

First Record of the Interesting Genus *Contumyces* in Türkiye: *Contumyces rosellus* (M.M. Moser) Redhead, Moncalvo, Vilgalys&Lutzoni

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Received Date: 28.07.2025

Accepted Date: 31.10.2025

Abstract

Aim of study: The aim is to identify *Contumyces rosellus*, a species belonging to the genus *Contumyces*, which has a controversial position within the Rickenellaceae family. According to multigenetic marker phylogenetic analyses, it is classified as monotypic. The aim is also to document it as a new genus record for the Turkish mycobiota.

Area of study: The specimen was collected in January 2025 from areas covered with black moss near Akçalı village (Çanakkale).

Material and method: The species was primarily identified using morphological characters based on field and laboratory analyses. Nucleotide sequences obtained from the ITS region were then used for phylogenetic analysis. The phylogenetic tree was inferred using Bayesian analysis implemented in MrBayes.

Main results: The specimen was characterized by a funnel-shaped cap, striated-sulcate margin, downward-pointing lamellae, cylindrical to semi-cylindrical stem structure, and color ranging from yellow to brownish-orange. Microscopically, small, white, smooth-surfaced, and non-amyloid spores were observed. The phylogenetic tree constructed based on ITS sequence analyses confirmed that the sample belongs to *Contumyces rosellus*.

Research highlights: *Contumyces rosellus* is the first *Contumyces* species to be recorded in Türkiye. This new record, characterised by morphological and molecular analyses, represents the third species of the genus worldwide, contributing to the diversity of bryophytic macrofungi in Türkiye.

Keywords: *Hymenochaetales*, ITS, Morphology, New Record, Türkiye

Türkiye’de İlginç Cins *Contumyces*’in İlk Kaydı: *Contumyces rosellus* (M.M. Moser) Redhead, Moncalvo, Vilgalys&Lutzoni

Öz

Çalışmanın amacı: Hymenochaetales takımı içerisinde yer alan ve multigenetik marker filogenetik analizlerine göre monotipik bir familya olarak konumlandırılan Rickenellaceae içerisinde tartışmalı bir konuma sahip olan *Contumyces* cinsine ait *Contumyces rosellus* türünü morfolojik ve moleküler verilerle teşhis ederek Türkiye mikrobiyotası için yeni bir cins kaydı olarak belgelemektir.

Çalışma alanı: Örnek, Ocak 2025 tarihinde Akçalı köyü (Çanakkale) civarındaki karayosunu ile kaplı alanlardan toplanmıştır.

Materyal ve yöntem: Türün tanımlanmasında öncelikle saha ve laboratuvar analizlerine dayanan morfolojik karakterleri kullanılmıştır. Moleküler analizler kapsamında ITS bölgesinden elde edilen nükleotid dizileri filogenetik analiz için kullanılmıştır. Filogenetik ağaç, MrBayes yöntemi ile oluşturulmuştur.

Temel sonuçlar: Toplanan örnek, huni şeklinde şapka, çizgili-sulcat kenar, aşağı doğru uzanan lameller, silindirik ila yarı silindirik ve sarıdan kahverengimsi turuncuya kadar değişen sap yapısı ile tanımlanmıştır. Mikroskopik olarak küçük, beyaz, düzgün yüzeyli ve inamiloid sporlar gözlemlenmiştir. ITS dizi analizleri ile oluşturulan filogenetik ağaç sonucunda örneğin *Contumyces rosellus* olduğu doğrulanmıştır.

Araştırma vurguları: *Contumyces rosellus*, Türkiye’den bildirilen ilk *Contumyces* türü olarak kaydedilmiştir. Dünyada sadece üç türü bulunan cinsin morfolojik ve moleküler analizlerle tanımlanan bu yeni kaydı, Türkiye’nin bryofitik makromantar çeşitliliğine bilimsel bir katkı sunmaktadır.

Anahtar Kelimeler: *Hymenochaetales*, ITS, Morfoloji, Yeni Kayıt, Türkiye



Introduction

Hymenochaetales Oberw., a diverse order within Basidiomycota, encompasses species exhibiting a wide range of basidiome forms, including clavarioid, effused-reflexed, and resupinate types. The majority of species in this order are represented by polypore and corticioid fungi. However, some species are agaric, as in *Blasiphalia*, *Contumyces*, and *Rickenella* genera. Several trophic types are present in *Hymenochaetales*, including saprotrophs (typically wood-decaying species), parasites, and mycorrhizal species (which can colonize both wood and moss) (Wang & Zhou, 2023; Cho et al., 2024). To date, 69 genera and more than 600 species have been reported in *Hymenochaetales* (Kirk et al., 2008; Zhou et al., 2023; Cho et al., 2024). As a result of recent phylogenetic studies, many of these species have been classified under the well-known families *Hymenochaetaceae* Imazeki & Toki and *Schizoporaceae* Jülich (Cho et al., 2024). Another family within the *Hymenochaetales* is *Rickenellaceae*. Many little-studied species were previously included in this family. However, recent studies based on multigenetic marker phylogeny analyses have narrowed the boundaries of *Rickenellaceae* to a monotypic family (Wang et al., 2023).

In the study by Redhead et al. (2002), *Jacobia*, named after Jakob Emanuel Lange, was replaced by *Contumyces*, named after the contemporary amateur Italian mycologist Marco E. Contu. The genus included *C. brunneolilacinus*, the generic species *C. rosellus*, and *C. vesuvianus* in *Hymenochaetales*. This was confirmed by recent phylogenetic studies (Larsson et al., 2006; Zhou et al., 2018). Recently, it has been suggested without justification that *Contumyces* is a subgenus of *Loreleia*. *C. rosellus*, a generic species of *Contumyces*, was transferred to the genus *Loreleia* (Redhead, 2019; Wang et al., 2023). Phylogenetic analyses separated *Contumyces rosellus* and *Loreleia marchantiae*. This separation was confirmed in the study by Larsson et al. (2006). The two sampled species of *Contumyces*, *C. rosellus*, and *C. vesuvianus*, are distinguished from *L. marchantiae*, even though they do not group

them into a clade well supported by molecular separation. Since there is no molecular sequence of *L. postii*, another species belonging to the genus *Loreleia*, and the type specimen of the genus, there is no reason to combine the genus *Contumyces* with the genus *Loreleia*. As a result of all these studies, *Contumyces* is still considered an independent genus from other known genera in *Hymenochaetales* (Wang et al., 2023). Bryophilous Basidiomycota are highly adapted to specialized habitats, often occurring in close association with mosses, either in symbiotic or commensal relationships (F et al., 1994; Vizzini et al., 2012). Such species are ecologically significant because their occurrence is strongly linked to moss-rich microhabitats, which require stable moisture and specific environmental conditions.

Türkiye checklists were analysed by Sesli et al. (2020), Solak and Türkoğlu (2022) and some recent studies (Acar et al., 2021; Acar & Uzun, 2022; Acar & Quijada, 2022; Dizkırıcı & Acar, 2022; Acar & Dizkırıcı, 2023; Akçay et al., 2023; Acar & Karabıyık, 2024a,b; Uzun et al., 2024; Akata et al., 2024a,b,c,d; Allı et al., 2024; Aslan et al., 2024; Karaduman et al., 2024; Kesici et al., 2024; Terman et al., 2024; Yeşilyurt et al., 2024; Ediş et al., 2025), *Contumyces rosellus* is a new genus record for the mycota of Türkiye.

Material and Methods

Morphological Studies

Fresh *Contumyces* basidiomata collected in the vicinity of Akçalı village, Çanakkale center, in 2025 constitute the material for this study. All morphological characters, collection sites, and substrates of the *Contumyces* specimens collected meticulously in the field were noted in the field notebook. The study material was documented photographically from different angles in its natural environment. After the field studies, the collected specimens were transported to the laboratory for further analysis. *Contumyces* specimens were dried under laboratory conditions in a non-illuminated climate and labeled as fungarium material for later use. Sections were taken from the dried samples and prepared in water

and Melzer's Reagent. Microscopic examinations were conducted under a Leica DM500 (Germany) light microscope. Data, such as basidia, spores, and cystidia, were photographed at 1000× magnification. objective. Microscopic characters were measured at least 20 times using Leica Application Suite (version 3.4.0) to determine the most reliable reference intervals. *Contumyces rosellus*, a new genus record for the mycobiota of Türkiye, was identified using the methods described by Moser (1950), Redhead et al., 1995; 2002; Moreno-Arroyo (2004), and Desjardin et al. (2015). The micromorphological characters of *C. rosellus* were drawn and illustrated using CorelDRAW (64-bit) (Canada) software for clarity and comprehensibility. After the identification process of the species was completed, *C. rosellus* was transformed into fungarium material and preserved under appropriate conditions in the fungarium of Van Yüzüncü Yıl University, Faculty of Science, Department of Biology (VANF).

Molecular Studies

Genomic DNA was extracted from the specimen using the CTAB (cetyltrimethylammonium bromide) protocol following Doyle and Doyle (1987), Acar (2022), and Kalmer et al. (2018). The ITS region was amplified using the primer pair Nnc/C26 (Rehner & Buckley, 2005). PCR amplification was carried out in a total volume of 25 µL containing 2× Solver PCR Mix, 0.5 µL genomic DNA (10 ng/µL), the respective primer pair (10 µM), and ddH₂O. The thermal cycling conditions consisted of an initial denaturation at 94°C for 10 min, followed by 40 cycles of denaturation at 94°C for 15 s, annealing at 56°C for 45 s, and extension at 72°C for 45 s, with a final extension step at 72°C for 10 min.

The amplified products were separated by electrophoresis on a 1.0% agarose gel stained with GelRed dye. PCR products were subsequently sequenced at Solver Lab, Van, using the corresponding primers employed for amplification. In addition to the sequences generated in the present study, representative sequences of *Hymenochaetales* species were

retrieved from the GenBank database and incorporated into the phylogenetic analyses.

Phylogenetic Analysis

Sequence editing and assembly were performed using Mesquite version 3.7 (Maddison & Maddison, 2009). Preliminary sequence identification and similarity searches were conducted against the GenBank database using the Basic Local Alignment Search Tool (BLAST) algorithm (Altschul et al., 1990). The sequences generated in the present study were compared with homologous sequences available in GenBank to identify closely related taxa.

The dataset comprised 27 ITS sequences, with *Boletopsis leucomelaena* (PV643831) selected as the outgroup. Phylogenetic relationships were inferred using a Bayesian inference (BI) approach implemented in MrBayes version 3.2.6 (Ronquist & Huelsenbeck, 2003). Bayesian analyses were performed using four Markov chain Monte Carlo (MCMC) chains for 3 million generations under the GTR+G (General Time Reversible + Gamma) substitution model. The first 25% of the sampled generations were discarded as burn-in, and the analysis was continued until the standard deviation of split frequencies fell below 0.01.

Node support was evaluated based on Bayesian posterior probabilities (BPP). A majority-rule consensus tree was generated from the post-burn-in trees, retaining all compatible groups for the estimation of posterior probabilities. The resulting phylogenetic tree was visualized and edited using FigTree version 1.4.3 (Rambaut, 2010).

Results

A brief description of *Contumyces rosellus*, macromorphological pictures, micromorphological pictures under a light microscope, and drawings of microcharacters are described.

Basidiomycota Whittaker ex R.T. Moore

Agaricomycetes Doweld

Hymenochaetales Oberw.

Rickenellaceae Vizzini

Contumyces Redhead, Moncalvo, Vilgalys & Lutzoni

Contumyces rosellus (M.M. Moser) Redhead, Moncalvo, Vilgalys & Lutzoni Figure 1, 2.

Pileus 4–18 mm, convex or convex-flat when young, often funnel-shaped when mature, margin curved inwards, vaguely striate, then straight, hygrophorous, sometimes appearing scalloped with age, surface smooth, sometimes slightly velvety (on closer inspection), light pale brownish to pinkish, very slightly purplish. The smell is almost odorless, and no taste was reported. *Lamellae* patently decurrent, close to subdistant, depth up to 3 mm, usually concolorous with the pileus, pale pink, fades to pinkish–cream and paler in color when mature. *Stipe* 13–23 × 0.5–3 mm, cylindrical, equal, sometimes thicker near the pileus, straight or curved, slightly swollen at the base, hollow, surface pruinose, becoming glabrous, light pale brownish to pinkish, very slightly purplish, paler when mature, usually nearly tan, whitish tomentum at the base, partial veil absent. *Basidia* 33–52 × 5.5–10.2 µm, clavate, hyaline, tetrasporic, with basal fibula. *Spores* (7–) 7.8–10 (–11.3) × (3.4–) 4–5.5 (–6.2) µm, ellipsoidal to cylindrical, lachrymoid, smooth, hyaline, apiculate, guttulate. *Cheilocystidia* (40–) 50.7–67.2 (–74.7) × (4.3–) 6–9 (–10.5) µm, mainly lageniform, sometimes subclavate to subfusiform, branched with clamp. *Pleurocystidia* not observed. *Pileipellis* with

parallel hyphae, up to 17.5 µm wide, clavate or lageniform endings, and fibulae.

Habitat: It is found in open areas, especially along footpaths, sparse grassland, and among mosses, scattered or in groups. In coastal areas, it bears fruit from mid-winter to spring. Although its exact distribution is unknown, it is considered a widespread species. Although rare in some areas, it can be seen locally in abundance (Desjardin et al., 2015).

Specimens examined: Türkiye, Çanakkale, Around Akçalı village, 40° 03'55"N, 26° 35'38"E, 268 m, mixes forest clearing, in meadow, on moss, 18.01.2025, Acar 1945.

Molecular Phylogeny

The phylogenetic analysis was conducted using a total of 27 sequences, including the outgroup and the studied specimen, for the ITS loci. The sequence lengths were 745 base pairs (bp).

Phylogenetic tree was constructed using specimens within the order *Hymenochaetales* that resemble *Contumyces rosellus*. This species is grouped within the same clade as other *C. rosellus* sequences available in GenBank, and this clade was positioned distinctly from the others. (Figure 3). The sample investigated in this study was grouped with its representative retrieved from the database, which had high Posterior Probabilities (1.0).



Figure 1. Macromorphological photos of *Contumyces rosellus* (Scale bar: 1 cm)

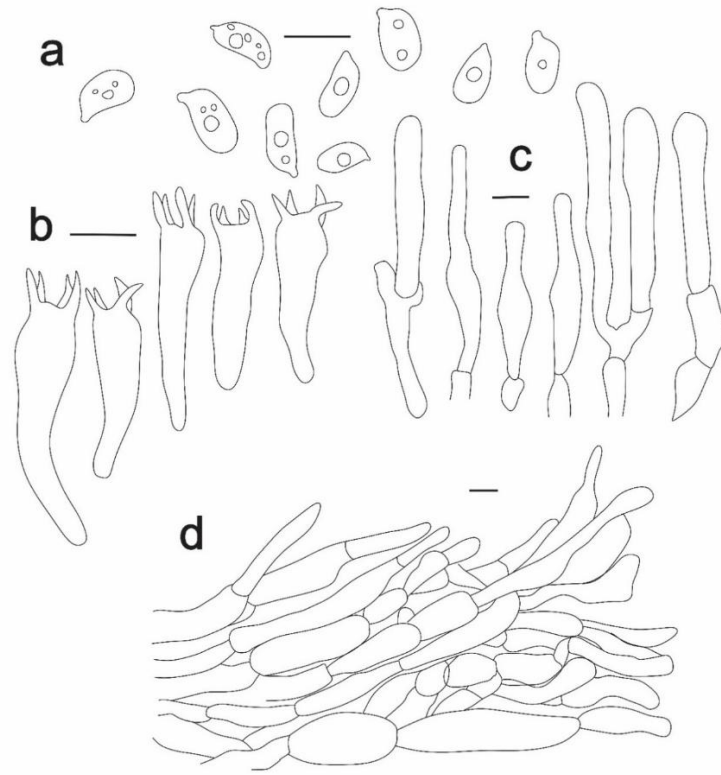


Figure 2. *Contumyces rosellus* a. Spores, b. Basidia, c. Cheilocystidia, d. Pileipellis (Scale bar: 10 μ m)

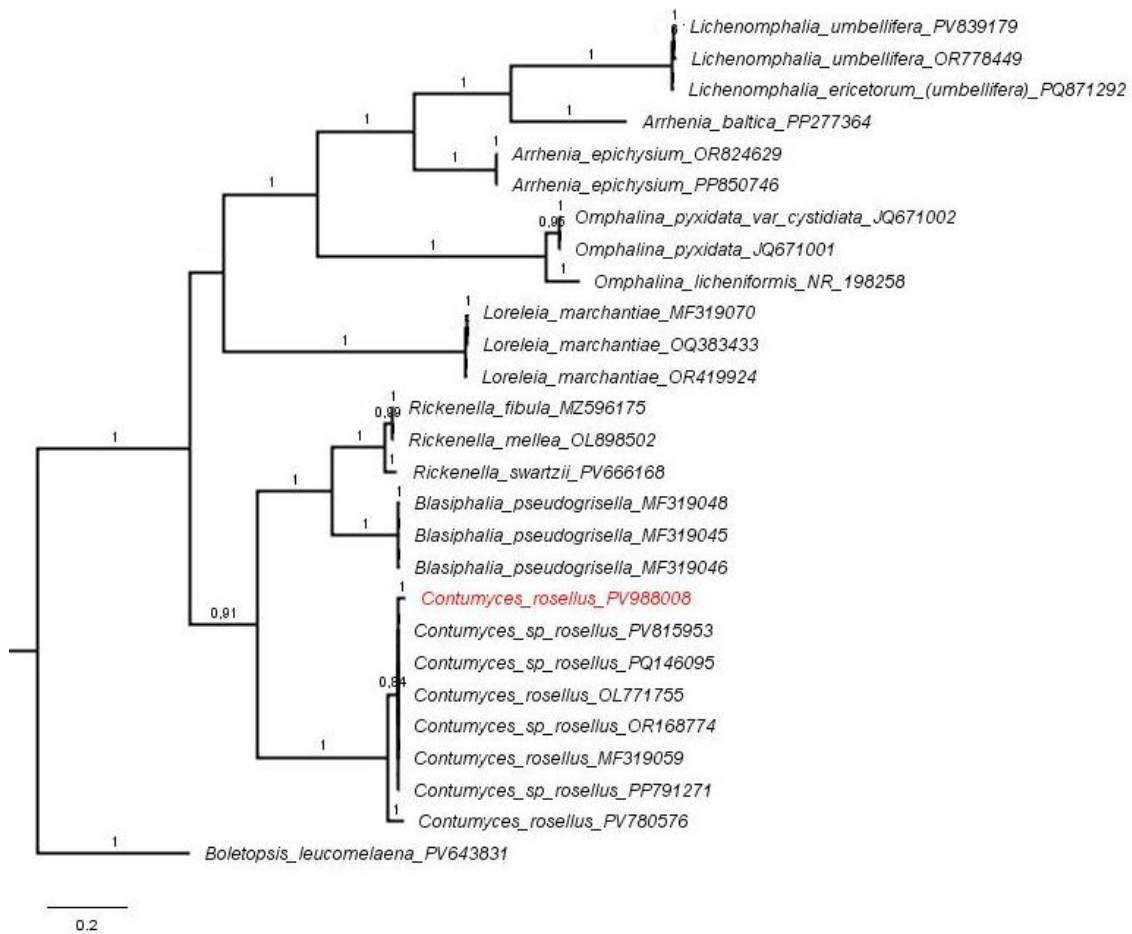


Figure 3. The Bayesian consensus tree inferred from the ITS region
PP> 0.7 is indicated above the branches. Sequences from the studied specimens are marked in red.

Discussion

The bryophyllous omphalinoid fungi (*Blasiphalia*, *Contumyces*, *Rickenella*) are characterized by a convex to deep-bellied pileus, central stalk, thin tissue, downward extending lamellae, white spore trail, and thin-walled inamyloid flat spores (Norvell et al., 1994; Vizzini et al., 2012). The genus *Contumyces* is similar to *Loreleia*, *Omphalina*, *Galerina*, *Blasiphalia*, and *Rickenella* in the field. The most similar genera to these are *Blasiphalia* and *Rickenella*. However, *Contumyces* differs in having cystidia in clusters on the cap, stem, and hymenium, whereas in *Rickenella* and *Blasiphalia*, the cystidia are solitary (Vizzini et al., 2012; Knopf, 2023). *Contumyces rosellus* can also be easily distinguished from both members of its genus and other genera due to the wine-colored to pinkish-brown shades all over the carpophore (Antonín & Noordeloos, 2004; Desjardin et al., 2015). As

C. rosellus matures, the cap may change to a faint tan, but the lamellae and stem usually retain a slightly pinkish color (Redhead et al., 1995; Desjardin et al., 2015).

Although somewhat morphologically similar to *Omphalina pyxidata* var. *cystidiata*, *Contumyces rosellus* is distinguished by its pink to pale salmon-colored fruit bodies, a white stalk, and longer and larger cystidia. Among the *Omphalinas* (s.l.), one notable species is *Loreleia postii* (formerly *Omphalina postii*), which has a bright orange to reddish-brown cap, cream-yellow gills, and a reddish-brown stalk. Another species, *Omphalina ericetorum*, formerly *Phytoconis ericetorum* (now known as *Lichenomphalia umbellifera*), represents the fruiting stage of a basidiomycete lichen. This species is recognizable by its light brown to yellow-brown cap, cream-colored gills, and reddish-brown to yellow-brown stalk. The darkest member of the group is *Arrhenia epichysium*

(formerly known as *Omphalina epichysium*). It is distinguished from the others by its color and distinctly woody structure, with a grey-brown cap, stem, and gills. All these species are, to some extent, morphologically similar to *Contumyces rosellus*. However, as mentioned above, the most important distinguishing characteristic is its wine-colored to pinkish-brown color (Redhead et al., 1995; Vizzini et al., 2012; Desjardin et al., 2015).

As a result of the phylogenetic analyses, the ITS dataset was composed of sequences belonging to *Contumyces rosellus* and related taxa within the order Hymenochaetales. Due to the limited availability of sequence data for this genus in GenBank and the consideration that an evaluation based solely on members of the family *Rickenellaceae* would be insufficient, a phylogenetic tree was constructed at the order level. In this phylogeny, *Contumyces rosellus* samples formed a distinct clade, and our specimen was positioned within this clade.

Contumyces rosellus, previously recorded in various regions of America and Europe but not in Türkiye, has now been added to the country's mycobiota as a new genus-level record, thereby increasing the number of bryophytic Basidiomycota in our country from 34 (Karaduman et al., 2024) to 35.

Ethics Committee Approval

N/A

Peer-review

Externally peer-reviewed.

Author Contributions

Conceptualization: H.K.; Ş.A.T. and I.A.; Investigation: H.K. and I.A. Material and Methodology: H.K.; Ş.A.T. and I.A. Visualization: H.K.; Ş.A.T. and I.A. Writing-Original Draft: H.K.; Writing-review & Editing: H.K.; Ş.A.T. and I.A. All authors have read and agreed to the published version of the manuscript.

Conflicts of interest

The authors declare that they have no conflict of interest.

Funding

This research was supported by the Scientific Research Projects Coordination Unit at Van Yüzüncü Yıl University under project number FHD-2025-12036.

References

- Acar, İ., Blando, F., Gul, B., Greco, A., Mukemre, M., Uzun, Y. & Dalar, A. (2021). The phenolic profile and biological activities of the wild-edible mushrooms *Helvella leucopus* and *Morchella pulchella*. *Journal of Food Measurement and Characterization*, 15(1), 555-566.
- Acar, İ. & Uzun, Y. (2022). *Stictis bengalensis* (Stictidaceae, Ostropales) – A New addition to Fungal Genera and Species for Turkey, *Österr. Z. Pilzk*, 30, 7–10.
- Acar, İ. & Quijada, L. (2022). A New Species Record from the Order of Pezizales; *Coprotus disculus*, *Mantar Dergisi*, 13(2), 120-123.
- Acar, I. (2022). New records from Turkey: *Cortinarius barbatus*, *C. osmophorus* & *C. saturninus*. *Mycotaxon*, 136(4), 819-830.
- Acar, İ. & Dizkırıcı A. (2023). *Agaricus micromegethus*, A New Record for Turkish Mycobiota, *Anatolian Journal of Botany*, 7(2), 128-130.
- Acar, İ. & Karabıyık, H., *Brunnipila calyculiformis* (Schumach.) Baral: A Novel Record for Türkiye. (2024a). *Cumhuriyet Science Journal*, 45(3), 486-489.
- Acar, İ. & Karabıyık, H. (2024b). *Lasiobelonium lonicerae* (Alb. & Schwein.) Raitv.= A Novel Record for Türkiye, *Turkish Journal of Agricultural and Natural Sciences*, 11(3), 791-796.
- Akata, I., Ediş, G., Kumru, E., Acar, İ. & Sahin E. (2024a). Taxonomic Studies on *Rhodocybe asyae* Specimens Discovered in a New Location, *Kahramanmaraş Sütçü İmam Üniversitesi Tarım ve Doğa Dergisi*, 27, 124-132.
- Akata, İ., Kumru, E., Ediş, G., Acar, İ. & Sahin, E. (2024b). Two Newly Reported *Agaricales* Species from Türkiye with Morphological and Molecular Data, *Kastamonu University Journal of Forestry Faculty*, 24(3), 260-280.
- Akata, I., Ediş, G., Kumru, E., Acar, İ. & Sahin, E. (2024c). Initial report of *Inocybe costinitii* in Türkiye with morphological and molecular data. *Kahramanmaraş Sütçü İmam Üniversitesi Tarım ve Doğa Dergisi*, 27(6), 1304-1312.
- Akata, I., Kumru, E., Sahin, E., Acar, İ. & Kaya, E. (2024d). *Amanita vidua*: A new record for Turkish *Amanita* Section Phalloideae based on

- morphological and molecular data. *Trakya University Journal of Natural Sciences*, 25(1), 97-110.
- Akçay, M. E., Acar, İ. & Uzun, Y. (2023). Three new records of Helotiales for the mycobiota of Türkiye. *Anatolian Journal of Botany*, 7(2), 117-121.
- Allı, H., Şen, İ., Tırpan, E. & Çöl, B. (2024). Two New Records from Türkiye with Morphological and Molecular Evaluations: *Gymnopus aquosus* and *Inocybe subporospora*, *Mantar Dergisi*, 15(2), 70-78.
- Altschul, S. F., Gish, W., Miller, W., Myers, E.W. & Lipman, D. J. (1990). Basic local alignment search tool. *Journal Molecular Biology*, 215(3), 403-410.
- Aslan, A. M., Uzun, Y., Kaya, A. (2024). *Agaricus brunneofibrillosus*, A New Record for Turkish Mycobiota, *Mantar Dergisi*, 15(1), 12-15.
- Antonín, V. & Noordeloos, M. E. (2004). A monograph of the genera *Hemimycena*, *Delicatula*, *Fayodia*, *Gamundia*, *Myxomphalia*, *Resinomycena*, *Rickenella*, and *Xeromphalina* (Tribus' *Mycenae*'sensu Singer, *Mycena* excluded) in Europe. IHW-Verlag.
- Cho, Y., Kim, D. & Lim, Y. W. (2024). Phylogenetic Assessment of Understudied Families in *Hymenochaetales* (Basidiomycota, Fungi) —Reporting Uncovered Species and Reflecting the Recent Taxonomic Updates in the Republic of Korea, *Journal of Microbiology*, 62, 429-447.
- Desjardin, D. E., Wood, M. G. & Stevens, F. A. (2015). *California mushrooms: The comprehensive identification guide*. Timber Press: Portland, OR. 560.
- Dizkırıcı, A. & Acar, İ. (2022). *Hymenoscyphus conscriptus* & *H. fucatus*, Newly Recorded from Turkey, *Mycotaxon*, 137(3), 555-567.
- Doyle, J.J. & Doyle, J.L. (1987). A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, 19, 11-15.
- Ediş G., Kumru E., Acar İ., Karabıyık H. & Akata I. (2025). First Report of *Rhodocybe fumanellii* (Entolomataceae) from Türkiye with Morphological and Molecular Characterisation. *KSU J. Agric Nat*, 28(5), 1197-1205.
- Kalmer, A., Acar, İ. & Tekpınar, A. D. (2018). Phylogeny of some *Melanoleuca* species (Fungi: Basidiomycota) in Turkey and identification of *Melanoleuca angelesiana* AH Sm. as a first record. *Kastamonu University Journal of Forestry Faculty*, 18(3), 314-326.
- Karaduman, Y., Yeşilyurt, F., Uzun, Y. & Kaya, A. (2024). *Eocronartium muscicola*, A New Bryophilic Fungus Record for Turkish Mycota. *Mantar Dergisi*, 15(1), 25-28.
- Kesici, S., Sadullahoğlu, C., Akçay, M. E. & Uzun Y. (2024). *Neocucurbitaria rhamnocola*: Türkiye İçin Yeni Bir Makromantar Kaydı. *Mantar Dergisi*, 15(2), 128-131.
- Kirk, P. M., Cannon, P. F., Minter, D. W. & Stalpers J. A. (2008). *Dictionary of the Fungi* (10th ed.). CAB International.
- Knopf, A. A. (2023). *National Audubon Society Mushrooms of North America*. USA: National Audubon Society, 711.
- Larsson, K. H., Parmasto, E., Fischer, M., Langer, E. & et al. (2006). *Hymenochaetales*: a molecular phylogeny for the hymenochaetoid clade. *Mycologia*, 98, 926-936.
- Maddison, W. & Maddison, D. (2009). MESQUITE: a modular system for evolutionary analysis. *Evolution*, 11(5).
- Moser, M. (1950). Neue Pilzfunde aus Tirol. Ein Beitrag zu Kenntnis der Pilzflora Tirols, *Sydowia*, 4, 84-123.
- Moreno-Arroyo, B. (2004). *Inventario micológico básico de Andalucía (IMBA)*. Consejería de Medio Ambiente, Junta de Andalucía, *Marasmiellus rosellus*, Córdoba. 226.
- Norvell, L. L., Redhead, S. A. & Ammirati J. F. (1994). *Omphalina sensu lato* in North America 1-2. 1: *Omphalina wynniae* and the genus *Chrysomphalina*. 2: *Omphalina sensu* Bigelow, *Mycotaxon*, 50, 379-407.
- Rambaut, A. (2010). *FigTree v1.3.1*. Institute of Evolutionary Biology, University of Edinburgh.
- Redhead, S. A., Walker, G. R., Ammirati, J. F. & Norvell, L. (1995). *Omphalina sensu lato* in North America 4: *O. rosella*, *Mycologia* 87(6), 880-885.
- Redhead, S. A. (2019). Nomenclatural novelties. *Index Fungorum*, 426, 1.
- Redhead, S. A., Moncalvo, J. M., Vilgalys, R. & Lutzoni, F. (2002). Phylogeny of Agarics: Partial Systematics Solutions for *Bryophilus* Omphaloid Agarics Outside the *Agaricales* (Euagarics), *Mycotaxon*, 82, 151-168.
- Rehner, S. A. & Buckley, E. (2005). A *Beauveria* phylogeny inferred from nuclear ITS and EF1- α sequences: evidence for cryptic diversification and links to *Cordyceps* teleomorphs. *Mycologia*, 97, 84-89.
- Ronquist, F. & Huelsenbeck, J.P. (2003). MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19, 1572-1574.
- Sesli, E., Asan, A., Selçuk, F., (Eds.), Abacı, Günyar Ö., Akata, I., Akgül, H., Aktaş, S., Alkan S., Allı H., Aydoğdu H., Berikten D., Demirel, K., Demirel, R., Doğan, H. H., Erdoğan, M., Ergül, C., Eroğlu, G., Giray, G., Halikî, Uztan, A., Kabaktepe, Ş., Kadaifçiler,

- D., Kalyoncu, F., Karaltı, İ., Kaşık, G., Kaya, A., Keleş, A., Kırbağ, S., Kıvanç, M., Ocak, İ., Ökten, S., Özkale, E., Öztürk, C., Sevindik, M., Şen, B., Şen, İ., Türkekul, İ., Ulukapı, M., Uzun, Ya., Uzun, Yu. & Yoltaş A. (2020). *The checklist of fungi of Turkey*. Ali Nihat Gökyiğit Vakfı Yayını, İstanbul, Türkiye.
- Solak, M. H. & Türkoğlu, A. (2022). *Macrofungi of Turkey, checklist, Volume-III*. Kanyılmaz Matbaacılık, Bornova-İzmir, Türkiye.
- Terman, Ş. A., Akçay, M. E. & Dizkırıcı A., (2024). First Record of *Helvella capucina* in Türkiye: Morphological and Molecular Characterization, *Mantar Dergisi*, 15, 66-72.
- Uzun, Y., Kesici, S. & Acar, İ. (2024). A New Genus Record for the *Phleogenaceae* Family from Türkiye. *Mantar Dergisi*, 15, 1-6.
- Vizzini, A., Curti, M., Contu, M. & Ercole E. A. (2012). New cystidiate variety of *Omphalina pyxidata* (Basidiomycota, tricholomatoid clade) from Italy. *Mycotaxon*, 120, 361-371.
- Wang, X. W., Liu, S. L. & Zhou, L. W. (2023). An Updated Taxonomic Framework of *Hymenochaetales* (Agaricomycetes, Basidiomycota). *Mycosphere*, 14(1), 452–496.
- Wang, X. W. & Zhou, L. W. (2023). *Umbellaceae* fam. nov. (*Hymenochaetales*, *Basidiomycota*) for *Umbellus sinensis* gen. et sp. nov. and Three New Combinations, *Journal of Fungi*, 10(1), 22.
- Yeşilyurt, F., Karaduman, Y., Uzun Y. & Kaya, A. (2024). *Simocybe centunculus*, a new record for the mycobiota of Türkiye, *Anatolian Journal of Botany*, 8(1), 46-49.
- Zhou, M., Dai, Y. C., Vlasák, J., Liu, H. G. & Yuan Y. (2023). Revision and updated systematics of *Trichaptum* s.l. (*Hymenochaetales*, *Basidiomycota*). *Mycosphere*, 14, 815–917.
- Zhou, L. W., Wang, X. W., Vlasák, J. & Ren G. J. (2018). Resolution of Phylogenetic Position of *Nigrofomitaceae* within *Hymenochaetales* (*Basidiomycota*) and *Nigrofomes sinomelanoporus* sp. nov. (*Nigrofomitaceae*) from China. *MycoKeys*, 29, 1–13.