



Entoloma hirtipes in Türkiye: First molecular confirmation based on ITS from Çanakkale

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Çanakkale'den *Entoloma hirtipes*: Türkiye'deki ilk ITS temelli moleküler doğrulama

Abstract: *Entoloma hirtipes* (Schumach.) M.M. Moser is a member of the *Entolomataceae* characterized by considerable morphological variability and taxonomic complexity, making accurate species delimitation challenging. In this study, a macrofungal specimen collected from Çanakkale Province in northwestern Türkiye was identified using an integrative taxonomic approach combining detailed macro- and micromorphological observations with ITS rDNA-based phylogenetic analyses. Macroscopic and microscopic examinations included the assessment of basidiospores, basidia, cheilocystidia, and pileipellis structures, which were compared with published descriptions. The examined material exhibited diagnostic features consistent with *E. hirtipes*, including a hygrophanous pileus, a fibrillose stipe surface, and heterodiametric angular basidiospores. The ITS region was amplified using the ITS1/ITS4 primer pair and analysed together with reference sequences retrieved from GenBank. Bayesian phylogenetic analysis recovered the newly generated sequence within a strongly supported *E. hirtipes* clade (PP = 1.00), fully corroborating the morphological identification. The combined morphological and molecular evidence enabled the reliable identification of the examined material as *E. hirtipes*. This study provides the first ITS rDNA-based molecular confirmation of *E. hirtipes* from Türkiye, expands the documented distribution of the species within the country, and demonstrates the importance of integrative taxonomy for the accurate delimitation of morphologically similar species in *Entolomataceae*.

Key words: *Entolomataceae*, fungal taxonomy, ITS rDNA, molecular phylogeny, Türkiye

Özet: *Entoloma hirtipes* (Schumach.) M.M. Moser, belirgin morfolojik değişkenlik ve taksonomik karmaşıklık gösteren *Entolomataceae* üyelerinden biri olup, doğru tür teşhisini güçleştirmektedir. Bu çalışmada, Türkiye'nin kuzeybatısında yer alan Çanakkale ilinden toplanan bir makromantar örneği, ayrıntılı makro- ve mikromorfolojik incelemeler ile ITS rDNA temelli filogenetik analizlerin birlikte kullanıldığı integratif taksonomik bir yaklaşımla değerlendirilmiştir. Makroskobik ve mikroskobik incelemeler kapsamında basidiyospor, bazidyum, keilosistidya ve pileipellis yapıları ayrıntılı olarak incelenmiş ve literatürde bildirilen verilerle karşılaştırılmıştır. İncelenen örneğin higrofan şapka yapısı, fibrilloz sap yüzeyi ve heterodiametrik, köşeli basidiyosporları gibi ayırt edici karakterlerinin *E. hirtipes* tür tanımlarıyla uyumlu olduğu belirlenmiştir. ITS bölgesi ITS1/ITS4 primer çifti kullanılarak çoğaltılmış ve GenBank'tan elde edilen referans dizilerle birlikte analiz edilmiştir. ITS rDNA veri setine dayalı Bayesyen filogenetik analiz sonucunda elde edilen yeni dizi, güçlü destek değerine sahip (PP = 1.00) *E. hirtipes* kladı içerisinde konumlanmış ve morfolojik teşhisi moleküler olarak doğrulanmıştır. Morfolojik ve moleküler verilerin birlikte değerlendirilmesi, incelenen materyalin güvenilir biçimde *E. hirtipes* olarak tanımlanmasını sağlamıştır. Bu çalışma, *E. hirtipes*'in Türkiye'den ITS rDNA verilerine dayalı ilk moleküler doğrulamasını sunmakta, türün Türkiye'deki bilinen yayılımını genişletmekte ve *Entolomataceae* içerisinde morfolojik olarak benzer türlerin doğru şekilde sınırlandırılmasında integratif taksonominin önemini ortaya koymaktadır.

Anahtar Kelimeler: *Entolomataceae*, fungal taksonomi, ITS rDNA, moleküler filogeni, Türkiye

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1. Introduction

Entoloma (Fr.) P. Kumm. is one of the most species-rich genera of the family *Entolomataceae* and the order *Agaricales*, currently represented by approximately 2000 recognised species worldwide (Kaygusuz et al., 2024; Uzun et al., 2025). Members of the genus are typically distinguished by their pink spore track and distinctive angular basidiospores, which are the result of the inner wall structure (Noordeloos and Gates., 2012). However, *Entoloma* exhibits a highly heterogeneous morphological structure; basidiomas can be tricholomatoid, mycenoid, clitosiboid, or pleurotoid in form, and micromorphological characters, such as pileipellis structure, pigmentation type,

and the presence and shape of cystidia, show wide variation (Noordeloos and Gates, 2012; Noordelos, 2012). Notwithstanding the considerable morphological diversity observed within *Entoloma*, delineating species boundaries remains a substantial taxonomic challenge. Morphological convergence, particularly in macroscopic characters such as cap color, hygrophanous status, lamellae attachment and stem surface features, poses a significant challenge to the accurate interpretation of phylogenetic relationships, often resulting in misdiagnosis (Vila et al., 2013; Morozova and Pham, 2023). This phenomenon is especially pronounced in species complexes within subgenera such as *Nolanea* (Fr.) P. Kumm., *Claudopus* Gillet and *Leptonia* (Fr.) P. Kumm., where extensive morphological overlap exists and

interspecies boundaries are frequently indistinct (Jančovičová and Adamčík, 2012; Vila et al., 2013).

In recent years, molecular phylogenetic studies based on protein-coding gene regions such as nrITS, nrLSU, tef1- α , and rpb2 have significantly reshaped the infrageneric classification of *Entoloma* (Vila et al., 2013; Morozova and Pham, 2023). These studies have revealed that taxa morphologically considered under a single species can, in fact, be comprised of cryptic or pseudocryptic species complexes. Conversely, some populations exhibiting significant phenotypic variation can be genetically classified within a single species. Consequently, in the contemporary context, the utilisation of DNA barcode data for the purpose of conducting detailed morphoanatomical studies has become the prevailing approach for the reliable identification of species within the taxonomic classification of Entolomataceae (Morozova and Pham, 2023; Chen et al., 2024).

Even though the diversity of *Entoloma* in Türkiye has been progressively documented through national checklists and an increasing number of taxonomic studies (Sesli and Sesli, 2017; Sesli et al., 2020; Allı, 2021; Altuntaş et al., 2021; Kaygusuz et al., 2024; Uzun et al., 2025; Sadullahoğlu & Uzun, 2025), the current knowledge of the Turkish *Entoloma* biota remains incomplete. Recent studies have introduced several new records and substantially improved our understanding of the genus, suggesting that its actual diversity is considerably higher than currently documented. Nevertheless, most available records are still based primarily on morphological observations, whereas molecularly validated studies remain scarce. Recent molecular studies conducted on several *Entoloma* species, particularly in Europe, have demonstrated that morphologically defined taxa may comprise cryptic or pseudocryptic species complexes (Vila et al., 2013; Morozova & Pham, 2023). Consequently, DNA sequence data have become increasingly important for reliable species delimitation within the genus.

Entoloma hirtipes is distinguished by its hygrophanous pileus, prominently fibrillose stipe surface, and angular basidiospores. However, it exhibits considerable morphological overlap with several closely related taxa. Therefore, identifications based solely on morphological characters, particularly within species complexes sharing similar macromorphological features, may lead to inaccurate species delimitation. Increasing evidence of cryptic diversity within *Entoloma* (Vila et al., 2013; Chen et al., 2024) highlights the importance of integrative taxonomic approaches combining morphology with molecular data. In Türkiye, *E. hirtipes* was first reported from Konya Province by Afyon (1997), subsequently recorded from Hakkari Province (Acar et al., 2020), and later included in the national checklist of Turkish fungi (Sesli et al., 2020). Despite these records, the species has remained poorly documented in the country, and, to the best of our knowledge, has not previously been confirmed using DNA sequence data.

In this study, specimens collected from northwestern Türkiye and morphologically consistent with *Entoloma hirtipes* were subjected to detailed macro- and micromorphological analyses and further supported by molecular phylogenetic data based on the nrITS region. The integration of morphological evidence with DNA barcode

data contributes to a more robust delimitation of species boundaries within *Entoloma* and enhances the understanding of Entolomataceae diversity in Türkiye.

2. Materials and Method

The macrofungus specimen examined in this study was collected on 9 January 2025, during fieldwork conducted in Çanakkale, Türkiye, near the Hasan Mevsuf Sports Hall on the Campus of Çanakkale Onsekiz Mart University (ÇOMÜ) (Fig.1). The specimens exhibited fruiting bodies on humic soil in an area characterised by *Pinus brutia* Ten. and *Quercus coccifera* L. trees. A comprehensive morphological evaluation encompassing both macroscopic and microscopic characteristics, in conjunction with molecular analyses predicated on the ITS region (ITS1/ITS4), was utilised to ascertain the species, thereby ensuring a reliable species-level identification.

2.1. Morphological studies

During field studies, locality information (including coordinates and altitude), collection date, habitat type, accompanying vegetation, substrate characteristics, and macroscopic findings were meticulously recorded for each specimen. Photographs of the basidiomas were captured in their natural environment using a Canon EOS 60D digital camera, to accurately reflect their colour, developmental stage, and habitus characteristics. Following collection, the specimens were dried under controlled conditions at 40–45 °C to preserve their morphological characteristics. They were then labelled and stored appropriately until the analysis stage. Micromorphological examinations were performed using a Leica DM500 light microscope. Thin sections of the material, desiccated prior to examination, were prepared in distilled water (H₂O), and the basidium, basidiospore, cheilocystidia, caulocystidia, and pileipellis structures were examined in detail. Spore measurements and other microscopic characteristics were analysed using Leica Application Suite (v3.4.0) software. A minimum of 25 measurements were obtained for each character, and spore measurements (n = 30) were presented in the format. Spore dimensions were expressed as length × width, and the spore ratio Q (length/width) and the average spore ratio Qav were calculated. Microscopic drawings of the structures were prepared using CorelDRAW (64-bit, Corel Corporation,

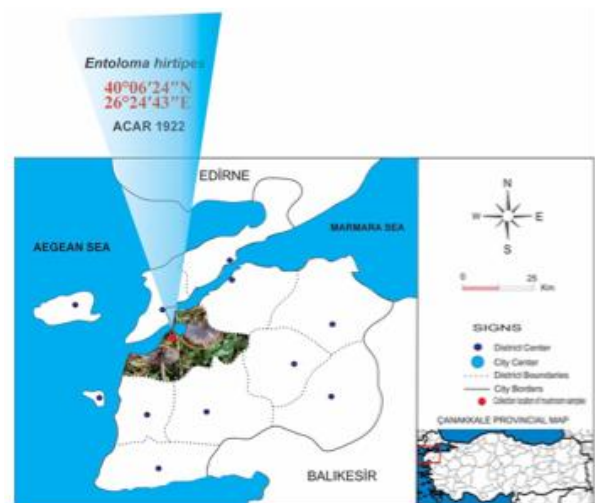


Figure 1. Map showing the collection locality of *Entoloma hirtipes* in Çanakkale, Türkiye.

Canada) program in accordance with scientific publication standards.

Species identification was carried out through a comparative evaluation of macro- and micromorphological characters. European species concepts, particularly those related to the genus *Entoloma*, were used as the taxonomic framework for this study. In this context, the studies of (Breitenbach and Kränzlin, 1995; Co-David et al., 2009; Noordelos, 2012; Reschke et al., 2022) were consulted for species identification. The examined specimens were prepared as fungarium material and deposited in the Fungarium of the Department of Biology, Faculty of Science, Van Yüzüncü Yıl University (VANF) as reference specimens.

2.2. Determination of ITS rDNA sequences

Genomic DNA of the macrofungus sample examined in this study was isolated using a CTAB-based method (Rogers and Bendich, 1994). Subsequent to the isolation process, the purity and concentration values of the obtained DNA samples were determined using a Thermo Scientific NanoDrop 2000c UV-Vis spectrophotometer (USA). Suitable DNA samples were then stored at -20 °C until PCR analysis. To facilitate species identification at the molecular level, the Internal Transcribed Spacer (ITS) region of ribosomal DNA was targeted. The ITS region was amplified using the universal primer pair ITS1 and ITS4 (White et al., 1990). The primer sequences utilized in this study were ITS1 (5'-TCCGTAGGTGAACCTGCGG-3') and ITS4 (5'-TCCTCCGCTTTATTGATATATGC-3'), respectively. The PCR reactions were prepared in a total volume of 25 µL, with the reaction mixture consisting of 10 µM primer pair, approximately 10 ng/µL genomic DNA, 10× PCR buffer, 25 mM MgCl₂, 10 mM dNTP mixture, 5 U/µL Taq DNA polymerase (FIREPol®, Solis BioDyne, Estonia), and sterile distilled water. The thermal cycling program that was utilized for the Polymerase Chain Reaction (PCR) amplification process included an initial denaturation step at a temperature of 95°C for a duration of three minutes, followed by denaturation at 95°C for 30 seconds, annealing at 55°C for 30 seconds, and extension at 72°C for one minute for a total of 35 cycles. The reaction was concluded with a final extension step at 72°C for five minutes. The PCR products were electrophoresed on a 1% agarose gel at 100 V for approximately 90 min, yielding a single band of approximately 650–700 bp. The samples that exhibited successful amplification were purified using a PCR cleaning kit, and subsequent sequence analyses were conducted by a commercial sequencing service utilizing an ABI 3730XL Sanger sequencing device. The resulting raw sequences were then arranged by combining forward and reverse reads and converted into contigs. The arrangement of these sequences was then subjected to comparison with the BLAST algorithm in the GenBank database, with the aim of confirming species identification (Altschul et al., 1990).

2.3. Molecular phylogeny

In this study, the ITS rDNA sequence of *Entoloma hirtipes* (Acar 1922) was assembled by combining Sanger sequencing reads obtained using the ITS1 and ITS4 primer pair in DNAMAN v10 (Lynnon Corporation). Forward and reverse reads were edited and assembled to generate a consensus sequence. The resulting consensus sequence was

compared with sequences in the NCBI GenBank database using the BLASTn algorithm to identify closely related taxa. Representative ITS sequences of *Entoloma* species were downloaded from GenBank and used to construct the phylogenetic dataset (see Appendix 1). The dataset consisted of the *E. hirtipes* (Acar 1922) sequence obtained in this study together with sequences retrieved from GenBank. The ingroup comprised *Entoloma* species, whereas *Rhodocybe fumanellii* Ferrari, Vizzini & Fellin (PV363011) was selected as the outgroup for rooting the phylogenetic tree, following the phylogenetic framework of Ediş et al. (2025). All sequences were aligned prior to phylogenetic analyses and manually adjusted where necessary. Bayesian phylogenetic analyses were performed using MrBayes v3.2.7a (Ronquist et al., 2012). The Markov Chain Monte Carlo (MCMC) analysis was run for 3,000,000 generations with two independent runs and four chains (one cold and three heated), with sampling every 100 generations and a burn-in of the first 25% of sampled trees. The GTR+I+Γ model was applied as the nucleotide substitution model (Tavaré, 1986; Yang, 1994), and branch support values were estimated as posterior probabilities (PP).

3. Results

3.1. Taxonomy

Entoloma hirtipes (Schumach.) M.M. Moser (Figs. 2,3)

Turkish Scientific Name: Düz kıvrıkbaş (Sesli et al., 2020)

Pileus 20–60(–70) mm diam., conical or conical-campanulate when young, soon becoming broadly convex, finally plano-convex in mature basidiomata; centre usually with a distinct but small papilla or low umbo; surface smooth or very finely fibrillose, distinctly hygrophane when moist; disc dark grey-brown, dark olive-brown or dark brownish-grey, becoming paler towards the margin, brownish-grey; colour markedly fading on drying to pale grey-brown. Margin translucent-striate when moist due to the thin flesh; in older basidiomata sometimes slightly undulate or irregular. Context thin, pale greyish-brown in the centre, becoming paler towards the margin. Lamellae moderately spaced to rather distant, broad; initially pale grey-beige or dirty cream, becoming pinkish-beige, pinkish-brown or grey-pink with spore maturation; attachment mostly adnexed or slightly sinuate, sometimes with a small tooth. Edge mostly even or slightly undulate, usually concolorous with the lamella surface or slightly paler. Stipe 40–90 × 2–6 mm, cylindrical, usually slender and elongated, sometimes slightly broadened towards the base; surface pale grey-brown or greyish-beige in the upper part, darker brown towards the base; usually finely longitudinally fibrillose or slightly pubescent; apex often paler and minutely pruinose; base often whitish tomentose. Stipe context solid when young, becoming hollow or spongy with age; flesh fibrous and fragile. Odour and taste weak or indistinct. Basidiospores (9–)10–12(–13) × 6–8(–8.5) µm, heterodiametric, mostly 5–7-angled, ellipsoid-polygonal; wall thin to moderately thickened, hyaline to very pale yellowish; Q = 1.3–1.6. Basidia 30–40 × 8–12 µm, mostly 4-spored, clavate, with basal clamp connections. Cheilocystidia 35–60 × 7–15 µm, cylindrical, clavate or sometimes lageniform; thin-walled, hyaline. Pleurocystidia not observed. Pileipellis composed of hyphae forming a periclinal cutis; hyphae 4–14 µm wide,



Figure 2. *Entoloma hirtipes* A-D. Basidiomata in natural habitat

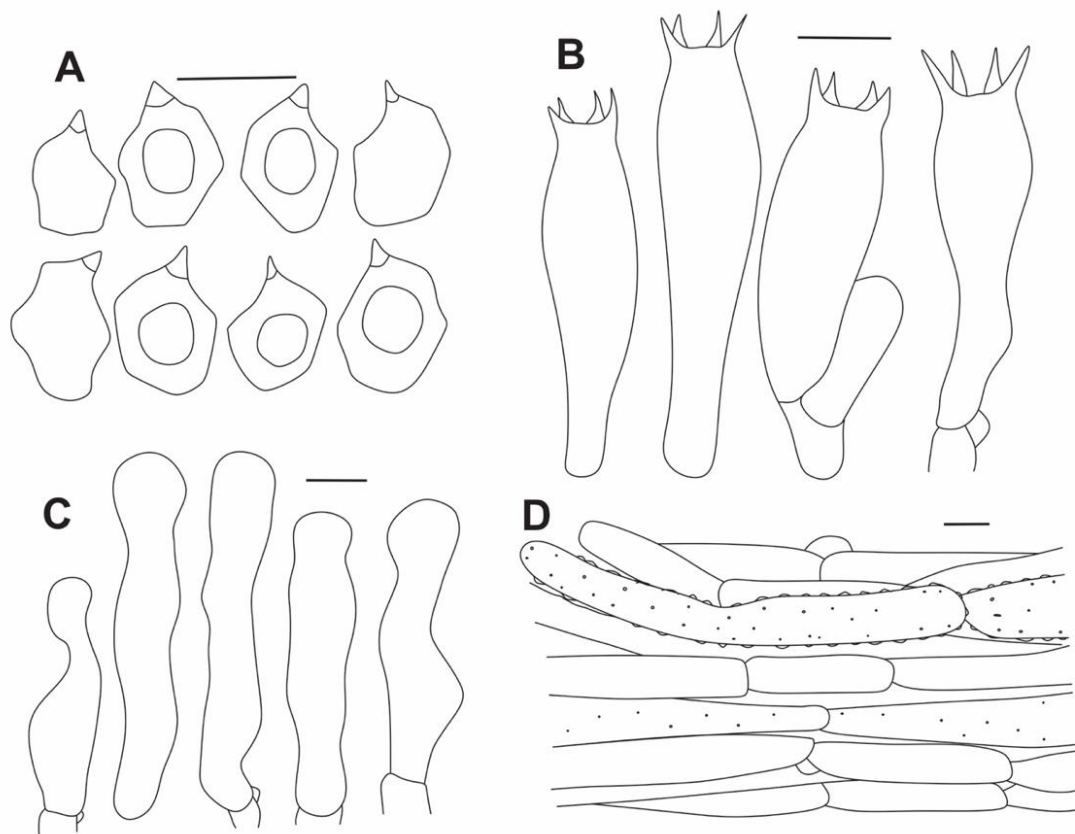


Figure 3. *Entoloma hirtipes* A. Spores, B. Basidia, C. Cheilocystidia, D. Pileipellis (Scale bars: 10 μ m)

mostly pigmented; pigment intracellular, brownish and granular. Clamp connections present in all tissues.

3.2. Ecology and distribution

Entoloma hirtipes predominantly grows saprotrophically on the ground. The species under consideration is found in open or semi-open habitats, especially meadows, forest clearings, roadsides and park-like areas. Furthermore, the species has been observed in both deciduous and mixed forests. The species is believed to demonstrate considerable ecological tolerance. As indicated by the extant literature, the species under consideration is widely distributed throughout the majority of the European continent. Furthermore, it has been documented in the Mediterranean basin, as well as in Western Asia and Oceania databases. In

Türkiye, the presence of this species has been documented in **various** regional macrofungus studies (Noordeloos, 2012; Solak ve Türkoğlu, 2022).

Specimen examined: Türkiye, Çanakkale Province, Çanakkale Onsekiz Mart University (ÇOMÜ) campus, near Hasan Mevsuf Sports Hall, under *Pinus brutia* and *Quercus coccifera*, 55 m a.s.l., 40°06'24"N 26°24'46"E, 09 Jan 2025, leg. İ. Acar, voucher no: Acar 1922 (VANF).

3.3. Phylogenetic results

The Bayesian phylogenetic analysis performed using the ITS rDNA dataset demonstrates that *Entoloma* species are grouped within several well-supported major clades (Fig. 4). The dataset utilised in the analysis was constructed from

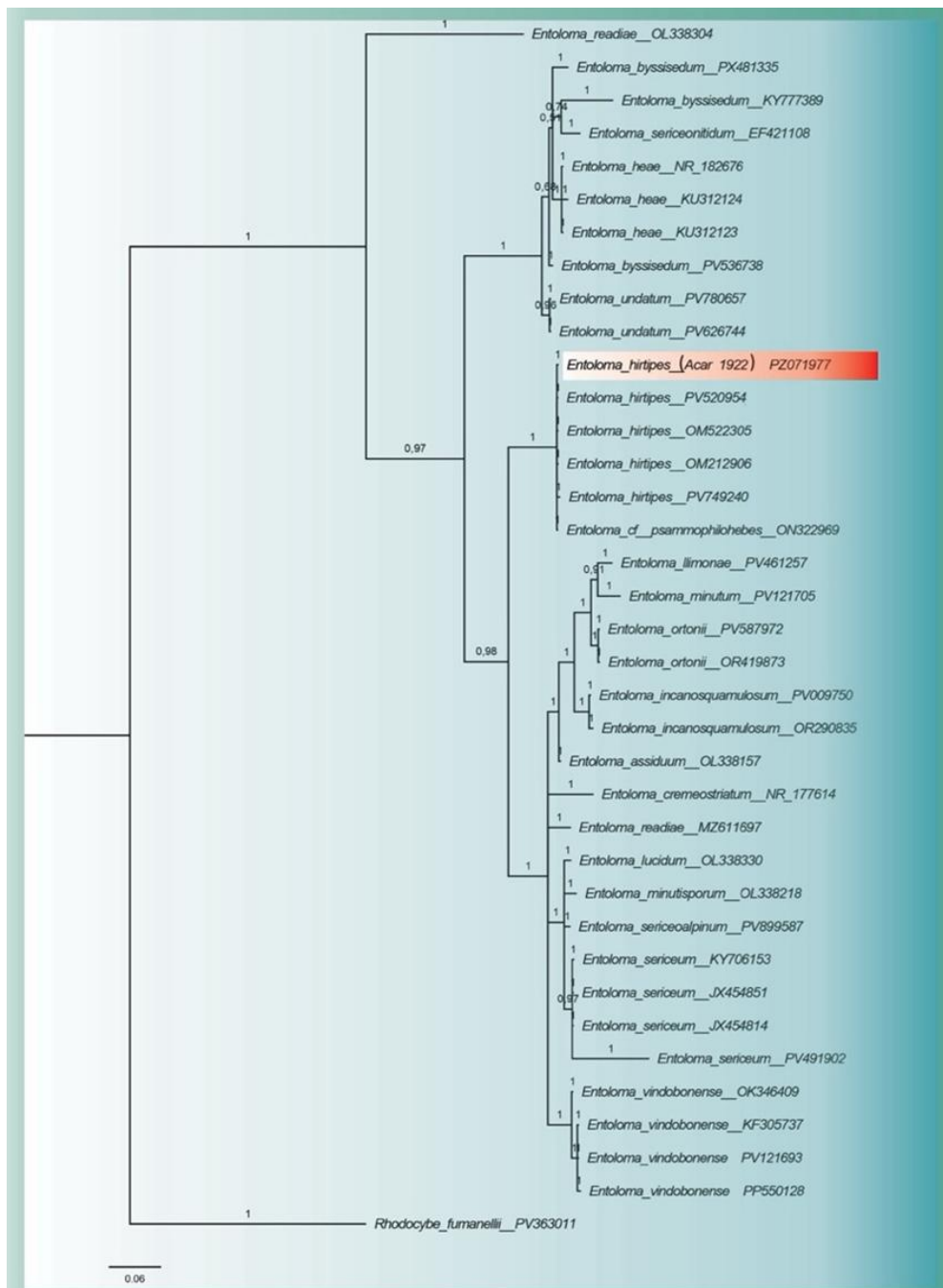


Figure 4. Bayesian phylogenetic tree inferred from ITS rDNA sequences of *Entoloma* species. The sequence generated in this study (*Entoloma hirtipes*, Acar 1922; PZ071977) is indicated by a red box. Posterior probabilities (PP ≥ 0.95) are shown at the nodes. The tree is rooted with *Rhodocybe fumanellii*

the *E. hirtipes* (Acar 1922; PZ071977) sequence obtained in this study, along with representative *Entoloma* sequences downloaded from GenBank, and the tree was rooted using the *Rhodocybe fumanellii* (PV363011) sequence. In the phylogenetic analysis, the *E. hirtipes* sequence obtained in this study was found to be within the same clade as other *E. hirtipes* sequences from GenBank (PV520954, OM522305, OM212906 and PV749240). This group was supported by high posterior probability values (PP = 1.00). Within this clade, the sequence designated as *Entoloma* cf. *psammophilohibes* (GenBank accession number ON322969) is also included. However, the clustering of this sequence within the same well-supported group as *E. hirtipes* sequences suggests that this record is very closely related to *E. hirtipes*, and that a possible misidentification cannot be excluded.

E. hirtipes clade occupies a related position in the phylogenetic tree with a close group including taxa such as *E. undatum* (Gillet) M.M. Moser, *E. byssisedum* (Pers.) Donk, *E. heae* Blanco-Dios, and *E. sericeonitidum* (P.D. Orton) Arnolds, but forms a separate lineage from these species. In other parts of the tree, species such as *E. sericeum* Quél., *E. vindobonense* Noordel. & Hauskn., *E. minutum* (P. Karst.) Noordel., *E. ortonii* Arnolds & Noordel., and *E. incanosquamulosum* (Largent) Noordel. & Co-David form independent clades. Overall, ITS rDNA-based phylogenetic analysis reveals that the examined "Acar 1922" collection has a phylogenetic position consistent with *Entoloma hirtipes* and is located within the same well-supported clade as the reference *E. hirtipes* sequences.

4. Discussions

In this study, samples collected from Çanakkale province were identified as *E. hirtipes* following a comprehensive evaluation of their macro- and micromorphological characteristics, in conjunction with ITS rDNA-based molecular data. Morphologically, the examined material largely agrees with the species concept given in the literature. The hygrophan pileus, dark gray-brown pigmentation, thin and fibrillose stipes, and distinctly angular basidiospores are among the distinctive characteristics. The spore size and morphology observed in this study fall within the ranges reported from European materials (Breitenbach and Kränzlin, 1995; Noordeloo, 2012).

Micromorphological characters also support species identification. Basidiospores measured in this study are mostly 5–7 angular heterodiametric in structure, and their dimensions are consistent with those reported in the literature. The cylindrical-clavate or lageniform form of cheilocystidia and the absence of pleurocystidia are also among the defining microscopic features of the species. In addition, the cutis-like structure of the pileipellis consisting of pigmented hyphae and the presence of clamp attachments in all tissues are consistent with the typical anatomical characters of the genus *Entoloma* (Co-David et al., 2009; Noordeloo, 2012).

In Türkiye, *Entoloma hirtipes* has been documented only rarely. The species was first reported from Konya Province by Afyon (1997), representing the first record for the Turkish mycobiota. It was subsequently recorded from Hakkari Province during a regional macrofungal diversity

survey, where it was collected under *Quercus* spp. (Acar et al., 2020), and was later included in the national checklist of Turkish fungi (Sesli et al., 2020). The present collection represents the third documented record of *E. hirtipes* from Türkiye and the first from Çanakkale Province. Unlike the previous Turkish collections, which originated from the Central Anatolian and Eastern Anatolian regions, our specimen was collected in a Mediterranean transitional ecosystem on the Çanakkale Onsekiz Mart University campus, growing under a mixed stand of *Pinus brutia* L. and *Quercus coccifera* L. These records indicate that *E. hirtipes* is capable of occurring in different phytogeographical regions and forest types in Türkiye, although the currently available data suggest that the species is rarely encountered or under-recorded. Furthermore, the present study provides, to the best of our knowledge, the first DNA sequence-based confirmation of *E. hirtipes* from Türkiye.

Phylogenetic analyses provided unequivocal support for the morphological identification. In the Bayesian phylogenetic tree inferred from the ITS rDNA dataset, the sequence generated from the Turkish specimen (*Entoloma hirtipes*, Acar 1922) clustered with authenticated *E. hirtipes* reference sequences with maximal posterior probability (PP = 1.00), unequivocally confirming the identity of the examined material at the molecular level. The complete congruence between the morphological observations and the ITS phylogeny further highlights the value of an integrative taxonomic approach for the reliable delimitation and identification of morphologically similar *Entoloma* species (Vila et al., 2013; Reschke et al., 2022).

Entoloma hirtipes is a species that can be morphologically confused with *E. sericeum* Quél., *E. vindobonense* Noordel. & Hauskn. and some members of the *Nolanea* group. However, these species are typically distinguished by characteristics such as divergent spore sizes, pileus pigmentation, or ecological preferences (Breitenbach and Kränzlin, 1995; Noordeloo, 2012). The molecular data obtained in this study also reveal that these species belong to different phylogenetic clades.

Recent molecular phylogenetic studies have demonstrated that many morphologically similar species within *Entoloma* actually belong to different phylogenetic lineages (Co-David et al., 2009; Reschke et al., 2022). Consequently, there is an increasing need to support morphological data with DNA barcode data for reliable species identification within the genus. The results of the present study further demonstrate that integrative taxonomy provides an effective approach for the accurate identification of *Entoloma* species.

In conclusion, the evaluation of morphological characters together with ITS rDNA-based phylogenetic data of the material collected from Çanakkale clearly demonstrates its conformity with *E. hirtipes*. This study represents one of the few cases in which *E. hirtipes* from Türkiye has been confirmed using molecular data, thereby contributing to a better understanding of Entolomataceae diversity in the country. Furthermore, the findings highlight the importance of integrating morphological and molecular data in the taxonomic assessment of *Entoloma* species.

Conflict of Interest

There are no conflicts of interest in this work.

Authors' Contribution

The authors contributed equally.

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Appendix:

Entoloma assiduum (OL338157), *E. byssisedum* (KY777389), *E. byssisedum* (PV536738), *E. byssisedum* (PX481335), *E. cf. psammophilohebes* (ON322969), *E. cremeostriatum* (NR_177614), *E. heae* (KU312123), *E. heae* (KU312124), *E. heae* (NR_182676), *E. hirtipes* (Acar 1922; PZ071977), *E. hirtipes* (OM212906), *E. hirtipes* (OM522305), *E. hirtipes* (PV520954), *E. hirtipes* (PV749240), *E. incanosquamulosum* (OR290835), *E. incanosquamulosum* (PV009750), *E. llimonae* (PV461257), *E. lucidum* (OL338330), *E. minutisporum* (OL338218), *E. minutum* (PV121705), *E. ortonii* (OR419873), *E. ortonii* (PV587972), *E. readiae* (MZ611697), *E. readiae* (OL338304), *E. sericeoalpinum* (PV899587), *E. sericeonitidum* (EF421108), *E. sericeum* (JX454814), *E. sericeum* (JX454851), *E. sericeum* (KY706153), *E. sericeum* (PV491902), *E. undatum* (PV626744), *E. undatum* (PV780657), *E. vindobonense* (KF305737), *E. vindobonense* (OK346409), *E. vindobonense* (PP550128), *E. vindobonense* (PV121693), and *Rhodocybe fumanellii* (PV363011) as outgroup.