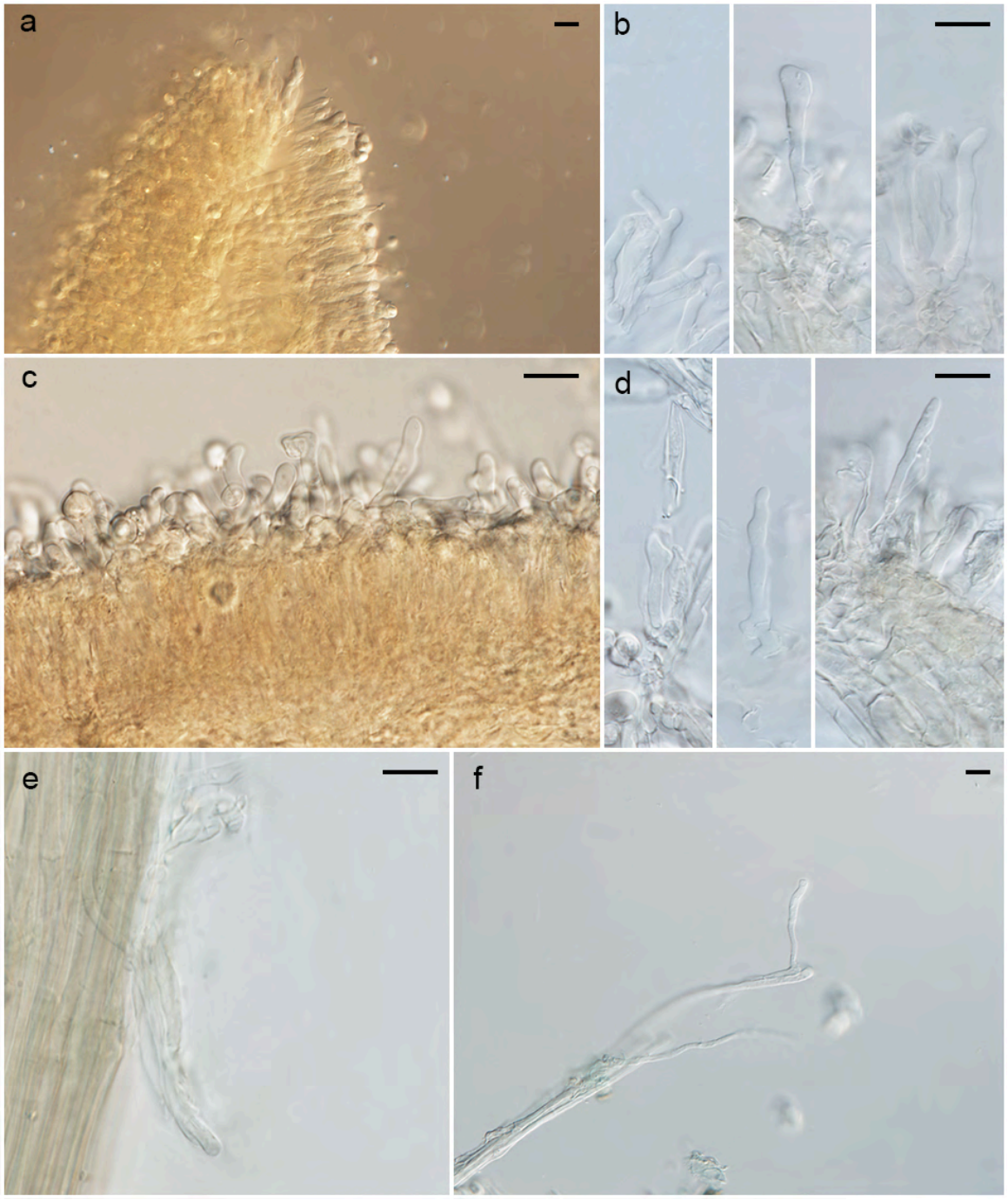

Figure 9. Cystidia of 2-spored collection of *Pseudobaeospora taluna* (MEL 2363200) in 5% KOH. **a** cheilocystidia emerging at lamellar edge, **b** detail of cheilocystidia, **c** pleurocystidia emerging from lamellar face, **d** detail of pleurocystidia, **e** clustered caulocystidia on stipitipellis, **f** single caulocystidium observed in crush mount. Scale **a**–**f**=10 µm.