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A new species of *Porpoloma* Singer (*Fungi*: *Agaricales*, *Tricholomataceae*) from eastern Australia

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Abstract

Porpoloma Singer is a genus of mushrooms distinguished by a tricholomatoid habit and amyloid spores. The genus is restricted to temperate regions of the southern hemisphere, with currently accepted species known from New Zealand and South America. Apart from *P. penetrans* (Cleland) Grgur., which most likely does not belong in *Porpoloma* but is suggested to be a species of *Heimiomyces* Singer, no species of *Porpoloma* have been described from Australia. However, molecular phylogenetic analyses indicate the presence of at least nine species in Australia. Here, we describe *P. flavilamellatum* from sporing body material from New South Wales. The species is also detected from sequences generated from soil samples collected in Queensland. *Porpoloma flavilamellatum* is distinguished macroscopically from some members of the genus by having yellow lamellae, and by other members of the genus that also have yellowish lamellae (*P. amyloideum* (G. Stev.) E. Horak, *P. coyan* Garrido, *P. sejunctum* Singer) by having darker yellow lamellae, lacking a membranous annulus or zone on the stipe, and being found in habitats with *Myrtaceae* Juss. rather than *Nothofagaceae* Kuprian. It is distinguished from all other members of the genus *Porpoloma* by its unique phylogenetic position.

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Introduction

Porpoloma Singer is a genus of mushroom-forming fungi with pale spores in the family *Tricholomataceae* R. Heim. It was originally described to accommodate *P. sejunctum* Singer, a species from southern South America associated with *Nothofagus* Blume (Singer 1952). Species of *Porpoloma* are macromorphologically similar to look-alike species of the genus *Tricholoma* (Fr.) Staude, but can be distinguished by a positive amyloid reaction of basidiospores in iodine solution (Singer 1952). Three species described by Singer (1952) from South America (*P. sejunctum*, *P. portentosum* Singer and *P. terreum* Singer) form ectomycorrhizal associations with species

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of *Nothofagus* (Trappe 1962, Sánchez-García et al. 2014). Additional species from the northern and southern hemispheres have since been described by various authors (Index Fungorum 2025). Singer (1962) classified *Porpoloma* into three subgenera based on differences in cheilocystidia and colour changes when cut or bruised: subg. *Porpoloma*, subg. *Pseudotricholoma* Singer, and subg. *Pogonoloma* Singer.

Sánchez-Garciá et al. (2014) presented a multi-locus phylogeny of *Tricholomataceae* that revealed *Porpoloma* was polyphyletic and recognised four genera: *Porpoloma* in the strict sense, *Corneriella* Sánchez-García, *Pseudotricholoma* (Singer) Sánchez-García & Matheny and *Pogonoloma* (Singer) Sánchez-García. Some species first described in *Porpoloma* were transferred to these segregate genera, such as *Porpoloma bambusarum* Desjardin & Hemmes from Hawaii, which is now the type species of *Corneriella* Sánchez-García (Sánchez-Garciá et al. 2014). The genus *Porpoloma* in the strict sense was restricted to species from temperate regions in the southern hemisphere, with smooth, amyloid, ellipsoid spores and brownish intracellular pigments in hyphae of the pileipellis (Sánchez-Garciá et al. 2014). The species confirmed in *Porpoloma* by the phylogeny of Sánchez-García (2014) include *P. portentosum, P. sejunctum, P. terreum*, and two undescribed species from Australia. The phylogenetic placement of other species remains unresolved due to an absence of molecular data from these species. *Porpoloma adrianii* Raithelh., *P. amyloideum* (G. Stev.) E. Horak, and *P. coyan* Garrido are all southern hemisphere species that are likely representatives of *Porpoloma*, but there are several species described from the northern hemisphere whose correct placement has not yet been established.

Recent observations from the citizen-science platform iNaturalist (https://www.inaturalist.org/) have brought attention to a *Porpoloma* species occurring in the Australian state of New South Wales. An ITS DNA barcode for fungi (Schoch et al. 2012) was obtained for one observation (https://www.inaturalist.org/observations/166391651) through the Ohio Mushroom DNA Lab (Canan et al. 2024). Analysis of this sequence indicated this species was phylogenetically distinct from other *Porpoloma* species with sequences available on GenBank but was a close match to sequences on the curated ITS database UNITE (Abarenkov et al. 2023) that were generated from soil samples collected in Queensland. Recently, a sporing body collection was lodged in the National Herbarium of Victoria (MEL) which has enabled characterisation of the micro-morphology and provided a physical type specimen. Here, we formally describe the new species *Porpoloma flavilamellatum* based on morphological and molecular phylogenetic analysis.

Methods

Specimen selection

In order to cover the diversity of the genus in Australia, fungarium specimens identified as *Porpoloma* were selected for sequencing from the National Herbarium of Victoria (MEL), the Western Australian Herbarium (PERTH) and the New Zealand Fungarium – Te Kohinga Hekaheka o Aotearoa (PDD).

Morphology

The macromorphological description is assembled from descriptive notes and photographs of fresh collections recorded by collectors, as well as examination of dried material. Colours are described from photographs of fresh collections in daylight conditions.

The micromorphological description is based on examination of dried fungarium specimens, from which hand cut sections were rehydrated in H_2O, 5% potassium hydroxide (KOH) or Melzer's reagent (MLZ), as specified. Detailed examination of the holotype specimen forms the basis of the description. Microscopic features were observed and photographed using an Olympus BX51 microscope (Olympus, Tokyo, Japan) with an Olympus DP-73 camera attachment. Measurements were taken at ×400 or ×1000 (with oil immersion) using measurement tools in Olympus cellSens Standard (v. 1.16). Basidiospore measurements were recorded in MLZ for 30 spores from the holotype specimen. Basidiospore measurements are provided as the observed range of values, to the nearest half micrometre, with the mean italicised. Basidium measurements are provided as the observed range of values with the mean italicised. All other microscopic measurements are provided as the range of observed values, to the nearest half micrometre.

Sampling and DNA isolation

Fragments of dried lamellae were sampled from specimens and disrupted in 2 ml microcentrifuge tubes using a Tissue Lyser II bead mill (Qiagen, Germany). DNA was isolated from samples using a modified CTAB method summarised in Craig et al. (2023), based on that of Gardes and Bruns (1993). Polymerase chain reactions (PCR) were performed to amplify the internal transcribed spacer (ITS) rDNA region in 20 µl reactions using MyTaq Red Mix (Bioline, UK), 1 µl of DNA template and the primers pairs ITS5/ITS4 or ITS1F/ITS4 (White et al. 1990, Gardes and Bruns 1993), using methods outlined by Craig et al. (2023). Sequencing was undertaken by the Australian Genome Research Facility (AGRF, Melbourne, Australia) and chromatograms were aligned, manually checked and edited using Geneious Prime 2021.0.3 (https://www.geneious.com) to generate consensus sequences.

Phylogenetic analyses

ITS sequences generated in this study (Table 1) were assembled with sequences from species of *Porpoloma* and the closely related genus *Dennisiomyces* that were downloaded from NCBI GenBank, based on Sánchez-García et al. (2014). Additional *Porpoloma* sequences were downloaded from UNITE (Abarenkov et al. 2023) by searching for sequences (search by NCBI+UNITE sequences; filter for *Porpoloma*) and using MassBLASTer through the PlutoF workbench (Abarenkov et al. 2010) to find sequences from NCBI and UNITE with high similarity to sequences generated for this study (Supplementary material 1: table of ITS sequences used in phylogenetic analyses from NCBI GenBank, UNITE and newly generated). The ITS dataset was aligned using MUSCLE Alignment (Version 3.8.425) (Edgar 2004) implemented in Geneious Prime (1000 maximum iterations, 100 maximum trees, all other settings default), followed by manual editing including trimming of sequence ends (Supplementary material 2: alignment of ITS sequences). Supplementary materials are deposited on figshare (https://doi.org/10.6084/m9.figshare.29362859).

Maximum-likelihood (ML) phylogenetic analyses were performed for the ITS alignment using command-line IQ-TREE 2.2.2.6 (Nguyen et al. 2015, Minh et al. 2020), which implemented ModelFinder (Kalyaanamoorthy et al. 2017) to test for the best-fit substitution model according to Bayesian Information Criterion (BIC) and UFBoot2 (Hoang et al. 2018) to calculate ultrafast bootstrap support (UFBS) values from 10,000 replicates. The best-fit model according to BIC was TN+F+G4. Sequences of *Dennisiomyces* species were included as the outgroup according to Sánchez-García et al. (2014).

Bayesian inference analyses (BI) were performed using MrBayes 3.2.6 (Huelsenbeck & Ronquist 2001, Ronquist et al. 2012) as implemented in Geneious Prime, with GTR+G4 substitution model and *Dennisiomyces griseus* (KJ417325) as the outgroup. Two million MCMC iterations were performed, with four heated chains, a heated chain temperature of 0.15, a subsampling frequency of 1000, and burn-in length of 250,000, which resulted in stable average standard deviation of split frequencies below 0.01. As the topology of ML and BI analyses were consistent, only the ML phylogeny with both ML UFBS values greater than 70% and BI posterior probability (PP) greater than 0.80 is presented (Fig. 1). For clades with ML UFBS values above 70% and BI PP below 0.80, BI PP are shown in parentheses.

Results

The ITS dataset contained sequences from 69 specimens of 19 putative species (Supplementary material 1), including sequences from 30 specimens from Australia and New Zealand published in this study (Table 1). The aligned ITS dataset comprised 734 characters, of which 448 were constant and 182 were parsimony informative.

In the ML and BI phylogenetic analyses of ITS, *Porpoloma* is monophyletic with high support (100% UFBS, 1.00 PP). The type species of the genus, *Porpoloma sejunctum*, forms a well-supported clade (100% UFBS, 1.00 PP) comprising sequences from the isotype (MICH 00011835), another sporing body collection, and from ectomycorrhizal root tips of *Nothofagus* species, all of which were collected in southern South America (Supplementary material 1). The pairwise identity of sequences in this clade are 97.36–99.66%. Among the other named species with multiple samples, *P. amyloideum* (100% UFBS, 1.00 PP) and *P. terreum* (100% UFBS, 1.00 PP) are monophyletic with high support while *P. portentosum* (96% UFBS, 0.70 PP) has moderate support in ML but low support in BI. Some comparisons within the *P. portentosum* clade are less than 97%, indicating there may be further species diversity within this clade. The pairwise identities within the clades of *P. amyloideum* and *P. terreum* are 99.42–99.84% and 97.92–100%, respectively. The *P. terreum* clade includes sequences from the isotype (MICH00011746) and other sporing body collections, as well as sequences generated from soil and ectomycorrhizal root tips (Supplementary material 1).

The remaining clades comprise sequences from sporing bodies collected in Australia and New Zealand, and environmental DNA sequences (eDNA) from soil samples collected in Australia, New Caledonia and Papua New Guinea (Supplementary material 1). The well-supported clades representing undescribed putative species from Australia are labelled as *Porpoloma* sp. A–H, including *P.* sp. A and *P.* sp. B., which correspond to *P.* sp. 1 and *P.* sp. 2 of Sánchez-García et al. (2014). *Porpoloma* sp. 'caespitose' is an undescribed species from New Zealand with sequences from sporing bodies. *Porpoloma* sp. NCL and *P.* sp. PNG comprise only eDNA sequences generated from soil samples.

Sequences from two specimens collected from the Australian state of New South Wales form a well-supported (100% UFBS, 1.00 PP) clade with eDNA sequences generated from soil samples collected in North Queensland. The pairwise identity of sequences within this clade are 97.40–99.84%. The pairwise identity of the sequences from the sporing bodies is 98.77%, and within the soil sequences is 99.35–99.84%. This clade is sister to the type species of *Porpoloma*, *P. sejunctum*, with moderate support (82% UFBS, 0.82 PP), and the clade formed of these species is moderately supported (70% UFBS, 0.84 PP) as sister to a clade with low support (<70% UFBS, 0.63 PP) comprising *P. amyloideum* and *P.* sp. B, C, D1, D2, G and H.

The lineage from New South Wales and Queensland is distinct from the phylogenetic diversity of *Porpoloma* that is known so far, including both formally named species and undescribed putative species, and warrants formal description.

Table 1. ITS sequences newly generated for this study, except (*), which was generated by the Ohio Mushroom DNA Lab (Canan et al. 2024). ^Corresponds to iNaturalist record https://inaturalist.ala.org.au/observations/166391651.

Taxon	Specimen barcode	Locality	Date	Collection	Habitat	ITS accession
P. amyloideum	PDD 101803	NZ	29 Jan 2010	P. Leonard PL 11110	With *Nothofagaceae*	PV739468
P. amyloideum	PDD 106844	NZ	16 Nov 2017	P.J. de Lange [JAC 14757]	Beech forest	PV739471
P. amyloideum	PDD 113006	NZ	6 Apr 2019	N. Siegel NS 3619	On litter with *Nothofagaceae*	PV739472
P. amyloideum	PDD 114921	NZ	11 May 2023	N. Siegel NS 5873	Solitary from duff under beech	PV739473
P. flavilamellatum	No voucher^	AUS: NSW	28 May 2023	T.T. Huang	Wet sclerophyll with *Syncarpia glomulifera* and *Eucalyptus* spp.	PQ734136*
P. flavilamellatum HOLOTYPE	MEL 2563761	AUS: NSW	18 Apr 2024	T.T. Huang OQT261	Dry rainforest/ wet sclerophyll with *Myrtaceae*	PV833593
P. sp. A	MEL 2358280	AUS: TAS	22 Nov 2001	D.A. Ratkowsky, G.M. Gates 1303	N-facing slopes	PQ659189
P. sp. A	MEL 2358281	AUS: TAS	10 Jun 2003	D.A. Ratkowsky, G.M. Gates 1304	N-facing slopes	PQ659190
P. sp. A	MEL 2231742	AUS: WA	27 Jul 2003	K. Syme KS 1287	*Acacia*, *Allocasuarina*, *Eucalyptus wandoo*	PQ659193
P. sp. A	MEL 2117041	AUS: WA	23 Jun 2001	B. Archer 1902	*Acacia*, *Carpobrotus*, *Santalum spicatum*	PQ659194
P. sp. B	PERTH 05255171	AUS: WA	5 Jul 1993	K. Syme, A.J. Syme KS 686	*Eucalyptus diversicolor*, *E. calophylla*	PQ659191
P. sp. B	PDD 96890	NZ	20 May 2013	J.A. Cooper JAC12786	Broadleaved forest with *Kunzea ericoides*	PV739467
P. sp. B	PDD 97169	NZ	27 Jun 2010	J.A. Cooper JAC13077	*Leptospermum* scrub	PV739469
P. sp. C	PERTH 08699925	AUS: WA	10 Jul 1995	K. Syme KS 851	*Agonis flexuosa*, *Spyridium globulosum*	PV776398
P. sp. C	MEL 2363152	AUS: VIC	14 Aug 2010	T.W. May 1840	Vegetated dunes behind beach	PV833591
P. sp. C	MEL 2385500	AUS: TAS	17 Jan 2002	G.M. Gates, D.A. Ratkowsky 3094	Wet sclerophyll	PV833592
P. sp. C	MEL 2300596	AUS: TAS	24 Jul 2001	S.J.M. McMullan-Fisher 1512	Wet eucalypt forest with *Pomaderris apetala*, *Eucalyptus globulus* and *E. obliqua*	PV833685

P. sp. 'caespitosa'	PDD 96731	NZ	2 May 2010	N. Siegel	On soil with *Nothofagaceae*	PV739465
P. sp. 'caespitosa'	PDD 96732	NZ	6 May 2010	P. Leonard FUNNZ2010/ 1062	On soil with *Nothofagaceae*	PV739466
P. sp. 'caespitosa'	PDD 105739	NZ	15 May 2014	R.E. Halling FUNNZ2014/ 0199	On soil with *Nothofagaceae*	PV739470
P. sp. 'caespitosa'	PDD 77513	NZ	27 Mar 2003	P. Leonard PL 20303	On soil	PV739474
P. sp. 'caespitosa'	PDD 102580	NZ	8 May 2009	P. Leonard PL 62509	On soil with *Nothofagaceae*	PV739475
P. sp. D1	MEL 2385497	AUS: TAS	12 Jul 2003	G.M. Gates, D.A. Ratkowsky 3092	Wet sclerophyll	PV833680
P. sp. D1	MEL 2320691	AUS: VIC	28 Dec 2007	P. George	*Nothofagaceae*	PV833684
P. sp. D2	MEL 2397519	AUS: TAS	23 May 2016	T.W. May, N.G. Karunajeewa, J.B. Walter, B.W. Picking, I.D. Bell, H. Noorda 1908	Cool temperate rainforest, regrowth *Nothofagus cunninghamii*	PV833676
P. sp. D2	MEL 268707	AUS: TAS	31 May 1992	T.W. May 796	Under *Nothofagus cunninghamii* with some *Eucalyptus*	PV833691
P. sp. E	PERTH 07901623	AUS: WA	3 Aug 2006	K. Syme KS 1714	*Eucalyptus salmonphloia* and *Acacia*	PQ659195
P. sp. E	MEL 2432719	AUS: WA	28 Jun 2005	K. Syme KS 1402	*Acacia acuminata*, *Santalum spicatum*	PQ659196
P. sp. F	MEL 2534967	AUS: WA	17 Jun 2023	S. Syme, P. Anderson, D. Edmonds KS 3225	*Eucalyptus marginata*, *Corymbia calophylla*, *Allocasuarina fraseriana* woodland	PQ659188
P. sp. F	MEL 2416575	AUS: WA	14 Jul 2006	K. Syme KS 1636	*Eucalyptus*, *Hakea*, *Callitris*, *Melaleuca*	PQ659192
P. sp. G	MEL 2049986	AUS: VIC	30 Jun 1997	S. Ford	Amongst moss on the ground in mature stand of cool temperate rainforest	PV833683

Discussion

Phylogenetic and morphological comparison to similar species

Porpoloma flavilamellatum is phylogenetically distinct from other named and undescribed *Porpoloma* species. The most closely related species in the phylogeny is *P. sejunctum* from South America, and the pairwise identity between these species in the ITS alignment is 89.57–91.29%. The next closest is *P. amyloideum* from New Zealand, and the pairwise identity between this species and *P. flavilamellatum* is 89.60–91.11%. These three species, as well as *P. coyan* Garrido (sequences not available to be included in analyses) from Chile, are morphologically similar, with yellowish lamellae, a white to pale yellow stipe, and yellowish pileus that is radially streaked with brownish fibrils. However, the pileus of *P. coyan* is typically more reddish brown-grey and the lamellae are white to yellowish white (Garrido 1988). *Porpoloma amyloideum* typically has a more yellow stipe

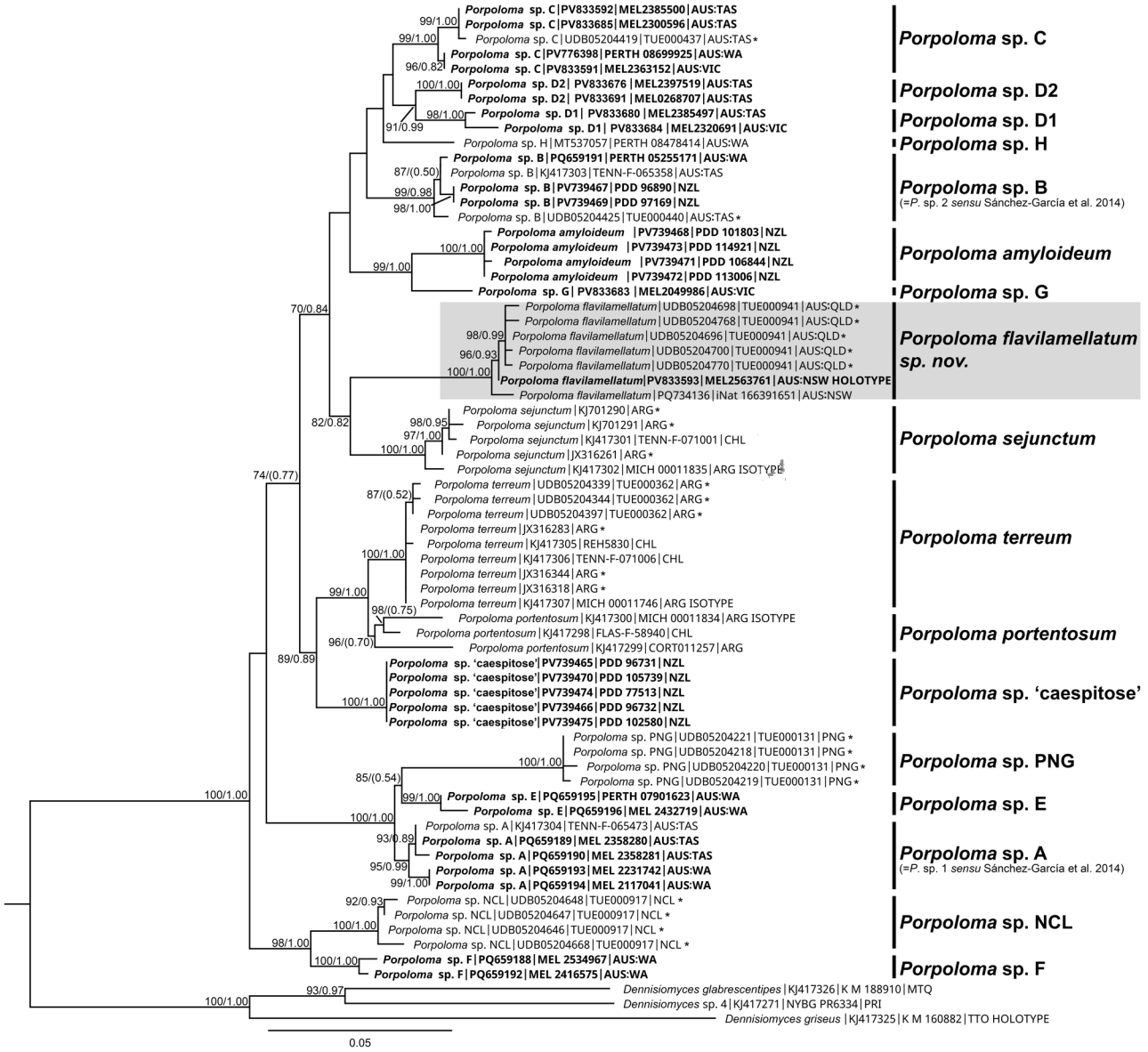

Figure 1. Maximum likelihood phylogeny of *Porpoloma* using an alignment of ITS sequences, with both ML UFBS values greater than 70% and BI posterior probability (PP) greater than 0.80 shown at nodes. For clades with ML UFBS values greater than 70% and BI PP less than 0.80, BI PP are shown in parentheses. *Dennisiomyces* is the outgroup following Sánchez-García et al. (2014). Sequences generated in this study are in bold type. Sequences from soil samples or ectomycorrhizal root tips are marked with an asterisk (*). GenBank or UNITE accessions for ITS sequences and location from which specimens were collected are given after taxon names.

than *P. sejunctum* and *P. flavilamellatum*, occasionally with reddish fibrils, and a conspicuous membranous annulus near the base of the stipe (Stevenson 1964). *Porpoloma flavilamellatum* can be clearly distinguished from *P. amyloideum* by lacking this conspicuous annulus (or a differently-coloured basal zone). It also typically has strongly yellow lamellae in combination with smaller spores (6.5–8.5 × 4–5.5 µm) in comparison to *P. amyloideum* (7–8 × 4.5–6.5 µm), *P. coyan* (8–11 × 6–8 µm) and *P. sejunctum* (8.2–9 × 5.5–6.3 µm), and is found in habitats associated with the plant family *Myrtaceae* Juss. rather than *Nothofagaceae* Kuprian.

Porpoloma penetrans (Cleland) Grgur., originally described from South Australia as *Collybia penetrans* Cleland (Grgurinovic 1997), is most likely referrable to *Heimiomyces* Singer due to the presence of nodulose cheilocystidia. Further investigation, involving examination of the type, is underway.

Comparison to undescribed Australasian species

The undescribed putative phylogenetic *Porpoloma* species included in the phylogeny (Fig. 1) roughly fall into two morphological groups: *Porpoloma* sp. C, D1, D2, G and H have yellowish lamellae, stipe and pileus; *Porpoloma* sp. A, B, E, F and *Porpoloma* sp. 'caespitose' have grey or white lamellae and stipe, and grey to brown pileus. The morphology of *Porpoloma flavilamellatum* is consistent with the yellow morphological group but it

is phylogenetically distinct from the other yellow Australian putative species (Fig. 1), which also have larger spores than *P. flavilamellatum*. The other yellow putative species have been found in wetter forests or woodlands with *Nothofagaceae* or *Myrtaceae* in Tasmania, southern Victoria, and south-west Western Australia, while *P. flavilamellatum* has been found in the central coast region of New South Wales in ecosystems dominated by *Myrtaceae*.

Potential mycorrhizal associations

The sequences of *Porpoloma amyloideum*, *P. portentosum*, *P. sejunctum* and *P. terreum* in the ITS phylogeny were all generated from specimens, soil samples or ectomycorrhizal root tips collected in the southern hemisphere from habitats with *Nothofagaceae*, which is consistent with the conclusion by Trappe (1962) and Sánchez-García et al. (2014) that *Porpoloma* is ectomycorrhizal with *Nothofagaceae*. The placement of sequences from ectomycorrhizal root tips of *Nothofagus* species within the clades of *P. sejunctum* and *P. terreum* provides especially strong evidence that these species form ectomycorrhizal associations with *Nothofagaceae* (Sánchez-García et al. 2014). However, several of the undescribed putative species with sequences recovered within *Porpoloma* were found in southern hemisphere habitats without *Nothofagaceae*, most commonly dominated by *Myrtaceae* taxa, including *P. flavilamellatum*. The eDNA sequences recovered in the *P. flavilamellatum* clade were generated from soil collected near Townsville, Queensland, in tropical broadleaf forest with *Eucalyptus* L'Hér. and *Casuarinaceae* R.Br. (Supplementary material 1). The occurrence of sporing bodies and genetic material in habitats with *Myrtaceae* suggests that some *Porpoloma* species, including *P. flavilamellatum*, likely form ectomycorrhizal associations with *Myrtaceae* taxa, especially *Eucalyptus*, as suggested by Sánchez-García et al. (2014).

Uncovering 'dark taxa'

The DNA sequences generated from specimens collected by Todd Huang in May 2023 and April 2024 connected the morphological concept of *Porpoloma flavilamellatum* to the UNITE phylogenetic species hypothesis comprising eDNA sequences (UNITE SH0079001.10FU), which was previously only known from sequences (Abarenkov et al. 2023). The connection of the sequences from specimens to the eDNA sequences has facilitated the typification, naming and formal description of the species, including enabling description of its morphology, distribution and possible ecological interactions, which would not be possible without preserved specimens in fungaria. *Porpoloma* sp. NCL and *P*. sp. PNG (Fig. 1) are species only known from sequences generated from soil samples that have not yet been matched to named species and therefore remain 'dark taxa' (Ryberg & Nilsson 2018).

Additional iNaturalist observation records from around the New South Wales Central Coast and South East Queensland near Brisbane are macromorphologically consistent with *Porpoloma flavilamellatum* and could assist with expanding understanding of the distribution of the species and its ecology. However, micromorphological and phylogenetic examination of additional specimens collected in Queensland and New South Wales lodged in fungaria is required in order to gain a clear understanding of the limits of the distribution of the species. The environmental sequences identified as *P. flavilamellatum* were detected in soil collected from Mount Zero near Townsville in North Queensland, which suggests the species may be present in ecosystems further north than sporing bodies have so far been observed. It is hoped that the formal description of *P. flavilamellatum* will draw attention to this under-detected species and allow further information on its occurrence in Australia to accumulate through observation data on platforms like iNaturalist and with additional collected specimen vouchers lodged in Australian fungaria.

Conclusions

This study is the first to describe an Australian species of *Porpoloma*, as the genus is currently delimited, and present a phylogeny of the diversity known so far from Australia and New Zealand. Further phylogenetic studies incorporating additional genetic loci will be needed to resolve the phylogenetic support for the interspecific relationships within *Porpoloma* and establish appropriate species boundaries for the undescribed putative species *Porpoloma* sp. A–H and *P*. sp. 'caespitose', especially considering the highly similar morphology shared by of some of the putative phylogenetic species. Continued sequencing of existing collections in fungaria as well as targeted searching for *Porpoloma* in likely habitats of the southern hemisphere may enable *Porpoloma* sp. NCL and *P.* sp. PNG to be linked to physical specimens so they can be formally described and named.

Taxonomy

Porpoloma flavilamellatum L.J. Vaughan & T.W. May, ***sp. nov.***

MycoBank 860004

Typification**:** AUSTRALIA, New South Wales, Springwood, Fairy Dell Track (33.7139° S, 150.5644° E), terrestrial in dry rainforest/wet sclerophyll forest with *Myrtaceae*, 18 April 2024, *T.T. Huang OQT261* (**holotype** MEL 2563761). GenBank: ITS = PV833593; 28S = PV746196.

Fig. 2

Diagnosis**:** *Porpoloma flavilamellatum* has darker yellow lamellae and smaller spores (6.5–8.5 × 4–5.5 µm) than the other yellowish *Porpoloma* species, *P. amyloideum* (7–8 × 4.5–6.5 µm), *P. coyan* (8–11 × 6–8 µm) and *P.*

Figure 2. *Porpoloma flavilamellatum* holotype MEL 2563761 (except **L.** https://www.inaturalist.org/observations/166391651). **A.** Basidiospores in MLZ**. B.** Basidiospores in H_2O. **C.** Basidiospores in KOH. **D.** Basidioles in KOH. **E.** Basidia in KOH. **F.** Hymenium in KOH. **G.** Pileipellis squash in MLZ. **H.** Pileipellis section in H_2O. **I.** Pileipellis section in KOH. **J–K.** Sporing bodies in habitat. Scale: A–C = 5 µm; D–F = 10 µm; G–I = 20 µm.

sejunctum (8.2–9 × 5.5–6.3 µm); lacks the membranous ring on the stipe of *P. amyloideum;* and is found in habitats with *Myrtaceae* Juss. rather than *Nothofagaceae* Kuprian. It is distinguished from other members of the genus *Porpoloma* by its unique phylogenetic position.

***Etymology*:** from Latin *flavus* (yellow) and *lamellatus* (lamellate).

Description

Habit sporing bodies terrestrial, occurring singly or in small groups.

Pileus 30–70 mm wide; at first convex, becoming broadly convex to almost plane, sometimes with broad umbo, sometimes becoming undulate toward margin, extreme margin often upturned, occasionally incurved, sometimes becoming tattered at edge; pale yellow to pale brown to dark brown, usually overlayed with radial brownish fibrils, especially in the centre, where a darker disc of fibrils is often present; surface dry, radially fibrillose. **Lamellae** adnate, sinuate, or appearing free, close, thin to moderately thick; yellow, margin concolourous with face; lamellulae present. **Stipe** 25–45 mm high, 7–15 mm wide, up to 25 mm wide at base; centrally attached, cylindrical, slightly clavate, tapered towards pileus, often slightly swollen at base; dry, firm, white to greyish to pale yellow; appressed longitudinally fibrillose, with soil adhering in a zone around the base, which is often darker. **Odour** and **taste** not recorded. **Spore print** not recorded.

Basidiospores 6.5–8.5 × 4–5.5 µm, mean *7.15* × *4.68* µm [30/1], Q = 1.30–1.75, mean Q = *1.53* [30/1], amyloid, hyaline in H_2O and KOH, except sometimes spores are filled with granular pigmented content, pigment brownish in MLZ, pinkish brown or burgundy in KOH, golden in H_2O. **Basidia** clavate, 32–*39.40*–47 µm long, 3–*3.70*–5 µm wide at base, 7–*7.75*–8.5 µm maximum width [10/1], 4-spored, rarely 1- or 2-spored, sterigmata 1.5–2 µm wide at base, up to 3.5–4 µm long; basidioles 20–*29.09*–39 µm long, 3–*3.41*–4 µm wide at base, 4.5–*6.23*–8 µm maximum width; basidia and basidioles hyaline, except, like some spores, occasionally they are partially or totally filled with granular pigmented contents, pigment brownish in MLZ reagent, pinkish brown or burgundy in KOH, golden in H_2O. **Cystidia** not observed. **Hymenophoral trama** comprising parallel hyphae, 4–14 µm diam., cylindrical, usually tapered at septa and slightly inflated between septa; individual hyphae appear hyaline. **Pileipellis** a cutis, composed of parallel hyphae, 4–8 µm diam., cylindrical, but often tapered at septa; sometimes surface encrusted, particularly for hyphae near the surface; terminal elements 47–105 × 5–8 µm, more or less cylindrical, rounded at apex, or slightly tapered toward apex before rounded apex; tissue in H_2O, hyphae of the upper pileipellis are reddish brown, becoming more hyaline towards the subpellis; in MLZ, hyphae take on the colour of the medium; in KOH, hyphae stain pinkish, with overlying elements in the suprapellis that stain darker reddish pink; terminal elements often darker pigmented than other elements; pileus trama with roughly parallel-arranged hyphae, 6–8 µm diam., hyaline, cylindrical, appearing thicker walled than upper pileipellis elements, with walls up to 1 µm thick. **Stipitipellis** composed of roughly parallel hyphae, 2.5–10.5 µm diam., with slight encrusting pigment in H_2O and slight pinkish staining in KOH; terminal elements not strongly differentiated from other hyphae, with rounded apices; hyphae in base of stipe also parallel. **Clamp** connections observed in all tissues.

***Sequenced specimen matching this species*:** New South Wales, Royal National Park, Couranga Track, near the Hacking River (34.14482° S, 151.02120° E), wet sclerophyll with *Syncarpia glomulifera* and *Eucalyptus* spp., 28 May 2023, *T.T. Huang s.n.* (iNaturalist: 166391651, voucher not kept), GenBank: ITS = PQ734136.

***Distribution & habitat*:** On the ground in dry rainforest or wet sclerophyll forest with *Myrtaceae*, including *Syncarpia glomulifera* and species of *Eucalyptus*. So far known from NSW, south of Sydney (Royal National Park) and near the Blue Mountains, and, by inference from soil eDNA, southern Queensland.

Disclosures

No disclosures to declare.

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