Australian Journal of Taxonomy
Open-access, online, rapid taxonomy
https://doi.org/10.54102/ajt

Citizen scientists detect the fungus *Onygena corvina* (*Onygenales*, *Ascomycota*) in New South Wales, Australia

T.W. May[1*], L.J. Vaughan[1], G.D.Holmes[1], E. Brand[2], F. Pegrem-Brand[2], L. Pegrem-Brand[2], N. Siegel[3]

[1] Royal Botanic Gardens Victoria, Birdwood Avenue, South Yarra, Victoria, 3141, Australia
[2] Citizen scientist, Wentworth Falls, New South Wales, 2782, Australia
[3] Independent researcher, Royalston MA 01368-9206, USA
*Corresponding author: tom.may@rbg.vic.gov.au

T.W. May https://orcid.org/0000-0003-2214-4972; L.J. Vaughan https://orcid.org/0000-0003-1659-9938; G.D. Holmes https://orcid.org/0000-0003-1120-8731

Abstract

A recent collection of a stipitate ascomycete with a powdery spore mass, collected from a bird carcass in New South Wales, is identified as *Onygena corvina*. This collection represents the first confirmed record of the species from Australia. *Onygena corvina* is otherwise rarely reported from the Southern Hemisphere, being known in the Oceanian region only from New Zealand and probably also occurring on the subantarctic Macquarie Island (part of Australia's Economic Territory). Phylogenetic analysis of ITS sequences from the two species currently accepted in the genus, *O. corvina* and *O. equina*, does not recover well-supported clades for each species. Consequently, we rely on morphology to identify the NSW collection as *O. corvina*, as it is a good match for this species in spore size and shape, and the host is also consistent. The "neotype" previously designated for *O. corvina* is shown to be not Code-compliant and a lectotype is designated, utilising the illustration in the protologue. The NSW collection was made by citizen scientists during the Great Aussie FungiQuest 2023, organised by Fungimap. We discuss the contribution of citizen scientists to locating and documenting new and interesting fungi and the scope for further supporting such contributions.

Cite this paper as: May TW, Vaughan LJ, Holmes GD, Brand E, Pegrem-Brand F, Pegrem-Brand L & Siegel N (2024). Citizen scientists detect the fungus *Onygena corvina* (*Onygenales*, *Ascomycota*) in New South Wales, Australia. *Australian Journal of Taxonomy* 72: 1–11. doi: https://doi.org/10.54102/ajt.i1ogn

Introduction

Onygena Pers. is a distinctive fungus of the order *Onygenales* (Ascomycota) that produces readily visible sporing bodies on animal remains, that are stipitate and with a powdery spore mass at maturity, initially bounded by a peridium. Within *Onygenales*, production of a sporing body with a stipe occurs only in *Onygena* and *Narasimhella marginispora* (Kuehn & Orr) v. Arx (=*N. poonensis* Thirum. & P.N. Mathur), but the latter lacks a peridium and has been isolated from buried substrates such as fabrics (Kandemir et al. 2022).

This paper was submitted on 18 April 2024 and published on 20 September 2024 (2024-09-19T22:15:08.705Z). It was reviewed by Hazal Kandemir and an anonymous reviewer, and edited by Kevin Thiele. Tom May is an Editor of the Australian Journal of Taxonomy. He did not at any stage have access to the manuscript while in peer review, and had no influence on its acceptance or handling, as is standard practice for manuscripts submitted by editors. Australian Journal of Taxonomy. ISSN: 2653-4649 (Online).

Although more than a dozen names have been introduced in the genus *Onygena*, Currah (1985) accepted only two species: *Onygena corvina* Alb. & Schwein. (=*O. hypsipus* Ditmar, *O. piligena* Fr.), usually found on bird carcasses and *O. equina* (Willd.) Pers (=*O. caespitosa* Pers.), usually found on bone, hooves or horn. Both species are sometimes reported from wool or fur or from material containing animal remains such as owl pellets. Kandemir et al. (2022) also accepted these two species, and provided neotypes for them, but did not typify any of the names suggested as synonyms by Currah (1985).

Among other species originally described in *Onygena*, Currah (1985) noted that *O. caprina* Fuckel (from horn) likely belonged in another genus, and suggested that *O. alpina* (Fresen.) Rytz represented *Phleogena faginea* (Fr. & Palmquist) Link (Atractiellales), a fungus that is of similar appearance to. *O. corvina* and *O. equina*, and which was originally described in *Onygena*, but grows on wood, and has spores produced on basidia rather than in asci. Leuchtmann & Clémençon (2012) showed that *O. alpina* was unrelated to *Onygena* or *Phleogena* Link and belonged in *Heydenia* Fresen. (Pezizales), as *Heydenia alpina* Fresen. along with *H. arietina* (E. Fischer) Leuchtm. & H. Clémençon (=*O. arietina* E. Fischer). Kandemir et al. (2022) noted that *O. mutata* Quél. is now placed in *Amaurascus* (also *Onygenales*) under *Amauroascus verrucosus* (Eidam) J. Schröt. Among the remaining species of *Onygena* that do not have modern placements, Kandemir et al. (2022) mention several others that occur on feathers, bone or hair, including *O. apus* Berk. & Broome (from decaying bones), *O. bommerae* Sacc. (on feathers and bones of birds), and *O. ungulina* Rostrup (on horse hooves) [for publication details of each see Kandemir et al. (2022)].

Growth on keratin-containing substrates is a feature of *O. corvina* and *O. equina*, and indeed for the other species described in the genus that are yet to be placed. According to Lange et al. (2016) "keratin is a fibrous and recalcitrant structural protein ... the third most abundant polymer in nature after cellulose and chitin". Keratin is a component of various parts of vertebrate animals, including skin, hair, wool, feathers, horns, hooves, nails, quills and beaks (McKittrick et al. 2012). Species of *Onygena* produce keratinases (types of proteases) that have been investigated for biotechnological potential, including for upgrade of keratinaceous waste to protein-rich animal feed and for breakdown of prion proteins (Lange et al. 2016). Investigations of genomes of *O. corvina* and other keratinophilic fungi reveal the surprising finding that they contain genes for production of not just keratinases but also the specialised enzymes important for "breaking the recalcitrance of cellulose and chitin" (Lange et al. 2016). However, care is needed in interpreting results as the strain of *O. corvina* used for whole genome analysis by Huang et al. (2015) has been reidentified as an *Arthoderma* (also *Onygenales*) by Kandemir et al. (2022) [see Materials & Methods].

There do not appear to be any published reports of *Onygena* from Australia but two fungarium collections of "*Onygena* sp." are compiled in the Global Biodiversity Information Facility (GBIF.org 2024): one collected from Macquarie Is. in 1995, on Royal Penguin feathers (WTU-F-019951) and the other collected in Western Australia in 1978 on a crab (PERTH 746177). Macquarie Island is a subantarctic island within Australia's Economic Territory, some 1500 km to the south-east of the Australian state of Tasmania.

In May 2023, the authors EB, FP-B and LP-B noticed unusual growths on feathers under a clump of coral fern while seeking fungi observations in Water Nymphs Dell to submit to The Great Aussie FungiQuest 2023 (https://www.biosmart.life/australian-fungi-quest-2023). Water Nymphs Dell is a public recreation area (Lot 1 DP 961858, Blue Mountains City Council) in the New South Wales town of Wentworth Falls. The Great Aussie FungiQuest is an annual event organised by Fungimap (https://fungimap.org.au/the-great-aussie-fungiquest/) to encourage upload of fungi observations to citizen science platforms such as QuestaGame and iNaturalist. An observation was submitted to iNaturalist on 9 May 2023 (https://www.inaturalist.org/observations/160697615) and added to the Fungimap Australia project. The 'what did you see?' function on the iNaturalist app suggested the growths were *Onygena corvina*. However, there were no other recorded observations in Australia, and an internet search suggested the species was confined to the Northern Hemisphere. EB found NS on the *O. corvina* 'identifiers' list on iNaturalist and contacted him for his opinion, and soon after also contacted Sophie Green, the Coordinator of Fungimap for clarification and advice. Sophie alerted Jordan Bailey (DAR) and Tom May (MEL) and NS also contacted TM. These contacts facilitated discussion with EB about how to obtain a specimen under the necessary permit, which was obtained in due course from the Blue Mountains City Council, allowing a collection to be made within three days of the original observation. We identify this collection on the basis of an examination of morphological characters and DNA sequences.

Methods

Morphological examination

Morphological data presented herein under *O. corvina* are based on the recent Australian collection MEL 2530453. Macromorphological characters, including colours, are described from field notes and photographs made at the time of collection where possible, and from dried fungarium material. Macromorphological measurements are described from dried fungarium material, which was observed, measured and photographed using an Olympus SZX16 Stereo Microscope with an Olympus DP-73 camera attachment and mea-

surement tools in Olympus cellSens standard (v. 1.16). Micromorphological characters are described from examination of dried fungarium material, from which hand-cut sections were rehydrated in water, Melzer's reagent or 5% KOH, as specified, to observe, measure and photograph tissues. Microscopic features were observed and photographed using an Olympus BX-52 light field microscope with Olympus DP-73 camera attachment and measurements were recorded in water at ×400 or ×1000 using measurement tools on Olympus CellSens standard (v. 1.16). Ascospore measurements are provided as observed ranges to the nearest half-micron with collection mean in italics, calculated from measurements of 60 ascospores. The quotient 'Q' is the ratio of spore length to spore width and is given as a raw range with collection mean in italics. All other measurements are given as observed ranges to the nearest 0.5 micrometre for microscopic features and to the nearest 0.25 millimetre for macroscopic features.

Sequencing and phylogenetic analyses

DNA was isolated from MEL 2530453 using a modified CTAB method summarised in Craig et al. (2023), based on that of Gardes & Bruns (1993). The internal transcribed spacer (ITS) and large ribosomal subunit (LSU) regions were PCR amplified using the primer pairs ITS1f/ITS4 (White et al. 1990, Gardes & Bruns 1993) and LR0R/LR5 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/), respectively, using methods outlined by Craig et al. (2023). Sequencing was undertaken by AGRF (Melbourne, Australia) and chromatograms were aligned, manually checked and edited using Geneious Prime (Version 2021.0.3, https://www.geneious.com) to generate consensus sequences.

DNA sequences with high similarity to the Australian sequences were identified in NCBI GenBank using BLASTn search (Altschul et al. 1990; Morguliset al. 2008) and in the UNITE database (Version 9.0, https://unite.ut.ee/repository.php; Abarenkov et al. 2023) using massBLASTer utility on PLUTOF (Abarenkovet al. 2010). Sequences with percent identity greater than 95% to the Australian sequences were assembled for analyses (Table 1). ITS and LSU sequences from CBS 225.60 and CBS 281.48, lodged in GenBank as *O. corvina*, were excluded because Kandemir et al. (2022) indicated that the two strains are in fact *Arthroderma crocatum* Udagawa, Kubo & Shibaki. CBS 281.48 was used for whole genome analysis by Huang et al. (2015).

ITS and LSU sequences were aligned separately using MUSCLE Alignment (Version 3.8.425) implemented in Geneious Prime (1000 maximum iterations, 100 maximum trees, all other settings default), then manually checked and edited with ends masked (Edgar 2004). Maximum-likelihood (ML) phylogenetic analyses were inferred separately for ITS and LSU alignments using IQ-TREE (Version 2.2.2.7, Nguyen et al. 2015, Minh et al. 2020) command-line program, 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 values from 1000 bootstrap replicates.

For analysis of LSU sequences, *Ascocalvatia alveolata* Malloch & Cain (sequence of type: AY176710) and *Ophidiomyces ophidiicola* (Guarro, Deanna A. Sutton, Wickes & Rajeev) Sigler, Hambl. & Paré (KF225601, and sequence of type: EU715820), identified as sister lineages to *Onygena* on the basis of ITS and LSU in Kandemir (2022), were used as the outgroup with the type of *Oph. ophidiicola* (EU715820) in root position. For analysis of ITS sequences, *A. alveolata* (UDB035119) was identified by BLAST on GenBank and UNITE as the next closest known taxon with available ITS sequences (after *Onygena* species), which is consistent with the phylogeny presented in Kandemir (2022). *A. alveolata* (UDB035119) and *Oph. ophidiicola* (KF225599, and sequence of type: EU715819) were used as the outgroup with the clade of *Oph. ophidiicola* in root position.

A second ITS alignment containing only sequences from the *Onygena* clade identified from the first ITS and LSU phylogenetic analyses was aligned as above and then treated with Gblocks 0.91b to remove ambiguous regions (Castresana 2000, Dereeper et al. 2008, 2010). Pairwise percent identity between members of the *Onygena* clade shown in table 2 was calculated from this Gblocks treated alignment.

Results

Molecular phylogeny

ModelFinder as implemented by IQTree identified K2P as the best-fit substitution model for the LSU alignment with BIC of 2277.421 and HKY+F+I for the ITS alignment with BIC score of 4067.823. The tree structure shown by Kandemir et al. (2022) was recovered in the LSU ML phylogenetic analysis, where *Ascocalvatia alveolata* and *Ophidiomyces ophidiicola* are sister to a well-supported clade (BS 100) of *Onygena* (Fig 1). *Ascocalvatia alveolata* and *Oph. ophidiicola* have percent identity of 93.59–93.76% and 92.86–93.21% to members of the *Onygena* clade, respectively. Within the *Onygena* clade, the pair of sequences identified as *O. corvina* are identical and have two base pair differences compared to the *O. equina* sequence, at nucleotide positions 387 and 434. The Australian sequence has a single base pair difference to both named species: at position 434 to *O. corvina*; at position 387 to *O. equina*.

In the ITS ML phylogenetic analysis, we note that the available sequences most similar to *Onygena* from *A. alveolata* and *Oph. ophidiicola* are very different to the *Onygena* sequences assembled and while the 5.8S region aligned well, ITS1 and ITS2 aligned poorly

Taxon	Specimen	Type status	Host	Country	ITS	LSU
Ascocalvatia alveolata	ATCC 22147	Type	Carnivore dung	Canada	UDB035119	AY176710
Ophidiomyces ophidiicola	CBS 122913	Type	Snake	USA	EU715819	EU715820
Ophidiomyces ophidiicola	MYCO ARIZ AN0400001		Snake	USA	KF225599	KF225601
Onygena corvina	JCM 9546		Decaying bone [1]	Japan	–	AB075355
Onygena corvina	CBS 152.73	"Neotype"	Bird remains	Netherlands	UAMH03795 [2]	MH878305
Onygena corvina	**MEL 2530453**		**Bird remains**	**Australia**	**PP278378**	**PP627009**
Onygena corvina	TUF 111520		Host not specified	Estonia	UDB034587	–
Onygena corvina	MGKF 337 [3]		Bird remains	USA	OR167982	–
Onygena equina	CBS 947.70	"Neotype"	Bovine hoof	Germany	UAMH03829 [2]	AY176717
Onygena equina	K(M) 178403		Bovine horn [4]	UK	MZ159461	–
Onygena equina	TUF 101989		Bovine horn	Estonia	UDB018096	–

Additional sequence and collection information from:
1 - https://www.jcm.riken.jp/cgi-bin/jcm/jcm_number?JCM=9546
2 - https://www.uamh.ca/ - two sequences not lodged on GenBank are provided in the metadata for UAMH specimens, hence the use of UAMH accession numbers as identifiers for the sequences.
3 - Personal fungarium Matthew Koons, see https://inaturalist.ala.org.au/observations/147928692.
4 - https://herbtrack.science.kew.org

Table 1: ITS and LSU sequences for *Onygena* and related taxa. Sequences newly generated in this study are in bold. Sequences are from GenBank except for sequences with UDB prefixes (from UNITE) and two sequences directly obtained from UAMH specimen metadata.

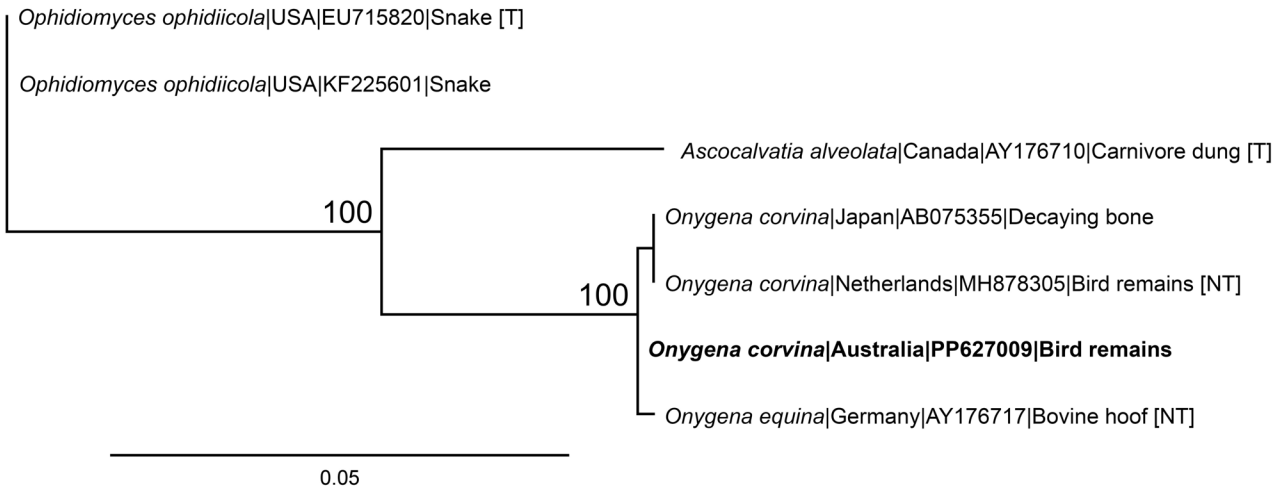

Figure 1. Maximum Likelihood phylogeny inferred from LSU sequences for *Onygena* with *Ophidiomyces ophidiicola* as outgroup. Ultrafast Bootstrap support values ≥ 95% are indicated at nodes. Sequence newly generated in bold.

between the genera. The ITS phylogenetic analysis recovered the same overall structure as the LSU analysis and Kandemir et al. (2022), and the clade of *Onygena* sequences has 99% ultrafast bootstrap support. Within the *Onygena* clade there were few base-pair differences between sequences and there is no separation into clades corresponding to *O. corvina* and *O. equina*, and nor is there separation on the basis of host (Fig 2). The Australian sequence is sister to two sequences (UDBB018096 and "Neotype": UAMH03829) of *O. equina* found on bovine hoof and horn in Europe. These three sequences form a clade with low support (<95) and basal to this clade are four sequences from Europe, three of which are identified as *O. corvina* and two of which were found on bird remains. The fourth sequence in this clade is identified as *O. equina* and was found on bovine horn. The separate ITS alignment of only sequences from the *Onygena* clade treated with Gblocks shows a minimum pairwise percent identity of 98.45% between the most distant sequences, with 11 base-pair differences across the 709 base-pair alignment (Table 2). One of these comparisons is between *O. corvina* (UDB034587) and *O. equina* (UDB018096), but another is between two sequences identified as *O. equina* (UDB018096, MZ159461), both collected from bovine horns.

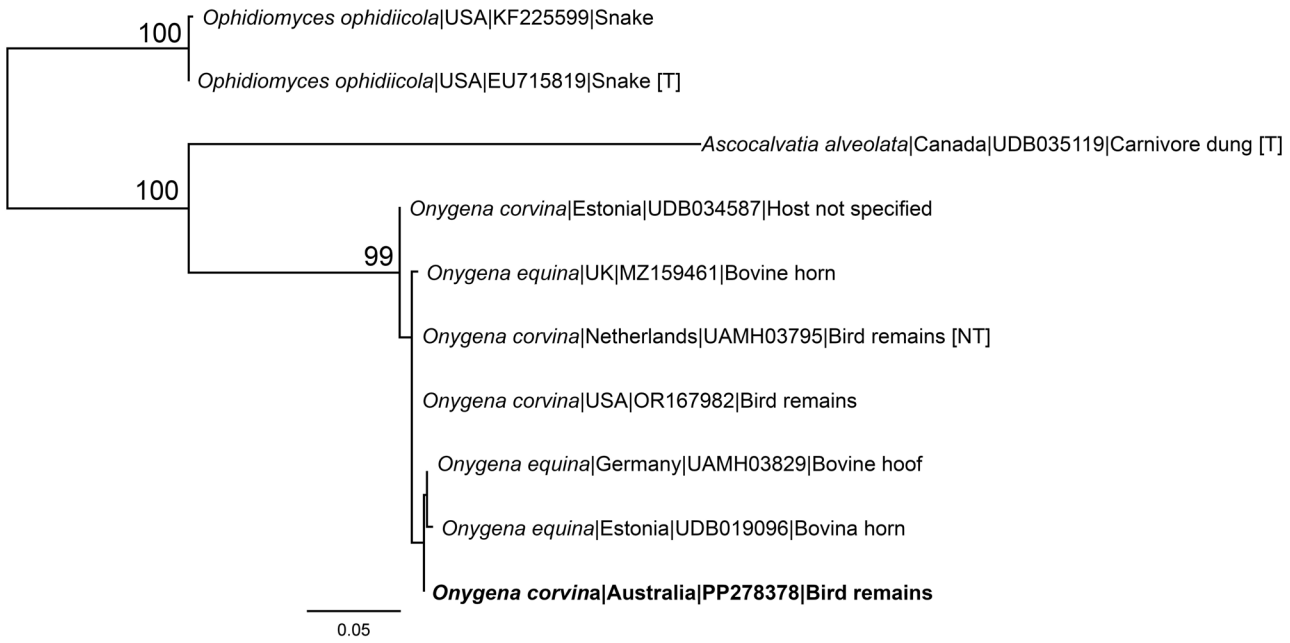

Figure 2. Maximum Likelihood phylogeny inferred from ITS sequences for *Onygena* with *Ophidiomyces ophidiicola* as outgroup. Ultrafast Bootstrap support values ≥ 95% are indicated at nodes. Sequence newly generated in bold.

	Onygena corvina Estonia UDB034587	Onygena equina UK MZ159461	Onygena corvina Netherlands UAMH03795 ("NT")	Onygena corvina USA OR167982	Onygena equina Germany UAMH03829	Onygena equina Estonia UDB018096
Onygena corvina | Estonia | UDB034587						
Onygena equina | UK | MZ159461	99.72					
Onygena corvina | Netherlands | UAMH03795 ("NT")	99.86	99.86				
Onygena corvina | USA | OR167982	99.29	99.29	99.44			
Onygena equina | Germany | UAMH03829	98.73	98.73	98.87	98.87		
Onygena equina | Estonia | UDB018096	98.45	98.45	98.59	98.59	99.72	
Onygena corvina | Australia | PP278378	**98.87**	**98.87**	**99.01**	**99.01**	**99.58**	**99.29**

Table 2. Matrix of % Identity for *Onygena* ITS sequence alignment treated with Gblocks. The sequence from the Australian specimen and the comparison of this with other *Onygena* sequences are indicated in bold.

Morphology

The macroscopic and microscopic features of the Australian specimen as well as the host substrate are consistent with *Onygena corvina* as described by Albertini & Schweiniz (1805), Fischer (1897), Breitenbach & Kränzlin (1984), and Beug et al. (2014). The spores of the NSW collection, that are elliptical rather than broadly elliptical and relatively narrow, match *O. corvina* rather than *O. equina*. Spore width of *O. corvina* in the literature is in the range 2–4 µm, while that of *O. equina* is mostly 4–5.5 µm [Fischer (1897), Hagen (1942), Breitenbach & Kränzlin (1984), Currah (1985), Beug et al. (2014), Uzun & Kaya (2019)]; although Currah (1985) gives width for *O. equina* as 3–5.5 µm and a report of *O. equina* from Poland (on horns or hooves) indicates width of 3–4 µm (Komorowska 1986).

Other collections

The Western Australian collection determined as *Onygena* sp. (PERTH 746177, on crab carapace) has small synnemata, when dry to 1.2 mm high, with a white stipe and pale orange, irregular non-powdery heads. Spores are ellipsoid to cylindrical, 4.5-6.5 x 2.5-3.5 (Q=1.43-2.17) [40/1]. These characters do not match either of the known species of *Onygena*, in particular due to the absence of a powdery spore mass.

Discussion

The collection from New South Wales documented here represents the first record from Australia of *O. corvina* accompanied by confirming morphological and molecular data. The WTU specimen from Macquarie Island (within Australia's Economic Territory) identified as *Onygena* sp. is recorded as occurring on a bird carcass and thus is likely to be *O. corvina*. On the basis of its morphological characters, the collection on a crab carapace from Western Australia is not an *Onygena*. It is also relevent that crab exoskeletons are typically chitin-based (Boßelmann et al. 2007) in comparison to the keratin-based susbtrates usually reported for *Onygena*. We note for the iNaturalist observation identified as *Onygena* sp. from crayfish in U.S.A. (https://inaturalist.ala.org.au/observations/178605492), the image is

not clear enough for accurate identification; but the fungus does not appear to have a powdery spore mass.

Most records of the genus *Onygena* are from the Northern Hemisphere (GBIF 2024). Among the 1,393 records of the genus, apart from the Australian report discussed herein and the collection from Macquarie Island, only five other records are from South America, Africa or New Zealand, and there are no reports from south-east Asia. There are two reports from New Zealand: PDD 106654, on pellet of Swamp Harrier (*Circus approximans*), identified as *O. corvina*; and PDD 49440, on goat skull, identified as *Onygena* sp. On the basis of the sparse records from the Southern Hemisphere, it is not possible to determine if *O. corvina* is native to Australia (but very rare) or is a recent introduction.

Further observations and collections will be of interest to establish the biostatus (native or exotic) of *O. corvina* in Australia, and the host range. Given the substrates reported in the Northern Hemisphere, the fungus should be sought not only on bird carcasses in an advanced state of decay but also on wool, fur, or regurgitated pellets such as produced by owls and raptors feeding on birds or mammals.

Phylogenetic analysis of ITS sequences from the two species currently accepted in the genus, *O. corvina* and *O. equina*, does not recover well-supported clades for each species and indeed sequences from the two species are intermixed, with a maximum distance between sequences of 1.55%. An ITS sequence from the NSW collection falls within the clade of sequences of *O. corvina* and *O. equina* (all from the Northern Hemisphere) but sits sister within the phylogenetic tree to sequences of *O. equina*. For LSU, a sequence from the NSW collection sits between sequences from the two species (although there are only three available sequences for this marker). Therefore, DNA sequence information does not allow a definitive identification to species.

For species delimitation in *Onygena*, one scenario suggested by the molecular data is that there is a single species that occurs on both feathers and bone. However, the spore characters seem constant for collections of each of *O. corvina* and *O. equina,* which also usually have specific hosts. In addition, Currah (1985) reported differences between the two species in spore surface features as visible under the Scanning Electron Microscope. Increased sampling of the genus is required across its cosmopolitan range and across additional genetic markers to resolve species boundaries and identify an appropriate DNA barcode region. Given the potential for use of *Onygena* as a souce of proteinases for use in biotechnology, establishing accurate species boundaries will be important as a guide in the search for novel compounds.

Many potentially new and interesting observations of fungi are posted on the internet by a growing network of citizen scientists spread across many geographic areas and habitats. As an example, for Australia on the iNaturalist platform there are already more than 460,000 observations of fungi made by more than 19,800 observers — providing a much denser sampling in time and space than can be achieved by the few mycologists working in reference collections. However, it is difficult for mycologists to promptly obtain material for lodging in fungaria as a basis for the detailed morphological examination and sequencing that is necessary for description and documentation of taxa. In this case, the posting of the record on iNaturalist (in particular) facilitated contact with mycologists because: (1) the Artificial Intelligence "computer vision" function of iNaturalist [known as "What did you see" on the app version and "Suggest an identification" on the web version] indicated the correct genus, and (2) iNaturalist provides a facility to direct message other contributers, and to select these from the list of "top identifiers".

There is much potential for active connection between the ever-growing network of citizen scientists, engaged with platforms such as iNaturalist, but this is limited at present by the few mycologists in fungaria and the demands on their time. Indeed, targeted contact with citizen scientists represents an alternative method for obtaining material to targeted collecting campaigns such as BushBlitz, which so far has a very low yield as far as novel fungi (see reports available at <https://bushblitz.org.au/reports/>). Resourcing for citizen science support staff in institutions would be a worthwhile investment, especially for reaching out to citizen scientists who have made interesting observations, at the time of these observations so that specimens can be secured. Support is also necessary, as in this case, for ensuring appropriate permits and for providing advice on suitable methods of collecting and documenting fungi for fungaria.

Taxonomy

Onygena corvina Alb. & Schwein., *Conspectus Fungorum in Lusatiae Superioris* 113, tab. IX, fig. 2 (1805)

Name identifier: MB 192740

Typification in protologue "Notabilem fungum in pennis ossiculisque superstitibus cadaveris unici corvini (*Corvi Cornicis* L.) putredine jam jam [as "jamjam"] conficiendi, loco umbroso jacentis, invenimus; ... (Sproizer Hügel). Septembri, Octobri." ["We found a notable fungus on the feathers and bones of the corpse of a single corvid (*Corvus cornix* L.) already putrefying, lying in a shady place; ... (Sproizer Hügel). September, October"]. **Lectotype** (**here designated**, typification identifier MBT 10019542): illustration - tab. IX, fig. 2 in Albertini & Schweiniz *Conspectus Fungorum in Lusatiae Superioris* ... (1805). Reference collection [the "neotype" assigned by Kandemir et al (2022)]: NETHERLANDS. Baarn, Landgoed Pijnenburg (52.172°, 5.244°), 1972, *H.A. van der Aa 3257* (Spec-

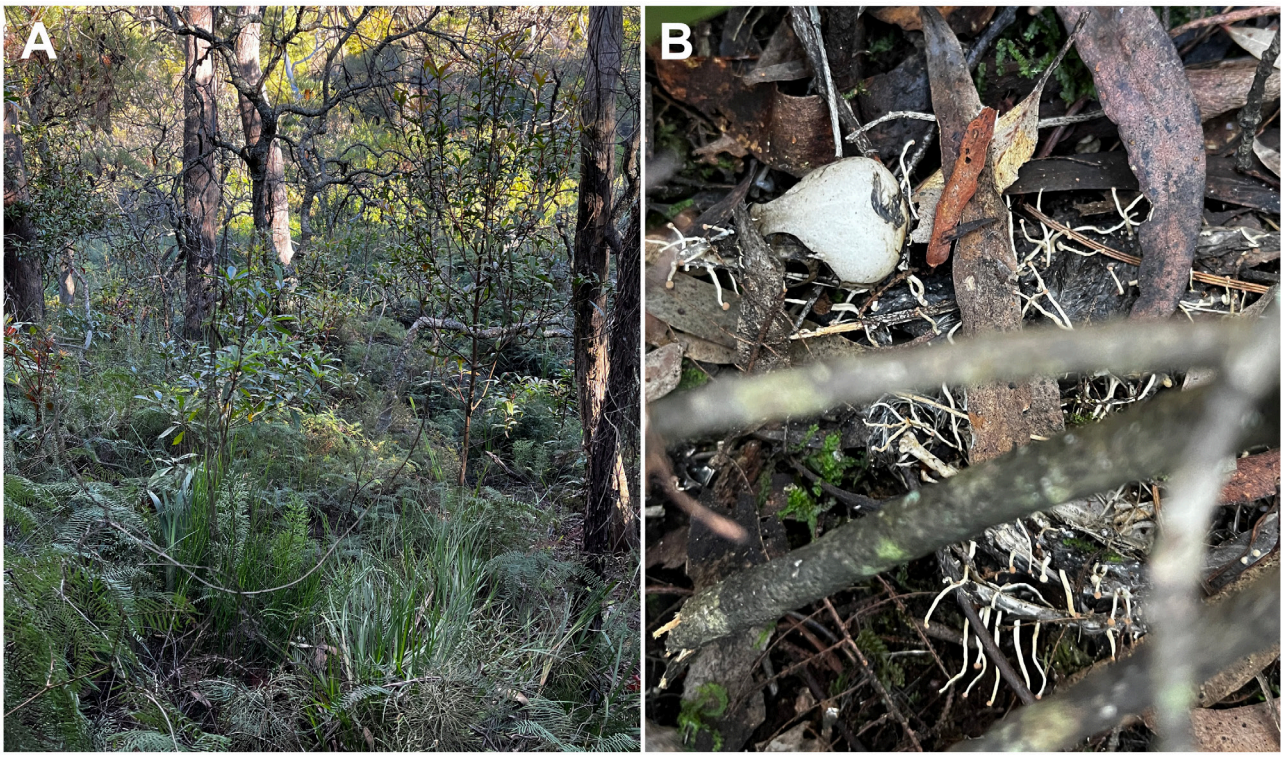

Figure 3. Habitat of *Onygena corvina* (MEL 2530453). A. Collection locality in Water Nymphs Dell public recreation area. B. Sporing bodies growing on bird skull and feathers in the field.

imen: CBS H-15266; Culture: CBS 152.73 =UAMH 3795). GenBank: ITS = UAMH 3795 [the sequence is not lodged in GenBank but is provided at <https://www.uamh.ca/details.php?id=3795>]; LSU = MH878305.

Figs. 3-5.

Macroscopic features

Sporing body capitate, comprised of sterile stipe supporting a roughly spherical spore mass. Spore mass rounded, 0.5–1.5 mm diameter, peridium 0.05–0.1 mm thick, pale cream, with lighter-coloured speckles on surface when young, breaking apart and becoming brown and densely fibrillose at maturity. Stipe cylindrical to irregular, often twisted, 2–15(–20) × 0.25–0.75 mm, white or pale cream, darker where damaged.

Microscopic features

Ascospores 6–*7.16*–8.5 × 3–*3.29*–4 µm [60/1], ellipsoid, often curved, thick-walled, appearing smooth, brown, with 2 internal oil drops. Asci 10–*11.00*–12.5 × 8–*9.05*–10.5 µm [10/1], rounded, 8-spored, with interascal hyphae 2–*3.12*–4.5 µm diam. [10/1], cylindrical, thin-walled, branching, hyaline. Paraphyses not observed. Peridium consisting of irregularly spherical hyphae approximately 4–10 µm diam. forming a pseudoparenchymatous tissue.

AUSTRALIA. New South Wales, Wentworth Falls, Water Nymphs Dell public recreation reserve (-33.7087222°, 150.3791667°), 16 May 2023, *E. Brand s.n., F. Pegrem-Brand & L. Pegrem-Brand* (MEL 2530453, DAR; https://www.inaturalist.org/observations/160697615). GenBank: ITS = PP278378; LSU = PP627009.

Host and habit. Gregarious, on the beak and feathers of a decomposing bird carcass of which the skull is 34 mm long and the is beak 12 mm long. The remaining feathers are not in good condition but appear to be dark in colour, especially on the crown, but also with some on the breast tinted reddish brown. The skull appears to be of a passerine (Leo Joseph, pers. comm.). Among passerine birds noted as present at the site, we can rule out Grey shrike-thrush (*Colluricincla harmonica*) as the beak for this species is at least 19 mm long (BirdLife Australia 2023). The Rufous Whistler (*Pachycephala rufiventris*) has been observed at the site and has a bill that is 15–19 mm long and plumage of similar tones to those on the remaining feathers (BirdLife Australia 2023). We cannot locate an image of the skull of the Rufous Whistler, but for a closely related species also present at the site, the Golden Whistler (*P. pectoralis*), the host skull shows a good match to an image on Skullsite (<https://skull-site.com/skullpage/pachycephala-pectoralis-golden-whistler/>; noted as with skull length 38 mm) — as far as the overall structure and the shape of the openings in the interorbital septum, but in the host skull the very fine downward tip to the bill is not present and the size is slightly smaller. The slightly larger size of the Golden Whistler is confirmed from the range of measurement in HANZAB (BirdLife Australia 2023) which gives the beak of this species at 14–18 mm long. Nevertheless, the comparison against *Pachycephala* species does indicate the general size expected for the host bird.

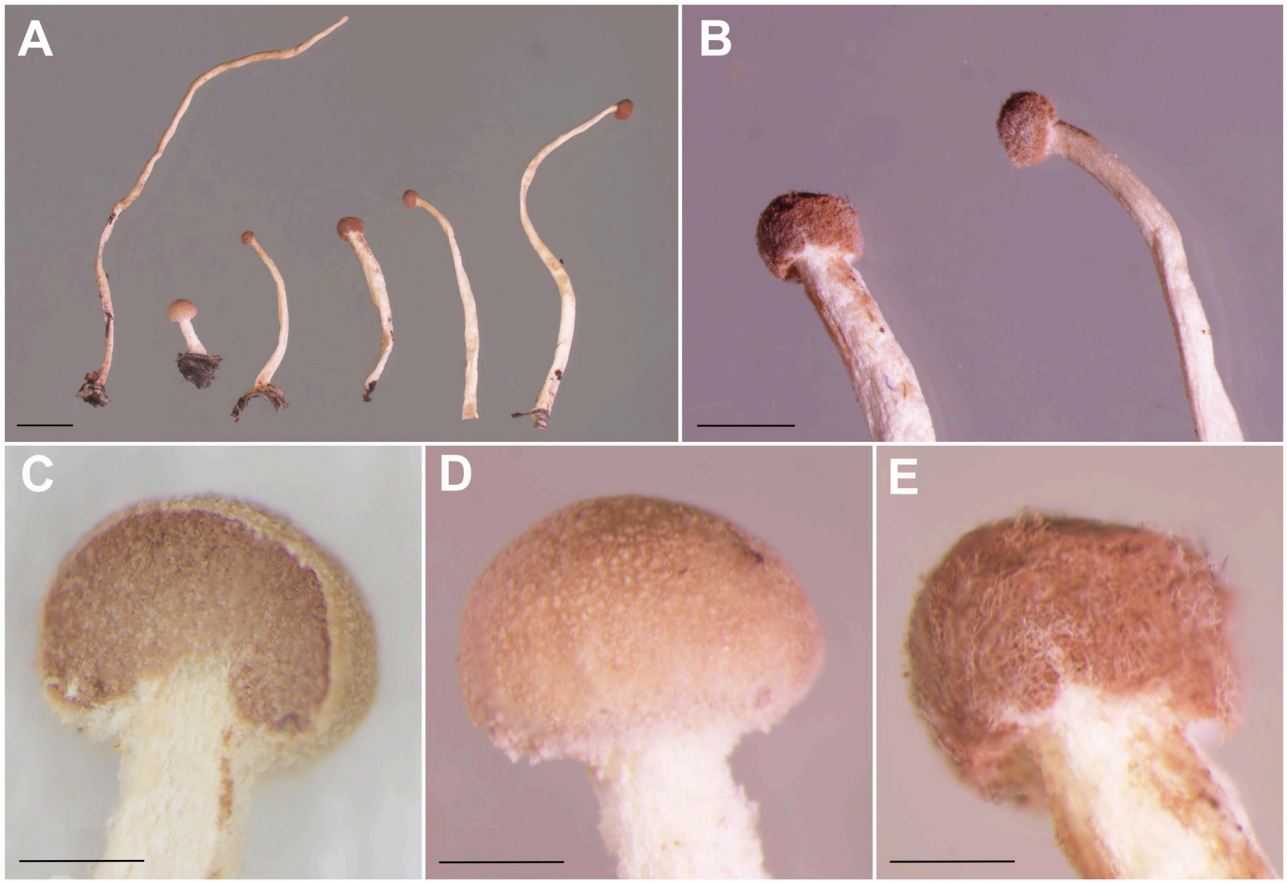

Figure 4. A–B. *Onygena corvina* (MEL 2530453) sporing bodies. C. Longitudinal section of immature spore mass showing outer peridium and inner tissue. D. Outer surface of immature spore mass with peridium. E. Mature spore mass. Scales: A=2 mm; B=1 mm; C–E=0.5 mm.

Distribution and habitat. In *Eucalyptus sieberi/E. piperita* Open Forest, a hanging swamp, several metres from creek line, on forest floor in dense coral ferns and leaf litter.

Typification. The selection of a neotype for *O. corvina* by Kandemir et al (2022) is not Code-compliant, because illustrations are considered part of the original material, and hence available for selection as lectotypes (Turland et al. 2018). Original material connected to the work by Albertini and Schweiniz *Conspectus Fungorum in Lusatiae Superioris* is held at MEL — specifically, at least 70 specimens attributed to Albertini that match up to novel taxa described in that work (Karakehian et al. 2024). However, a search of early collections of Ascomycota held in MEL failed to locate a collection of *O. corvina* that could be connected to Albertini. Therefore, we lectotypify on the illustration included in the protologue. The proposed "neotype" can be regarded as a reference collection and has associated reference sequences. There is no need at present to nominate an epitype, because an epitype should only be designated when the original material is "demonstrably ambiguous" (Turland et al. 2018). The plate shows a fungus growing on bird feathers, which is sufficient at the moment as a type for a species long-associated with bird carcasses. Should multi-gene molecular data become important in delimiting species of *Onygena*, the reference collection could then be designated as an epitype.

Disclosures

The authors do not have any conflicts of interest to disclose.

Acknowledgments

A generous donation from the late Wendy Dodd (Canberra, 1946--2023) funded the establishment of Luke Vaughan's position at RBGV. We are grateful to Eugenia Pacitti, Rebecca Le Get and Heather Merrylees at Royal Botanic Gardens Victoria for assisting with access to the collections at MEL; Sebastien Santini (CNRS/AMU IGS UMR7256) and the PACA Bioinfo platform for the availability and management of the phylogeny.fr website used to apply Gblocks 0.91b to the *Onygena* ITS sequence alignment; Leo Joseph and Richard Schodde (Australian National Wildlife Collection) for advice on bird skull identification; and Blue Mountains City Council for granting permission to collect a biological specimen on BMCC managed public recreation land.

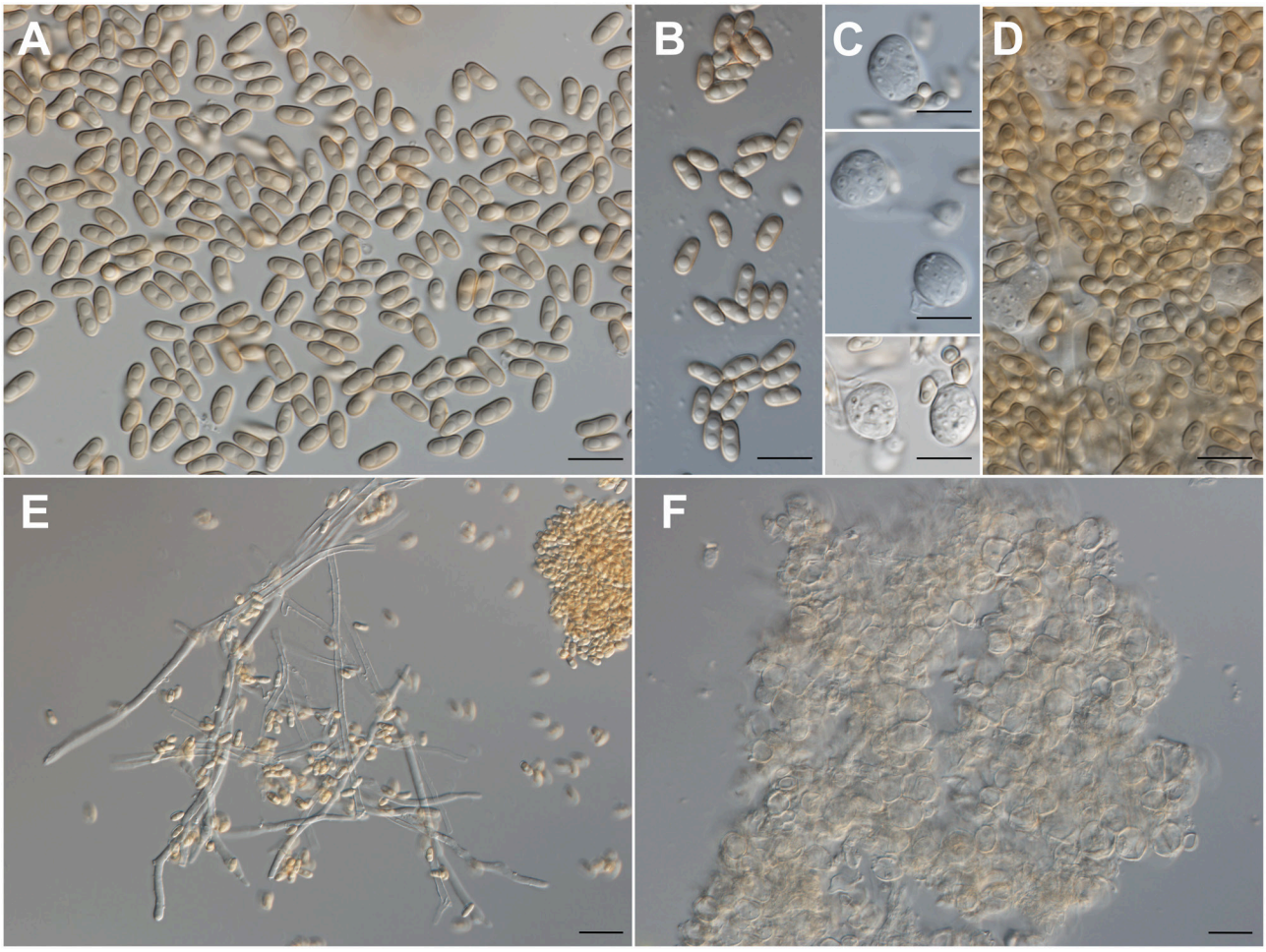

Figure 5. *Onygena corvina* (MEL 2530453) microscopic features. A. Ascospores in 5% Potassium hydroxide. B. Ascospores in water. C. Asci in 5% Potassium hydroxide. D. Asci, ascospores and interascal hyphae in 5% Potassium hydroxide. E. Hyphae and ascospores in water. F. Peridium of pseudoparenchyma tissue. Scales: A–D=10 µm; E–F=20 µm.

References

Abarenkov K, Tedersoo L, Nilsson RH et al. (2010) PlutoF - a web based workbench for ecological and taxonomic research, with an online implementation for fungal ITS sequences. *Evolutionary Bioinformatics* 6: 189–196.

Abarenkov K, Nilsson RH, Larsson K-H et al. (2023) The UNITE database for molecular identification and taxonomic communication of fungi and other eukaryotes: sequences, taxa and classifications reconsidered. *Nucleic Acids Research* 52: D791–D797. <https://doi.org/10.1093/nar/gkad1039>

Albertini JB, Schweiniz LD von (1805) *Conspectus Fungorum in Lusatiae Superioris agro Niskiensi crescentium, e methodo Persooniana*. Lipsiae, Sumtibus Kummerianis.

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. *Journal of Molecular Biology* 215: 403–410. <https://doi.org/10.1016/S0022-2836(05)80360-2>

Beug MW, Bessette AE, Bessette AR (2014) *Ascomycete Fungi of North America, a Mushroom Reference Guide*. University of Texas Press, Austin.

BirdLife Australia (2023). HANZAB. Text before updates sourced from: Marchant, S. et al (eds) 1990–2006 *Handbook of Australian, New Zealand and Antarctic Birds*. Volume 1 to 7. Birdlife Australia. <https://hanzab.birdlife.org.au>

Boßelmann F, Romano P, Fabritius H, Raabe D, Epple M (2007) The composition of the exoskeleton of two crustacea: the American lobster *Homarus americanus* and the edible crab *Cancer pagurus*. *Thermochimica Acta* 463(1–2): 65–68. <https://doi.org/10.1016/j.tca.2007.07.018>

Breitenbach J, Kränzlin F (1984) *Fungi of Switzerland* vol.1. Verlag Mykologia: Lucerne.

Castresana J (2000) Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Mol Biol Evol.* 17(4): 540-52. <https://doi.org/10.1093/oxfordjournals.molbev.a026334>

Craig S, Vaughan LJ, Holmes GD, May TW (2023) *Pseudobaeospora taluna* (Fungi: Agaricales) newly described from southern Australia. *Australian Journal of Taxonomy* 24: 1–16. <https://doi.org/10.54102/ajt.yuij6>

Currah RS (1985) Taxonomy of the Onygenales: Arthrodermataceae, Gymnoascaceae, Myxotrichaceae and Onygenaceae. *Mycotaxon 2*4: 1–216.

Dereeper A, Audic S, Claverie JM, Blanc G (2010) BLAST-EXPLORER helps you building datasets for phylogenetic analysis. *BMC Evol Biol.* 10:8. <https://doi.org/10.1186/1471-2148-10-8>

Dereeper A, Guignon V, Blanc G et al. (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Res*. 36(Web Server issue): W465-9. <https://doi.org/10.1093/nar/gkn180>

Edgar RC (2004) MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32(5): 1792–1797.

Fischer E (1897) *Dr. L. Rabenhorst's Kryptogamen-Flora von Deutschland, Oesterreich und der Schweiz. Zweite Auflage. Band 1. Abteilung V. Ascomyceten: Tuberaceen und Hemiasceen*. Verlag von Eduard Kummer: Leipzig. [See pp. 102: fig. 1, 104–105.]

Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for basidiomycetes - application to the identification of mycorrhizae and rusts. *Molecular Ecology* 2: 113–118. <https://doi.org/10.1111/j.1365-294X.1993.tb00005.x>

GBIF: the Global Biodiversity Information Facility. GBIF Occurrence Download, accessed 6 April 2024. <https://doi.org/10.15468/dl.sw6472>

Geneious Prime Version 2021.0.3. <https://www.geneious.com>

Hagen A (1942) *Onygena equina* and *corvina* in Norway. *Norsk Botanisk Forening Meddelelser* 1941: 93–99.

Hoang DT, Chernomor O, von Haeseler A, Minh BQ, Vinh LS (2017) UFBoot2: Improving the ultrafast bootstrap approximation. *Mol Biol Evol*. 35: 518–522. <https://doi.org/10.1093/ molbev/msx281>

Huang Y, Busk PK, Herbst FA, Lange L (2015) Genome and secretome analyses provide insights into keratin decomposition by novel proteases from the non-pathogenic fungus *Onygena corvina*. *Applied Microbiology and Biotechnology* 99: 9635–9649. <https://doi.org/10.1007/s00253-015-6805-9>

Kalyaanamoorthy S, Minh BQ, Wong TK, von Haeseler A, Jermiin LS (2017) ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat Methods*. 14: 587–589. <https://doi.org/10.1038/nmeth.4285>

Kandemir H, Dukik K, de Melo Teixeira M, et al. (2022) Phylogenetic and ecological reevaluation of the order Onygenales. *Fungal Diversity* 115: 1–72. <https://doi.org/10.1007/s13225-022-00506-z>

Karakehian JM, Rödel T, Damm U, Pfister DH, Miller AN, Truong C, May TW (2024) Specimens in the National Herbarium of Victoria, Australia (MEL) and at Naturalis Biodiversity Center of Leiden, Netherlands (L) associated with Albertini and Schweinitz's *Conspectus fungorum in Lusatiae superioris*. *Taxon* <https://doi.org/10.1002/tax.13239>

Komorowska H (1986) *Onygena equina* (Willd.) Pers.: Fr. in Poland. *Acta Mycologica* 22(1): 49–52.

Lange L, Huang Y, Busk PK (2016) Microbial decomposition of keratin in nature - a new hypothesis of industrial relevance. *Applied Microbiology and Biotechnology* 100: 2083–2096. <https://doi.org/10.1007/s00253-015-7262-1>

Leuchtmann A, Clémençon H (2012) The taxonomic position of the genus *Heydenia* (Pyronemataceae, Pezizales) based on molecular and morphological data. *Mycological Progress* 11: 699–710. <https://doi.org/10.1007/s11557-011-0779-5>

McKittrick J, Chen PY, Bodde SG, Yang W, Novitskaya EE, Meyers MA (2012) The structure, functions, and mechanical properties of keratin. *JOM* 64: 449–468. <https://doi.org/10.1007/s11837-012-0302-8>

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, Lanfear R (2020) IQ-tree 2: new models and efficient methods for phylogenetic inference in the genomic era. *Mol Biol Evol*. 37: 1530–1534. <https://doi.org/10.1093/molbev/msaa015>

Morgulis A, Coulouris G, Raytselis Y, Madden TL, Agarwala R, Schäffer AA (2008) Database indexing for production MegaBLAST searches. *Bioinformatics* 24(16): 1757–1764. <https://doi.org/10.1093/bioinformatics/btn322>

Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol*. 32: 268–274. <https://doi.org/10.1093/molbev/msu300>

Turland NJ, Wiersema JH, Barrie FR et al. (Eds) (2018) *International Code of Nomenclature for algae, fungi, and plants (Shenzhen Code) adopted by the Nineteenth International Botanical Congress Shenzhen, China, July 2017*. Regnum Vegetabile 159. Koeltz Botanical Books: Glashütten.

Uzun Y, Kaya A (2019) *Onygena*, a new ascomycete genus record for Turkey. *KSU Journal of Agriculture and Nature* 22(Suppl 1): 98–101. <https://doi.org/10.18016/ksutarimdoga.vi.535130>

White TJ, Bruns TD, Lee S, Taylor J (1990) 38 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics, In *PCR Protocols.* (Eds MA Innis,

DH Gelfand, JJ Sninsky, TJ White) pp. 315–322. Academic Press: San Diego. <https://doi.org/10.1016/B978-0-12-372180-8.50042-1>