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Auriscalpium greyorum sp. nov. (*Fungi*: *Russulales*: *Auriscalpiaceae*): an endangered earpick fungus from southern Australia

B. Clauss[1,2], L.J. Vaughan[1], G.D. Holmes[1], R. Richter[3] & T.W. May[1]*

[1] Royal Botanic Gardens Victoria, Birdwood Avenue, Melbourne, Victoria 3004, Australia
[2] Independent researcher, Denver, Colorado 80220, U.S.A.
[3] Citizen scientist, Monbulk, Victoria 3793, Australia
*Corresponding author: tom.may@rbg.vic.gov.au
Luke J. Vaughan https://orcid.org/0000-0003-1659-9938; Gareth D. Holmes https://orcid.org/0000-0003-1120-8731; Tom W. May https://orcid.org/0000-0003-2214-4972

Abstract

Auriscalpium greyorum is described for the fungus previously known as *Auriscalpium* sp. "Blackwood", an endangered species known from few sites in *Eucalyptus* forests in Victoria, Australia. Microscopically, *A. greyorum* is consistent with other species of the genus by the presence of amyloid, ornamented spores and gloeoplerous hyphae and cystidia — but the very reduced stipe, at most 7 mm long, embedded in the bark of the substrate, differs from the well-developed stipe present in most other species of the genus. Phylogenetic analysis of internal transcribed spacer (ITS) rDNA demonstrated that *A. greyorum* is well-separated from the seven other named species of *Auriscalpium* for which sequence data are available, including from *A. andinum*, a South American species with a very short stipe. Within the clade of *Auriscalpium* species, sequences of collections from the southern hemisphere, including *A. greyorum*, form a grade, with sequences from *Gloiodon, Dentipratulum* and *A. villipes* (from Mexico) interspersed between this southern hemisphere grade and the clade of the remaining northern hemisphere species of *Auriscalpium*. Therefore, further exploration of the generic limits of these three genera is warranted. *Auriscalpium greyorum* is threatened by inappropriate fire regimes, habitat disturbance and climate change.

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Introduction

Auriscalpium Gray is a long-established genus, the type of which, *Auriscalpium vulgare* Gray, was originally described by Linnaeus as *Hydnum auriscalpium* L. (Linnaeus 1753). The word *Auriscalpium* derives from Latin *auris* (ear) and *scalpo* (to scratch) and *A. vulgare* is commonly called the ear-pick fungus, due to the resem-

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blance of the small and laterally attached pileus on a long stipe to an ear-pick. Ryvarden (2001) accepted eight species in *Auriscalpium*, to which have been added *A. microsporum* P.M.Wang & Zhu L.Yang and *A. orientale* P.M.Wang & Zhu L.Yang (Wang & Yang, 2019). Macroscopically, species of *Auriscalpium* are pileate, stiptitate and with a spinose hymenophore; microscopically, the genus is characterised by amyloid spores that are ornamented, either a monomitic or dimitic hyphal system and the presence of gloeoplerous hyphae and cystidia (Maas Geesteranus 1966, 1971, 1978; Maas Geesteranus & Rammeloo 1979; Stalpers 1996; Ryvarden 2001; Wang & Yang 2019).

Maas Geesteranus (1963) introduced the family *Auriscalpiaceae* for *Auriscalpium*, *Gloiodon* P.Karst. and *Lentinellus* P.Karst. These three genera display quite different hymenophores (spines in the first two but lamellae in *Lentinellus*), but were united by the presence of gloeocystidia and production of minutely echinulate, amyloid spores. Phylogenetic analyses of sequence data consistently recovers the family *Auriscalpiaceae* as including *Auriscalpium, Gloiodon* and *Lentinellus*, but also including *Artomyces* Jülich (coral-like, with multiple branches and smooth hymenium) and *Dentipratulum* Domański (with a spinose hymenophore) (Larsson & Larsson 2003; Miller et al. 2006; Chen et al. 2015).

A rare spinose fungus with a rudimentary stipe, known from few locations in Victoria, has been designated as *Auriscalpium* sp. "Blackwood" and assessed as Endangered on the IUCN Red List of Threatened Species (May 2019). We here formally describe this fungus on the basis of morphological and phylogenetic analyses.

Methods

Presentation of names

Names of taxa at all ranks are italicised following Thines et al. (2020).

Morphological examination.

Macromorphological characters were described from fresh collections, field notes and photographs made at the time of collection. Colours were described from fresh collections in daylight conditions, and where possible according to Kornerup & Wanscher (1978). Macroscopic features were observed and photographed using an Olympus SZX16 stereomicroscope with an Olympus DP73 camera attachment and measured using measurement tools on Olympus cellSens Standard (v. 1.16, Olympus Corporation, Tokyo, Japan). Habitat, host tree, associated species, and appearance season information are based on field notes. Additional seasonal appearance information is based on iNaturalist observation records.

Micromorphological characters were described from examination of dried herbarium specimens, from which hand-cut sections were rehydrated in H_2O or 5% KOH, as specified, to observe pellis, trama and hymenium tissues. Spine sections were 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 bright field microscope with differential interference contrast and an Olympus DP73 camera attachment. Measurements were taken at ×400 or ×1000 (with oil immersion) using measurement tools on Olympus cellSens standard.

Spore measurements are shown as a raw range followed by the range of collection means from measurements of 10 randomly selected mature spores per collection observed from spine tissue, with grand mean in italics. The number of spores measured (A), from the number of collections examined (B), is shown as (A/B). The quotient 'Q' is the ratio of spore length to spore width and is given as the range of individual values, followed by the range of collection means with the grand mean in italics. All other measurements are given as observed ranges.

DNA isolation, PCR and sequencing.

DNA was isolated from selected herbarium specimens (Table 1) using a modified CTAB method based on that of Gardes & Bruns (1993) and outlined in Craig et al. (2023). The internal transcribed spacer (ITS) region was PCR amplified using the primers ITSF and ITS4 (White et al. 1990; Gardes & Bruns 1993). Domains D1–D2 of the large subunit (LSU) of rDNA were PCR amplified using primers LR5 and LROR (Vilgalys & Hester 1990; Vilgalys Lab 1992). Sequencing was undertaken by AGRF (Melbourne, Australia) using the same primers as used for PCR amplification. The resulting chromatograms were aligned, manually checked and edited using Geneious Prime (Version 2021.0.3, https://www.geneious.com) to generate consensus sequences (Table 1). LSU sequences were generated to provide reference sequences for the new species, but were not analysed further.

Phylogenetic analyses.

ITS sequences identified as *Auriscalpium* in NCBI GenBank and UNITE (Abarenkov et al. 2023) were selected and added to sequences newly generated from MEL specimens. Additional sequences from GenBank and UNITE that had a percentage identity of greater than 80% in BLAST searches to *Auriscalpium greyorum* (OQ750680) and *Auriscalpium* sp. (OQ750681) were also acquired (Altschul et al. 1990; Morguliset al. 2008). Sequences representing genera in *Auriscalpiaceae* (*Artomyces, Dentipratulum*, *Gloiodon* and *Lentinellus*) and the outgroup *Gloeocystidiellaceae* (*Gloeocystidiellum*) were selected based on a phylogeny of the Russulales (Miller et al. 2006) and phylogeny of *Artomyces* (Cai et al. 2025). Sequences less than 675 bp and those with missing data were removed from the alignment, unless they were

Table 1. ITS and LSU sequences newly generated for this study.

Taxon	Specimen	Locality	GenBank Accession		Type status
			ITS	LSU	
Auriscalpium greyorum	MEL 2305170	Australia: Victoria	OQ750676	KP311332	
Auriscalpium greyorum	MEL 2323326	Australia: Victoria	OQ750677	PP715652	Holotype
Auriscalpium greyorum	MEL 2524521	Australia: Victoria	OQ750678		
Auriscalpium greyorum	MEL 2524522	Australia: Victoria	OQ750679	PP715638	
Auriscalpium greyorum	MEL 2524894	Australia: Victoria	OQ750680	PP715644	
Auriscalpium sp. AUS1	MEL 2524898	Australia: Victoria	OQ750681		
Auriscalpium sp. AUS1	MEL 2524899	Australia: Victoria	OQ750682		
Auriscalpium sp. AUS1	MEL 2533852	Australia: Tasmania	PP508274		

among the only representative sequence available for taxa (e.g. *Gloiodon nigrescens*, AF506450).

The selected ITS sequences (Supplementary material 1: https://doi.org/10.6084/m9.figshare.28856345) were aligned using MUSCLE Alignment (Version 3.8.425) as implemented in Geneious Prime (1000 maximum iterations, 100 maximum trees, all other settings default) (Edgar 2004). The alignment was manually checked and edited and the ends were trimmed. Maximum Likelihood (ML) phylogeny was estimated with IQ-TREE 2.2.2.6 (Nguyen et al. 2015; Minh et al. 2020), using TIM+F+G4 substitution model selected by ModelFinder (Kalyaanamoorthy et al. 2017), and 10,000 Ultrafast bootstrap (UF) replicates (Hoang et al. 2018). The ITS alignment for the above analyses is deposited in figshare (Supplementary material 2: https://doi.org/10.6084/m9.figshare.28856345).

Results

The aligned ITS dataset contained sequences from 112 specimens representing 22 species and comprised 759 characters, of which 365 characters were constant and 310 were parsimony informative. In the ML phylogenetic tree based on ITS sequence data (Fig. 1) the *Auriscalpiaceae* clade has 100% support (cited support values are Ultrafast bootstrap). Within *Auriscalpiaceae*, sequences from representative species of the genera *Artomyces*, *Lentinellus* and an un-named clade of environmental sequences from Colombia form well-supported clades (100%). The remaining sequences form a well-supported clade (99%) that is sister to this group, and contains species of *Auriscalpium, Dentipratulum* and *Gloiodon*. Australian sequences within this group are placed in three of six southern hemisphere species-level clades. Of these, only *Auriscalpium barbatum* from Western Australia, *A. umbella* from New Zealand, and *Gloiodon nigrescens* from Indonesia are so far formally named.

A well-supported clade (100%) representing *Auriscalpium greyorum sp. nov.* is sister to a clade (100%) containing *A. umbella* (99%) and an unnamed Australian species, AUS1 (100%). This group is sister to the remaining sequences of *Auriscalpiaceae*. *Auriscalpium barbatum* (94%) from Western Australia and an undescribed species from New Caledonia, NC1 (99%), are placed within a well-supported (100%) clade that is sister to other *Auriscalpiaceae* (except the *A. greyorum* / *A. umbella* / *A.* sp. AUS1 clade). Within these other *Auriscalpiaceae* sequences, *Dentipratulum*, *Gloiodon* and a clade of *Auriscalpium* sequences from Mexico and Ecuador each have high support (100%, 99%, 100%, respectively), and together form a clade (99%) that is sister to a well-supported clade (100%) containing northern hemisphere *Auriscalpium* species, including the type species, *A. vulgare*. Within this clade, the *Auriscalpium orientale* clade (91%) is sister to a clade (100%) containing the *A. microsporum* clade (100%) and the clade of *A. vulgare* group (92%). Within the *A. vulgare* group, there is a clade of Eurasian sequences (97%) that contains two North American specimens labelled *A.* cf. *vulgare* and the other North American specimens labelled *A.* cf. *vulgare* form a separate clade (with moderate support).

Discussion

Auriscalpium greyorum extends the range of morphological characters exhibited by *Auriscalpium* to include a much-reduced stipe embedded in substrate tissue. *Gloiodon* has been distinguished from *Auriscalpium* on the basis of the lack of a stipe, but in addition the habit is resupinate to effused-reflexed and the context is fibrous rather than compact as in *A. greyorum*. Therefore, on morphological grounds, *A. greyorum* fits best within *Auriscalpium*.

Australasian species of *Auriscalpium* have not previously been included in phylogenetic analyses of the genus. The Australasian species, including the named species *A. barbatum* and *A. greyorum* (from Australia) and *A. umbella* (from New Zealand), as well as several un-named species from Australia and New Caledonia, fall in a grade at the base of the clade containing *Auriscalpium* +

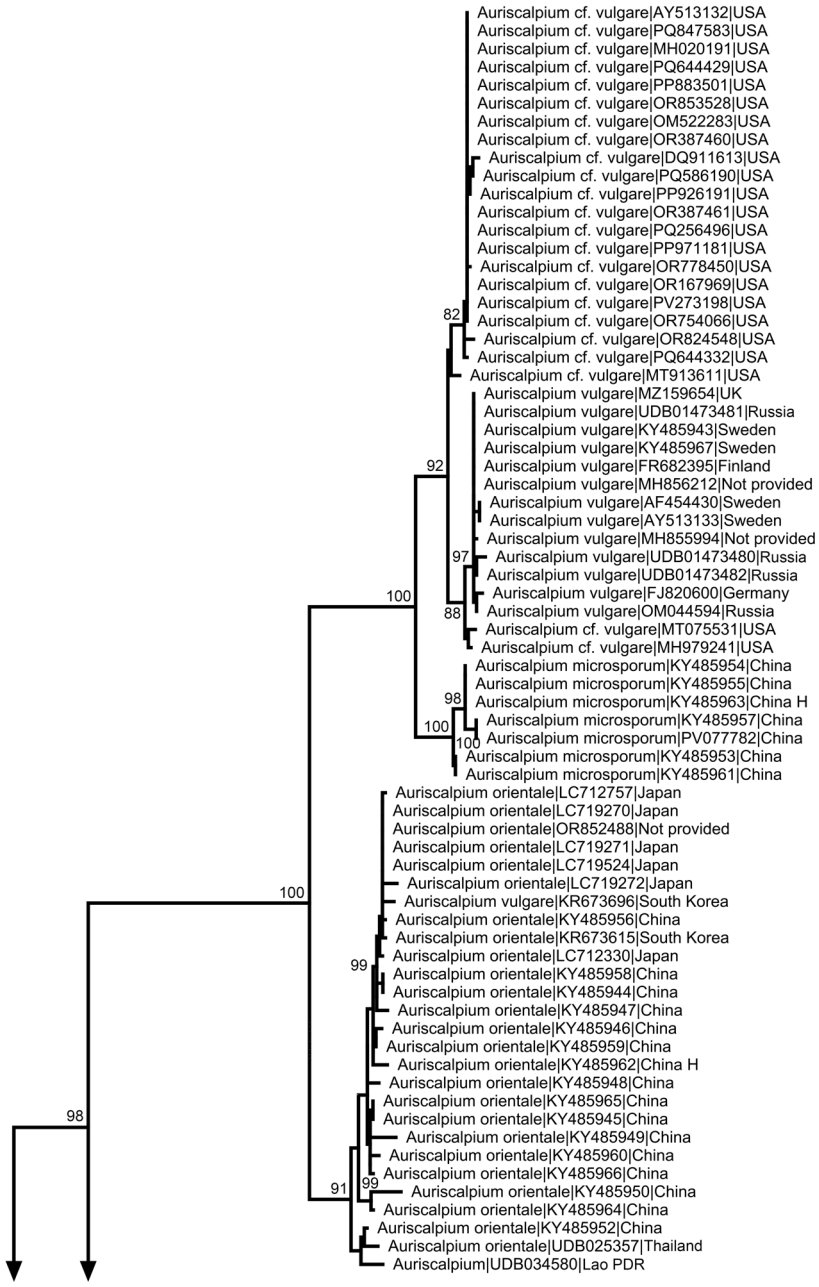

Figure 1. Maximum Likelihood phylogenetic tree based on ITS sequences of *Auriscalpiaceae* and *Gloeocystidiellaceae* from NCBI and UNITE or newly generated for this study. Support for clades is indicated by UF bootstrap percentage at nodes for values >80%. *Gloeocystidiellum porosum* was used as outgroup. Sequences in bold type were generated through this project. The clade highlighted in light red represents the newly described species. Two clades comprised of sequences from New Caledonian and Australian collections that are not formally named are shown in light grey highlight. H = holotype.

Gloiodon + *Dentipratulum.* Therefore, the option of erecting a new genus for the Australasian species (in order to retain *Gloiodon* and *Dentipratulum* as independent genera) is not phylogenetically sound, and in any case, we consider this cannot be supported by morphological synapomorphies. Indeed, the molecular phylogeny calls into question the distinction between *Auriscalpium* and *Gloiodon* as already noted by Larsson & Larsson (2003). Analysis of further DNA markers is advisable before formal synonymy of the two genera is proposed. However, in relation to the placement of the species newly described here, because *Auriscalpium* has priority over *Gloiodon*, the former genus would remain the correct home for *A. greyorum* if *Auriscalpium* and *Gloiodon* were to be synonymised.

Taxonomy

Auriscalpium greyorum B.Clauss, L.J.Vaughan & T.W.May, sp. nov.

MB 848128

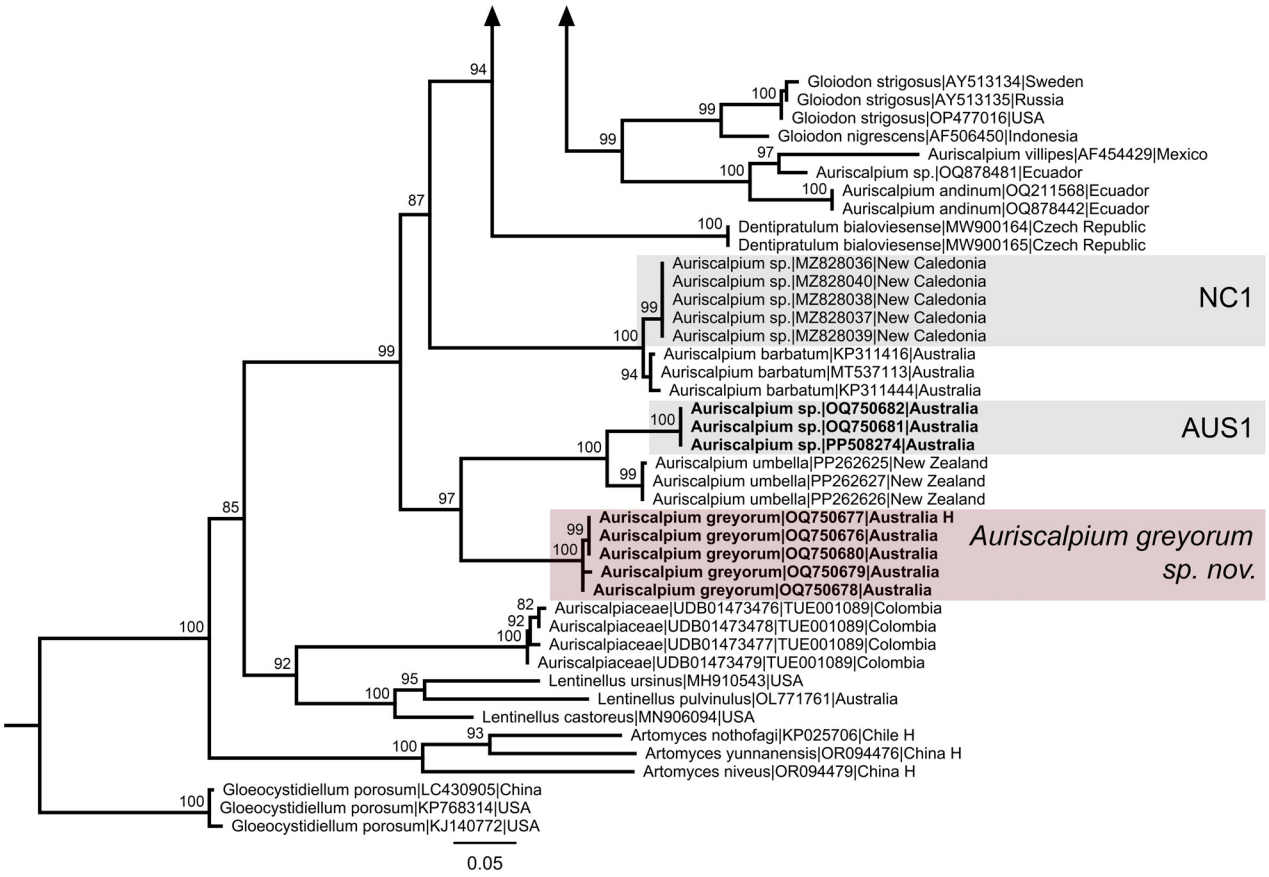

Figure 1. (Continued).

Type: AUSTRALIA, VICTORIA, Blackwood, Jack Cann Reserve, 1 July 2007, *Field Naturalists Club of Victoria Fungi Group 69* (**holotype** MEL 2323326). GenBank: ITS = OQ750677, LSU = PP715652.

Synonymy: *Auriscalpium* sp. "Blackwood" as used in May (2019).

Figs 2–3.

Basidiomes annual, pileate, laterally attached to substrate with reduced stipe. **Pileus** (3–)6–19 mm wide, 6–10(–14) mm deep horizontally from bark attachment to margin, up to 4 mm high from top of pileus to margin, semi-circular to kidney-shaped in top-view, side view hemispherical or campanulate, then plano-convex to almost plane; at first reddish brown (8D7), then chocolate brown (6F4), with darker patches of dark brown (9F8) at margin and in radial fibrils, often paler toward margin when young, often very dark brown when old; surface texture sparsely hispid, often more dense near attachment to bark and on younger specimens, bristles up to 1 mm, erect or forming appressed radial fibrils when flattened, hyaline to pale buff (4A2–3) to greyish red (8B6); margin sometimes becoming inrolled when dry, wavy, splitting radially, not translucent-striate. **Spines** pendant, up to 4 mm long, 0.2–0.5 mm diameter at base, close, terete, tapering slightly toward apex; apex rounded or acute; at first spines strongly decurrent running down stipe, with spines more well-developed on stipe than underside of pileus, then sometimes not decurrent, and with spines more well-developed close to stipe and less-developed closer to margin; almost white (1A1) to greyish white (1B1) to pale buff (1B3), sometimes with reddish tinge, with white dusting under lens, if acute, with vinaceous portion at apex. **Stipe** 1–4(–7) mm long, 1–2(–3) mm diameter, mostly embedded in bark, up to depth of 2–3 mm, sometimes narrowing in middle with slightly bulbous base; brown (6F4), with similar variations to pileus; surface with a layer of dense fine fibrils, from which arise erect, hispid processes that are up to 1 mm long, hyaline to pale buff (4A2) to greyish red (8B6); the fibrous layer with hispid processes contiguous with similar layer at base of pileus. **Context** in pileus 0.5–2 mm deep, concolourous with surface, or with very fine scattered pale buff mottling, when drying, pale buff (4A2–3), contiguous with stipe context; in stipe similar in colour to pileus context; in spine buff (4A3), to greyish red (8B6) when old.

Hyphal system monomitic, with septate, thick-walled generative hyphae (2–)3–6(–10) µm wide, and aseptate, thin-walled gloeoplerous hyphae 3–7 µm wide. **Clamp connections** detected in all tissues except gloeoplerous hyphae. **Trama** in pileus and stipe consisting of interwoven generative hyphae, cylindrical or varying in diameter, sometimes inflated in sections, often slightly flexuose, branching, sometimes with right-angled branches, with occasional gloeoplerous hyphae, cylin-

Figure 2 Macroscopic features of *Auriscalpium greyorum.* **a**,**b** Sporing bodies in habitat, on bark of living *Eucalyptus radiata* (MEL 2524521), photographs by Reiner Richter (CC) BY-NC-SA, **c** Pileus in oblique top view (MEL 2524521), **d** Cross-section of sporing body embedded in bark substrate, stipe and pileus surface with a layer of dense fine fibrils (MEL 2524521), **e** Detail of spines (MEL 2524522), **f** Cross-section of sporing body when drying, with stipe embedded in bark substrate (MEL 2524894). Scale=1 mm.

drical; in spine consisting of parallel generative hyphae, cylindrical to slightly inflated or fusiform, often with short segments, gloeoplerous hyphae cylindrical, often slightly flexuose, sometimes with right-angled bend, terminating as cystidia arising above basidia. **Subhymenium** narrow, consisting of interwoven, parallel, generative hyphae. **Pileipellis** an interwoven layer of hyaline, thick-walled generative hyphae, cylindrical, flexuose, with rounded terminal elements, coalescing perpendicular to pileus surface in places, forming interwoven erect bristle formations up to 1300 µm; gloeoplerous hyphae arising from context and terminating in surface layer, to half-way up bristles, as pileocystidia, widening to 7–10 µm toward apex, apex rounded

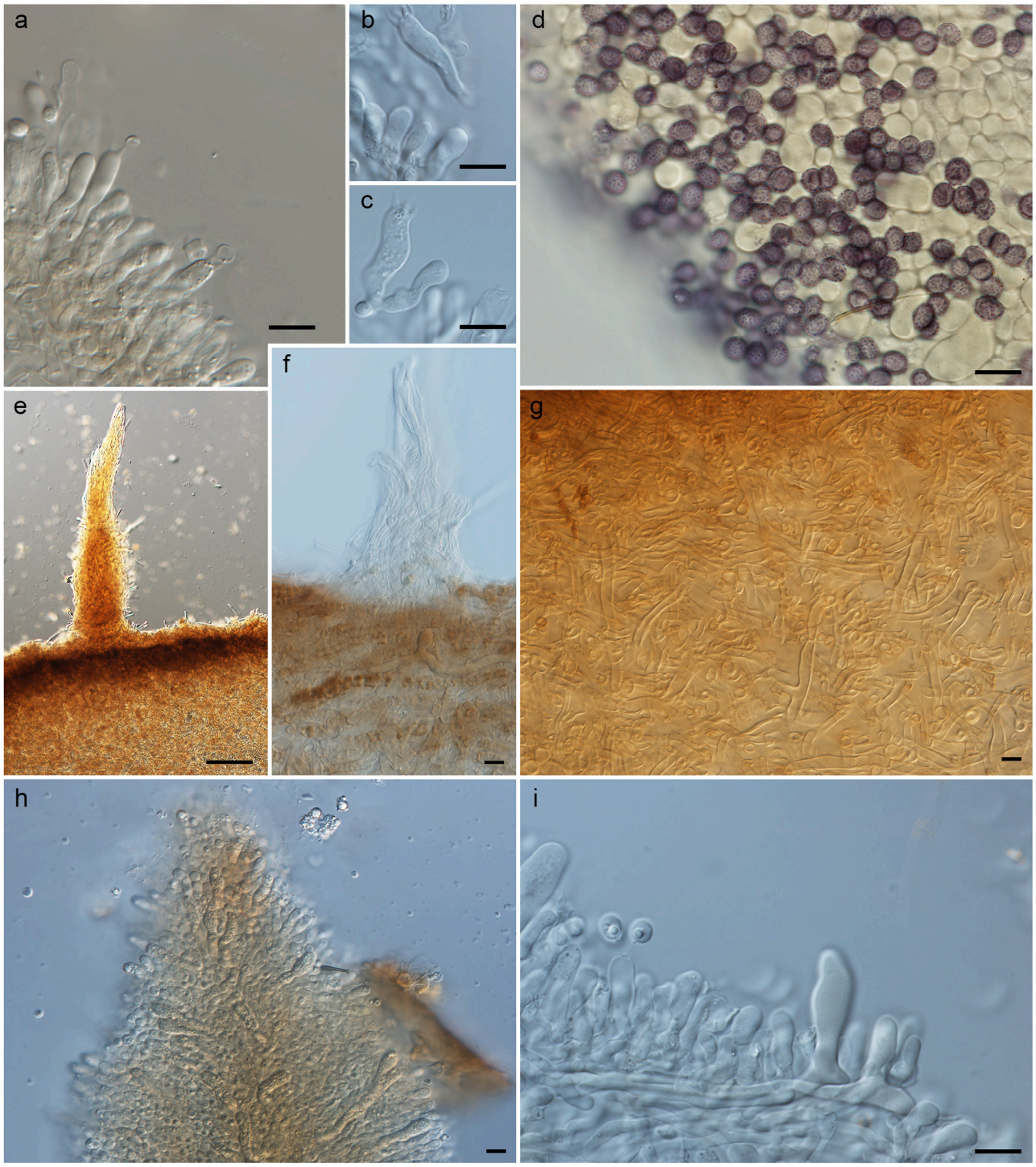

Figure 3 Microscopic features of *Auriscalpium greyorum*. **a**–**c**, **e**–**i** in 5% KOH; **d** in Melzer's reagent. **a**–**c** Basidia and basidioles (**a** H: MEL 2323326, **b**,**c** MEL 2305170), **d** Amyloid spores with finely verrucose ornamentation, on spine (MEL 2305170), **e** Pileipellis with bristle at low magnification (H: MEL 2323326), **f** Pileipellis at higher magnification with interwoven, erect, hyaline bristle formation, pigment-banded subpellis and emergent gloeoplerous hyphae (H: MEL 2323326), **g** Pileus trama just below pileipellis (H: MEL 2323326), **h** Spine with pleurogloeocystidia at edge, and cheilogloeocystidia at apex (MEL 2524522), **i** Pleurogloeocystidia emergent above hymenium, with right-angle bend and bump near bend, arising from parallel hymenophoral trama (MEL 2305170). Scale **a**–**d**, **f**–**i**=10 µm; **e**=100 µm. H = holotype.

to slightly inflated. **Subpellis** of roughly parallel thick-walled generative hyphae with bands of reddish-brown pigment. **Stipitipellis** like pileipellis with thicker interwoven hyaline surface layer, bristles up to 2000 µm. **Stipe context** like pileus context. **Basidia** (15–)20–30(–34) × (4–)5–7(–8) µm, narrowly clavate to clavate, 2–4 µm wide at base, 4-spored; sterigmata 3–5 µm long, 1–1.5 µm wide at base, tapering toward tip. **Basidiospores** (4.5–)5–7 × 4–6 µm (60/6), means 5.45–*5.75*–6.18 × 4.37–*4.73*–4.95 µm, Q:

1.00–1.38(–1.46), means 1.12–*1.22*–1.27, globose, subglobose or broadly ellipsoid, sometimes ellipsoid, ornamentation finely verrucose, of small, isolated, blunt, round to elongated warts, amyloid, apiculus to 1 µm. **Pleurogloeocystidia** (5–)8–10 µm wide, cylindrical to clavate, apex rounded to subcapitate, originating from parallel gloeoplerous hyphae in the spine context, often with abrupt right-angled bend, sometimes with bump near bend, or rarely branching without septa, arising parallel with basidia and terminating above hymenium, 30–60 µm long from bend to apex. **Cheilogloeocystidia** of similar size and shape, mostly without abrupt bend, also originating from parallel gloeoplerous hyphae in the spine context and extending conspicuously beyond basidia at spine apex.

Additional specimens examined: AUSTRALIA, VICTORIA: Blackwood, Jack Cann Reserve, 3 July 2005, *Field Naturalists Club of Victoria Fungi Group 11* (MEL 2524519); Blackwood, Jack Cann Reserve, 2 July 2006, *Field Naturalists Club of Victoria Fungi Group 55* (MEL 2305170); Macedon, Lagoon Park, 27 August 2022, *T.W. May 2142* (MEL 2524894); Gembrook, Kurth Kiln Regional Park, Shortcut Track, 30 August 2022, *L.J. Vaughan 2, T.W. May & R. Richter* (MEL 2524521); Gembrook, Kurth Kiln Regional Park, Scout Loop Track, 30 August 2022, *L.J. Vaughan 3, T.W. May, R. Richter* (MEL 2524522).

Diagnostic features. Auriscalpium greyorum is distinctive because of the combination of the habit on the trunk of living eucalypts, the very reduced stipe (the base of which is embedded in bark) and the small sporing bodies that are eventually dark brown with a hispid to appressed fibrillose surface. *Auriscalpium greyorum* is well-separated on the basis of ITS sequences, with the closest taxa having at most 91.3% similarity (Fig. 1).

Distribution & habitat. Found in Victoria in mixed *Eucalyptus* forest with *Eucalyptus obliqua*, *E. radiata* and *E. viminalis* and understory of species of *Acacia*, *Banksia*, *Olearia*, *Pomaderris*, *Pteridium esculentum* and grasses, at altitudes 157–612 m above sea level. Occurring from single sporing bodies to large colonies on the bark of living *E. radiata*, 1–6 m above ground; long-lived, persistent on host trees from April–October.

Conservation status. This species was assessed as Endangered for the IUCN Red List of Threatened Species in 2019 based on an estimated population size of less than 250 mature individuals (May 2019). At that time it was known from only two sites, the type locality at Blackwood and at Olinda, and at each site it was present on a single tree. It has since been found at several more sites in Victoria, in Kurth Kiln Regional Park (e.g. https://inaturalist.ala.org.au/observations/54820259) and Bunyip State Park (https://inaturalist.ala.org.au/observations/45047751) and at Lagoon Park, South of Woodend (https://inaturalist.ala.org.au/observations/131947470). Even with these additional sites, the estimates used in the Red List assessment of between 10 and 100 sites and between 40 and 400 mature individuals remain plausible. Threats to *A. greyorum* include inappropiate fire regimes, climate change and disturbance; with some of the sites being close to motor- and mountain bike trails.

Etymology. Named in honour of Edmund "Ed" Grey (1930–2021) and Patricia "Pat" Grey, who have made significant contributions to the knowledge of Australian fungi, including recognition of the distinctiveness and rarity of this species which was first collected in 2005 by Ed and Pat during an excursion of the Field Naturalists Club of Victoria Fungi Group.

Notes. Auriscalpium greyorum is highly distinctive among species of the genus *Auriscalpium* due to the inconspicuous stipe that is buried in the fibrous bark of the host tree. Most other species of *Auriscalpium* have a well-developed stipe, either central or lateral, but usually more than around 10 mm long (and often much longer), including the three species of the genus that lack sequences, *A. dissectum* Maas Geest. & Rammeloo (Congo), *A. gilbertsonii* Ryvarden (Costa Rica) and *A. fimbriatoincisum* (Teng) Maas Geest. (China) (Ryvarden 2001). The species with the shortest stipe is *A. andinum* (Ecuador), where the stipe is 5 mm long supporting a lateral pileus. This species has spores of similar size to *A. greyorum*, but the ITS sequences of the two species are quite dissimilar and *A. andinum* does not fall in the clade of Australasian species of *Auriscalpium*.

In comparison to species of *Gloiodon, A. greyorum* is morphologically most similar to *G. nigrescens*, which is the only species of the genus known from the southern hemisphere, but *G. nigrescens,* as documented from a collection from Bali, Indonesia by Desjardin and Ryvarden (2003), differs by the growth habit on dead hardwoods, deeply incised, digitiform margin, densely tomentose upper surface, lack of a stipe, distinctly shorter spines, and smaller spores.

In the field, as far as other hydnoid fungi occurring in Victoria, *A. greyorum* is superficially similar to *Pseudohydnum gelatinosum* (Scop.) P.Karst. in the broad sense and *Beenakia dacostae* D.A.Reid, which are both small, hydnoid fungi that may grow on or near trees in *Eucalyptus forests*. However, *A. greyorum* is easily differentiated from *P. gelatinosum* because it lacks a gelatinous texture, the pileus is smaller and dark brown, and the spines are up to 4 mm long compared to 1 mm long in *P. gelatinosum* and the Tasmanian species *P. tasmanicum* Y.C.Dai & G.M.Gates (Zhou et al. 2022). *Beenakia dacostae* is similar in size and general morphology to *A. greyorum* but typically has a more conspicuous stipe, a decurrent spine layer and a pale pileus, and is found growing on trunks of *Dicksonia antarctica* or on the soil under logs rather than on standing *Eucalyptus*. Microscopically, the amyloid spores clearly separate *A. greyorum* from both *P. gelatinosum* and *B. dacostae* (Reid 1955; Zhou et al. 2022).

Disclosures

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Author contributions: BC and LV contributed equally to preparation of the manuscript. LV, RR and TM collected specimens. BC and LV conducted microscopy and LV carried out photo-microscopy and prepared plates and tables. LV sampled specimens for DNA. GH performed DNA isolations, PCR and chromatogram processing. LV assembled sequence alignments and produced the phylogeny. BC, GH and LV wrote methods; BC and LV prepared the species description; BC, LV and TM wrote introduction, results and discussion; and TM edited the final manuscript. All authors read and approved the final manuscript.

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