

# RARE BASIDIOMYCETE RESUPINATUS ROUXII REPORTED FOR THE FIRST TIME IN TÜRKİYE

## REDKA GLIVA IZ SKUPINE BAZIDIOMICET RESUPINATUS ROUXII PRVIČ ZAZNANA V TURČIJI

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**ABSTRACT**

In this study, *Resupinatus rouxii* Consiglio & Setti was collected from Çanakkale province, Türkiye, and identified using both morphological and molecular data. Macroscopically, the species is characterised by its small size, kidney-shaped pileus, light grey colour, and slightly hairy surface. Microscopic examination confirmed diagnostic features of the genus *Resupinatus*, and detailed evaluations were made of the basidia, basidiospores, and cystidia. The internal transcribed spacer (ITS) region of nuclear ribosomal DNA was sequenced and used in phylogenetic analyses. The resulting ITS sequence showed more than 99% similarity to the reference sequence of *R. rouxii*, supporting the morphological identification. This study represents the second scientific report of *R. rouxii* worldwide and provides the fourth known record of this species, extending its known distribution to Türkiye (Çanakkale province) and contributing valuable data to its biogeography.

**Key words:** *Resupinatus*, fungi, new record, internal transcribed spacer region, molecular phylogeny, Turkey

**IZVLEČEK**

V tej študiji je bil *Resupinatus rouxii* nabran v provinci Çanakkale v Turčiji in identificiran na podlagi morfoloških ter molekularnih podatkov. Makroskopsko so za vrsto značilni majhen, ledvičasto oblikovan klobuk, svetlo siva barva in rahlo dlakava površina. Mikroskopski pregled je potrdil diagnostične značilnosti rodu *Resupinatus*, pri čemer smo podrobno analizirali bazi-dije, bazidiospore in cistidija. Sekvenciranje je bil notranje transkribirani vmesni prostor (ITS) jedrne ribosomske DNA, ki je bil uporabljen za filogenetske analize. Pridobljena ITS-sekvenca je pokazala več kot 99-odstotno podobnost z referenčno sekven-co *R. rouxii*, kar dodatno potrjuje morfološko identifikacijo. Ta študija je drugo znanstveno poročilo o razširjenosti *R. rouxii* na svetovni ravni. To je četrti znani zapis te vrste, pri čemer se Turčija (provinca Çanakkale) dodaja k njenemu znanemu območju razširjenosti in prispeva dragocene podatke k biogeografiji vrste.

**Ključne besede:** *Resupinatus*, glive, nov zapis, del jedrne ribosomalne DNA (ITS), molekularna filogenija, Turčija

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**1 INTRODUCTION****1 UVOD**

*Resupinatus* Nees ex Gray is a genus of macrofungi composed of small, saprotrophic species with a lignicolous lifestyle. The genus comprises approximately 50 to 55 species worldwide and is distinguished by small (<2.5 mm in diameter), dark-coloured, resupinate or cupulate carpophores (Thorn and Barron, 1986; Watling and Gregory, 1989; Kirk et al., 2008; Akçay, 2021). Although individual species are rarely encountered, members of *Resupinatus* contribute to the decomposition of woody debris in forest ecosystems. They are frequently found on the decaying wood of broadleaf trees, including *Quercus*, *Fagus*, and *Populus*, and occasionally on conifers. Their lignicolous habit,

together with morphological traits such as hairy to velvety pileus surfaces and reduced stipes, reflects adaptation to niches conducive to wood decay (Thorn and Barron, 1986; Akçay, 2021).

Microscopically, *Resupinatus* species are distinguished by hyaline, smooth, inamyloid, spherical to ellipsoid-shaped basidiospores, clamped hyphae, and distinctly gelatinised pileal tramae (Singer, 1986; Thorn and Barron, 1986; Bijeesh et al., 2020). The general absence of metuloid cystidia is also an important diagnostic feature. Traditionally, most species have been reported to possess a lamellar hymenophore; however, recent morphological, taxonomic, and phylogenetic studies have revealed that species with meruloid, poroid, and siphelloid hymenophores are also in-

cluded in *Resupinatus* (Redhead and Nagasawa, 1987; Thorn et al., 2005; Gonou-Zagou et al., 2011; McDonald and Thorn, 2019; Akçay, 2021).

Morphologically, *Resupinatus* shares many features with the genus *Hohenbuehelia* Schulzer; both are characterised by gelatinised, hairy trama and inamyloid basidiospores (Thorn et al., 2005; McDonald, 2015). However, *Resupinatus* is distinguished by its diverticulate, pointed pileipellis and assimilating hyphae observed in culture. Furthermore, unlike *Hohenbuehelia*, *Resupinatus* does not produce asexual morphs with mycelium specialised for adhering to and capturing nematodes (Thorn et al., 2005; Consiglio et al., 2018).

For many years, the phylogenetic position of *Resupinatus* remained controversial. Various studies have placed the genus under different families within *Agaricales* or listed it as *incertae sedis*, of uncertain placement (Vizzini et al., 2024). However, multi-locus phylogenetic analyses have revealed that *Resupinatus* is closely related to the family Pleurotaceae, while forming a distinct lineage outside of it (Justo et al., 2011; Matheny et al., 2006; Consiglio et al., 2018). Integrated interpretations of morphological and molecular data indicated that *Resupinatus* has distinct differences from members of Pleurotaceae, and some researchers, such as Jülich (1981) and Kalichman et al. (2020), proposed the establishment of an independent family, Resupinataceae.

A recent comprehensive phylogenetic study (Vizzini et al., 2024) supported these suggestions and re-

established the validity of Resupinataceae. This family is placed in the Pleurotineae clade, alongside Fistulinaceae, Pleurotaceae, and Schizophyllaceae. Thus, *Resupinatus* has consolidated its position in the scientific literature as an important genus in Agaricales, thanks to its unique morphological structure and phylogenetic position supported by molecular data.

This study focuses on the morphological and molecular characterisation of *Resupinatus rouxii* Consiglio & Setti, collected in natural habitat in Çanakkale province. Although the species appears to occur naturally in the region, it represents a new record for Türkiye, as confirmed by Sesli et al. (2020) and subsequent studies on the country's mycobiota (Acar et al., 2021; Akçay, 2021; Sesli, 2022; Acar and Dizkırıcı, 2023; Sesli, 2023; Acar and Karabıyık, 2024a, 2024b; Akata et al., 2024a, 2024b, 2024c; Aslan et al., 2024; Karaduman et al., 2024; Kesici et al., 2024; Uzun et al., 2024; Acar and Karabıyık, 2025; Akata et al., 2025). This study aims to clarify the taxonomic position of this species and to provide scientific data that broaden understanding of Türkiye's macrofungal diversity.

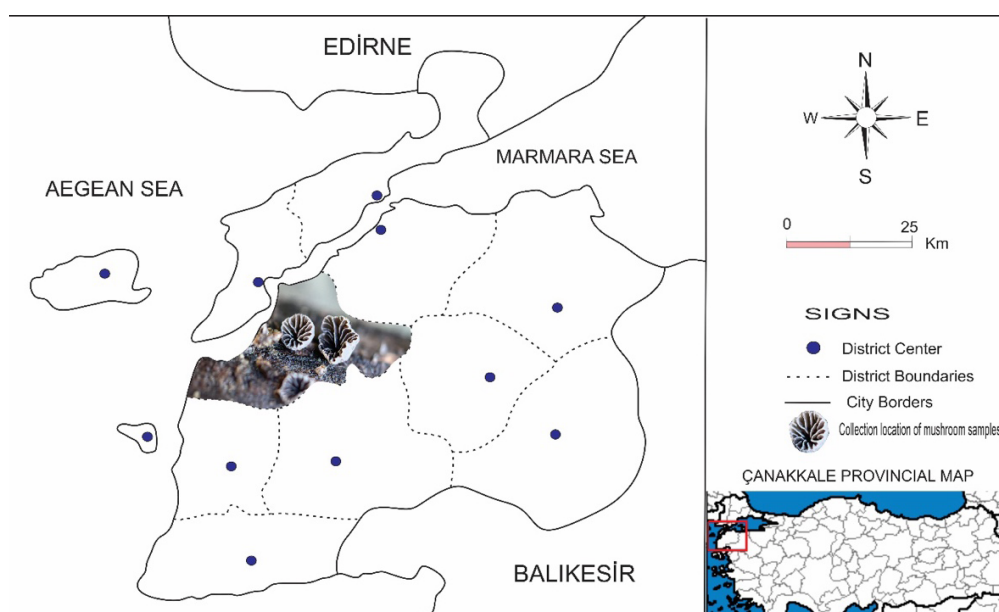
## 2 METHODS

### 2 METODE

#### 2.1 Sample Collection

##### 2.1 Zbiranje vzorcev

The macrofungus specimen examined in this study was collected from a single locality in the natural habitat of Çanakkale Province on 6 January 2025 (Fig. 1). A



**Fig. 1:** Map of the research area (Çanakkale Province). The fungal symbol indicates the collection locality of the *Resupinatus rouxii* specimen. The scale bar applies only to the main map (left). The inset map (lower right) is for general reference and not drawn to scale. (Map drawing: İ. Acar)

**Slika 1:** Zemljevid raziskovalnega območja (provinca Çanakkale). Simbol glive označuje lokacijo zbiranja vzorca glive *Resupinatus rouxii*. Merilna lestvica velja le za glavni zemljevid (levo). Vstavljeni zemljevid (spodaj desno) je namenjen splošni orientaciji in ni narisano v merilu. (Risba zemljevida: İ. Acar)

comprehensive taxonomic approach integrating morphological examinations and molecular analyses was adopted to identify the specimens. The macroscopic characteristics of the specimens were observed and recorded in the field, while microscopic features were analysed and molecular analyses were conducted in the laboratory.

## 2.2 Morphological Studies

### 2.2 Morfološke študije

The macroscopic features of the *Resupinatus rouxii* specimen were documented in its natural habitat using a Canon EOS 60D digital camera, and morphological characters were recorded in detail through direct field observation. Ecological data, including collection location, date, habitat characteristics, and substrate type, were systematically documented in the field record book. Following collection, the specimen was transported to the laboratory, where it was dried at approximately 25 °C in a ventilated room for 48 hours and subsequently preserved in labelled polyethylene bags. Each specimen was assigned a unique collection number and deposited in the fungarium for further morphological and molecular analyses. Micro-morphological examinations were carried out using a Leica DM500 light microscope. Basidia, basidiospores, cystidia, and pileipellis structures were analysed in detail, with at least 30 measurements taken from each microscopic character. The data were analysed using Leica Application Suite (v3.4.0) software. Illustrations of microscopic structures were prepared according to scientific standards using CorelDRAW (64-bit, Corel Corporation, Canada). Species identification was based on the diagnostic criteria described by Consiglio and Setti (2018). The specimen identified as *R. rouxii* was converted into fungarium material and archived in the Fungarium Collection of the Department of Biology, Faculty of Science, Van Yüzüncü Yıl University, under the collection number 'Acar 1899'.

## 2.3 Molecular Characterization

### 2.3 Molekularna karatkerizacija

Molecular analyses focused on amplification of the internal transcribed spacer (ITS) region from genomic DNA. The resulting sequences were subjected to BLAST analysis against international reference databases, and phylogenetic analyses were performed using various software packages to reveal the phylogenetic relationships between the species. Morphological and molecular findings were assessed together to ensure reliable species-level identification.

### 2.3.1 Determination of ITS rDNA Sequences

#### 2.3.1 Določanje ITS rDNA zaporedij

Genomic DNA was extracted from *Resupinatus* samples using the CTAB method according to the protocol described by Dizkırıcı et al. (2019a, 2019b) and Acar et al. (2022). After isolation, DNA purity and concentration were measured using a NanoDrop 2000c UV-Vis spectrophotometer (Thermo Scientific, Waltham, MA, USA). Extracted DNA was stored at -20 °C before polymerase chain reaction (PCR) to maintain its stability. The ITS (internal transcribed spacer) rDNA region, was amplified using the universal primers ITS1 and ITS4 as described by White et al. (1990). The PCR reaction was performed in a total volume of 25 µl, and the reaction mixture contained 10 µM of each primer (ITS1 and ITS4), 5 u/µl FIREPol® Taq DNA polymerase (Solis Biodyne, Tartu, Estonia), 10X PCR buffer, 25 mM MgCl<sub>2</sub>, 10 mM dNTP mix, 10 ng/µl genomic DNA, and sterile distilled water. PCR amplification was carried out under the following cycling conditions: initial denaturation at 95 °C for 3 minutes; 35 cycles of denaturation at 95 °C for 30 seconds, annealing at 55 °C for 30 seconds, and extension at 72 °C for 1 minute; and final extension at 72 °C for 5 minutes.

Amplification products were checked by electrophoresis on a 1.5% agarose gel at 100 V for 90 minutes, yielding single band products of approximately 700 bp. PCR products were purified using the High-Prep™ PCR Cleanup Kit (Cat. No: AC60005; MagBio Genomics, Gaithersburg, MD, USA), following the manufacturer's instructions. Purified products were then bidirectionally sequenced using an ABI 3730XL DNA analyser (Applied Biosystems, Foster City, CA) and BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, Foster City, CA) at MacroGen Laboratory in the Netherlands (Chen et al., 2014; Acar, 2022). All genomic DNA isolation and ITS region amplification procedures were carried out following the methodologies laid out by Rogers and Bendich (1994) and White et al. (1990), as well as the updated protocols by Kalmer et al. (2018) and Akata et al. (2024b, 2024c) to ensure the reliability and reproducibility of the study.

### 2.3.2 Molecular Phylogeny Study

#### 2.3.2 Študija molekularne filogenije

The Sanger sequence obtained with the ITS1/ITS4 primer pair was assembled using DNAMAN v10 (Lynnon Corporation) software. The resulting consensus sequence was subjected to species identification using the BLASTn algorithm. Ingroup and outgroup sequences were retrieved from the GenBank database (Appendix 1) and aligned with the newly generated se-

quence for phylogenetic analysis. The aligned dataset was then imported into MrBayes v3.2.7a for Bayesian inference of phylogeny. Phylogenetic reconstruction was conducted using the HKY+G (Hasegawa-Kishino-Yano + Gamma) nucleotide substitution model, which accounts for unequal base frequencies and variation in substitution rates among sites. This model was specified based on prior knowledge and implemented directly within the MrBayes v3.2.7a framework (Hasegawa et al., 1985). The analyses consisted of two independent MCMC (Markov Chain Monte Carlo) runs of four chains each, conducted over 3 million generations with sampling every 1000 generations. The first 25% of sampled trees were discarded as burn-in. The resulting trees were summarised by probability distributions and visualised with FigTree v1.4.4 software.

### 3 RESULTS

### 3 REZULTATI

The collected macrofungus specimen was identified as *Resupinatus rouxii* at the morphological and

phylogenetic levels. A brief morphological description, high-resolution photographs of macroscopic structures, drawings of microscopic characters, sampling date, and geographical coordinates are presented below.

#### *Taxonomy*

**Basidiomycota** Whittaker ex R.T. Moore

**Agaricomycetes** Doweld

**Agaricales** Underw.

**Resupinataceae** (Singer) Jülich

***Resupinatus*** Nees ex Gray

***Resupinatus rouxii*** Consiglio & Setti (Figs. 2–3)

**Pileus** 7–20 mm, black to dark brown, completely covered with greyish hairs, fan-shaped; margins often grooved, wavy, and indented. **Lamellae** sparse, greyish black to black, with distinctly white margins. **Pseudostipe** present, lacking a true stalk; pileus base extends into substrate, forming a false stalk. **Flesh** gelatinous, soft, and dark brown to black. **Basidiospores**



**Fig. 2:** *Resupinatus rouxii* a–d. Basidiomata in natural habitat (photo: İ. Acar)  
Scale bar: 10 mm for 'a'

**Slika 2:** *Resupinatus rouxii* a–d Bazidiomata v naravnem okolju (fotografija: İ. Acar)  
Merilna lestvica: 10 mm za sliko 'a'

4–5 × 3.5–4.5 µm, subglobose to broadly ellipsoid, with opaque granular contents or containing multiple oil droplets, inamyloid, smooth. **Basidia** 20–27 × 6.5–8.5 µm, clavate, 4-spored, sterigmata up to 5 µm long. **Cheilocystidia** 10–24 × 4–7.5 µm, cylindrical, basidioloid, coralloid, branched, often with one or two digitate processes. **Pleurocystidia** not observed. **Pileipellis** composed of two-layered, intertwined, branched hyphae forming a suprapellis cutis. In these hyphae, brown pigments are incrustated intracellularly and on the surface. Terminal cells filamentous, slightly gelatinous, 3.5–8 µm wide, present on surface. Subcutis about 500 µm thick, consisting of hyphae 1.5–6 µm wide, embedded in a gelatinous matrix. Clamp connections abundant throughout carpophore tissues.

**Specimens examined:** Türkiye, Çanakkale province, between Güzelyalı and Kumkale Observation Terrace, near Firdevs Bozkurt Fountain, 40°00'15"N, 27°17'36"E, 40 m a.s.l., on a dead branch of *Pinus brutia*, 6 January 2024, leg. İ. Acar, specimen no. Acar 1899; deposited in the Fungarium of the Department of Biology, Faculty of Science, Van Yüzüncü Yıl University (VANF).

#### Phylogenetic results

In this study, the ITS region was amplified and analysed for the molecular identification of *Resupinatus* specimens collected from Çanakkale (Türkiye). The sequences amplified using the ITS1 and ITS4 primers were aligned, the end regions were trimmed,

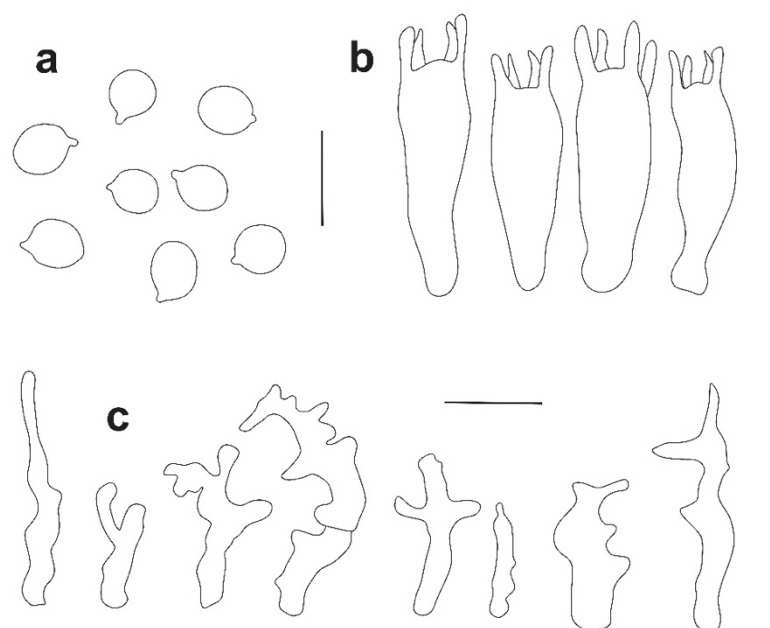
and the resulting consensus sequence was 566 bp in length (sample code: Acar 1899). This sequence was deposited in NCBI GenBank under accession number PV716457. A total of 60 additional ITS sequences belonging to *Resupinatus*, along with one outgroup sequence (*Hohenbuehelia atrocoerulea* (Fr.) Singer), were retrieved from GenBank for phylogenetic analyses (Appendix 1). The sequence lengths varied between 339 bp (MT594788) and 1593 bp (MW727690).

The ITS sequence of the Acar 1899 sample was compared with the NCBI GenBank database using the BLASTn algorithm, and the highest similarity (99%) was observed with *Resupinatus rouxii* (isolate OP282920). Two sequences differed by only a single nucleotide (gap), and the alignment was supported by a bit score of 1024. Bayesian phylogenetic analysis using the HKY+G nucleotide substitution model placed the Acar 1899 sample within the *R. rouxii* clade, with a high posterior probability of 1.00. Taken together, BLAST results and phylogenetic inference provide strong support for identifying the examined specimen as *Resupinatus rouxii* (Ronquist et al., 2012).

## 4 DISCUSSION AND CONCLUSIONS

### 4 RAZPRAVA IN ZAKLJUČKI

The holistic evaluation of morphological, ecological, and molecular data suggests that the analysed specimen overlaps with *Resupinatus rouxii* at the species level. In particular, ITS sequence data showed 99% similarity with the *R. rouxii* holotype, differing

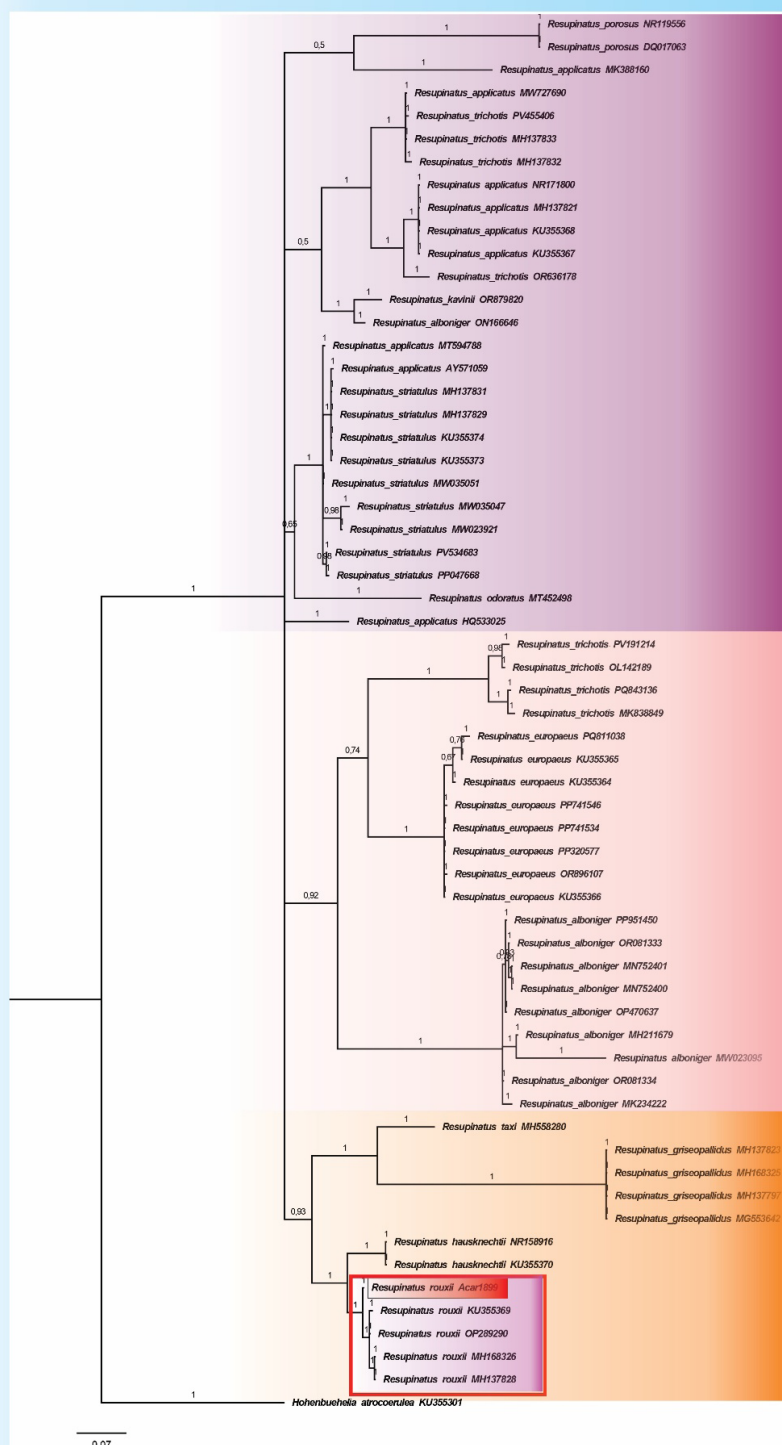


**Fig. 3:** *Resupinatus rouxii* a. Basidiospores, b. Basidia, c. Cheilocystid  
Scale bar: 10 µm (photo: İ. Acar)u

**Slika 3:** *Resupinatus rouxii* a. Bazidiospore, b. Bazidije, c. Heilicistidije  
Merilna lestvica: 10 µm (fotografija: İ. Acar)

by only a single nucleotide gap, one of the key findings supporting the accuracy of the identification. The ITS region is a widely used molecular marker with high discriminatory power for distinguishing species within the order Agaricales (Schoch et al., 2012). Phylogenetic analysis conducted under the HKY+G sub-

stitution model (Figure 4) placed the specimen firmly within the *R. rouxii* clade, with strong posterior probability support (PP=1.00). By accounting for variable substitution rates and evolutionary heterogeneity, this model increased the reliability of phylogenetic inference (Höhna et al., 2017).



**Fig. 4:** Bayesian 50% majority-rule consensus tree for *Resupinatus* based on ITS sequence data. The taxon recorded in this study (*Resupinatus rouxii* Acar1899) is highlighted in red. Bayesian posterior probabilities (PP) are shown above the branches. *Hohenbuehelia atrocoerulea* was used as the outgroup.

**Slika 4:** Bayesovo 50-odstotno konsenzno drevo po pravilu večine za rod *Resupinatus* na podlagi podatkov ITS-sekvenc. Takson, zabeležen v tej študiji (*Resupinatus rouxii* Acar1899), je označen z rdečim okvirjem. Bayesove posteriorne verjetnosti (PP) so prikazane nad vejami. *Hohenbuehelia atrocoerulea* je bila uporabljena kot zunanja skupina (outgroup).

**Table 1:** Comparison of the *Resupinatus rouxii* specimen from this study with the description by Consiglio & Setti (2018)

| Resupinatus rouxii | Consiglio & Setti (2018)                                                                                                           | Current study                                                                                                                      |
|--------------------|------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|
| Pileus             | 1.5–2.5 cm, blackish brown                                                                                                         | 7–20 mm, black to dark brown                                                                                                       |
| Lamellae           | Black with white edge                                                                                                              | Sparse, greyish black to black with distinctly white margins                                                                       |
| Pseudostipe        | Formed by a pseudostipe (extension of pileus towards the attachment point)                                                         | No true stalk; pileus base extends into substrate, forming a false stalk.                                                          |
| Basidiospores      | 4.4–5.2 × 3.7–4.6 µm, globose to broadly ellipsoid; opaque granular content or one or more oily drops; inamyloid, smooth           | 4–5 × 3.5–4.5 µm, subglobose to broadly ellipsoid; opaque granular contents or containing multiple oil droplets; inamyloid, smooth |
| Basidia            | 21–25 × 6–7.8 µm, clavate, tetrasporic, sterigmata up to 6 µm long                                                                 | 20–27 × 6.5–8.5 µm, clavate, 4-spored, sterigmata up to 5 µm long                                                                  |
| Cheilocystidia     | 9.6–18 × 3.9–7.2 µm, cylindraceous, basidioloid, coralloid, branched; typically with one or more digitate swellings in apical zone | 10–24 × 4–7.5 µm, cylindrical, basidioloid, coralloid, branched; often with one or two digitate processes                          |

At the macroscopic level, the pileus diameter (7–20 mm), dark brown to nearly black colour, black lamellae with distinct white margins, and pseudostipe formation are largely consistent with specimens of *R. rouxii* described by Consiglio & Setti (2018). Microscopically, minor variations in spore size ( $\pm 0.2$  µm) and the number of apical processes in cheilocystidia fall within the expected range of intraspecific variability. As shown in Table 1, the specimen examined in this study closely matches the original morphological description of *R. rouxii*.

The first report of *R. rouxii* from Türkiye represents a significant contribution to understanding the species' biogeographic distribution. The original description by Consiglio & Setti (2018) was based on a holotype from Switzerland and additional specimens from France and the USA. Consequently, the present study constitutes the second scientific report on this species and provides the fourth known geographical record worldwide. Previous reports that indicate that *R. rouxii* typically occurs on dead wood and moss-covered substrates of deciduous trees (e.g., *Fagus*). Its occurrence in this study on a coniferous host (*Pinus brutia* L.) indicates the habitat plasticity of the species and suggests a broader host spectrum than previously recognised.

When compared with the closely related species *Resupinatus applicatus* (Batsch) Gray, *R. rouxii* can be distinguished by several diagnostic characters. *R. applicatus* has a smaller pileus, denser lamellae, and underdeveloped or almost absent cheilocystidia (McDonald, 2015). In contrast, *R. rouxii* has distinctive features at macroscopic and microscopic levels, such as white lamellae margins and cheilocystidia with coralloid structures and digitate projections (see Table 1). These features reinforce its morphological distinctiveness

**Preglednica 1:** Primerjava primerka vrste *Resupinatus rouxii* iz te študije z opisom Consiglio & Setti (2018)

and reduce the likelihood of misidentification.

In conclusion, this study documents the presence of *Resupinatus rouxii* in Türkiye for the first time, expanding knowledge of the country's mycobiota. It also confirms the effectiveness of the ITS region as a reliable molecular marker for species identification within *Resupinatus*. Furthermore, the findings provide new insights into the morphological variability and habitat preferences of *R. rouxii*. Collectively, these results will serve as a valuable basis for future studies on the molecular taxonomy, biogeography, and ecological interactions of this little-known genus.

## 5 SUMMARY

### 5 POVZETEK

V raziskavi je bila vrsta *Resupinatus rouxii* Consiglio & Setti prvič zabeležena v Turčiji, v provinci Çanakkale, kar je pomembna dopolnitev poznavanja razširjenosti te redke bazidikomikotne glive. Vrsta, ki je bila do sedaj znana le iz Švice, Francije in ZDA, je bila identificirana z integracijo morfoloških in molekularnih podatkov, kar zagotavlja visoko stopnjo zanesljivosti.

Makroskopsko je *R. rouxii* prepoznaven po majhnem, ledvičasto oblikovanem klobuku (7–20 mm), temno rjavi do črni barvi, sivkasto poraščeni površini in manjkajočega pravega betiča, saj se klobuk podaljšuje v substrat in tvori psevdostipe. Lamellae so redke, črnkaste z izrazito belimi robovi, meso pa je želatinasto in temno obarvano. Mikroskopske analize so pokazale subglobozne do široko elipsoidne, gladke, neamiloidne bazidiospore (4–5 × 3,5–4,5 µm), klavate bazidije s štirimi sporami ter značilne cheilocistidije z razvejenimi koraloidnimi strukturami in izrastki. Vse tkivne strukture vsebujejo kleščaste povezave, kar je diagnostična značilnost rodu.

Za molekularno potrditev identifikacije je bila sekvencirana regija ITS jedrne ribosomske DNA. Pridobljeno zaporedje (566 bp) je pokazalo več kot 99-odstotno podobnost z referenčnim zaporedjem holotipa *R. rouxii* (GenBank OP282920). Bayesova filogenetska analiza (HKY+G model) je potrdila uvrstitev vzorca v isto skupino kot holotip, z visoko posteriorno verjetnostjo (PP = 1,00). Pridobljeno zaporedje je bilo deponirano v bazo GenBank pod številko PV716457.

Odkritje v Turčiji je četrti znani zapis te vrste na svetovni ravni in prvi na območju Male Azije. Poleg tega je bil primerek najden na odmrlem lesu iglavca (*Pinus brutia*), medtem ko so bili prejšnji zapisi povezani predvsem z listavci, kar nakazuje širšo ekološko razširjenost vrste. Ta ugotovitev odpira nova vprašanja o ekoloških preferencah in potencialni razširjenosti *R. rouxii*.

Rezultati potrjujejo, da je regija ITS zanesljiv molekularni marker za identifikacijo vrst znotraj rodu *Resupinatus* in poudarjajo pomen kombinacije morfoloških in molekularnih podatkov pri taksonomskih raziskavah. Prispevek dopolnjuje znanje o biogeografiji in raznolikosti bazidiomicetnih gliv ter je osnova za nadaljnje raziskave filogenetskih odnosov in ekoloških interakcij znotraj družine *Resupinataceae*.

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## Appendix 1

*Resupinatus rouxii* (KU355369), *R. rouxii* (OP289290), *R. rouxii* (MH168326), *R. rouxii* (MH137828), *R. hausknechtii* (NR158916), *R. hausknechtii* (KU355370), *R. porosus* (NR119556), *R. porosus* (DQ017063), *R. taxi* (MH558280), *R. griseopallidus* (MH137823), *R. griseopallidus* (MH168325), *R. griseopallidus* (MH137797), *R. griseopallidus* (MG553642), *R. applicatus* (MW727690), *R. applicatus* (NR171800), *R. applicatus* (MH137821), *R. applicatus* (MT594788), *R. applicatus* (HQ533025), *R. applicatus* (MK388160), *R. applicatus* (KU355368), *R. applicatus* (KU355367), *R. applicatus* (AY571059), *R. odoratus* (MT452498), *R. striatulus* (MW035051), *R. striatulus* (MW035047), *R. striatulus* (MW023921), *R. striatulus* (PV534683), *R. striatulus* (PP047668), *R. striatulus* (MH137831), *R. striatulus* (MH137829), *R. striatulus* (KU355374), *R. striatulus* (KU355373), *R. trichotis* (PV455406), *R. trichotis* (PV191214), *R. trichotis* (PQ843136), *R. trichotis* (OR636178), *R. trichotis* (OL142189), *R. trichotis* (MH137833), *R. trichotis* (MH137832), *R. trichotis* (MK838849), *R. kavinii* (OR879820), *R. alboniger* (PP951450), *R. alboniger* (MH211679), *R. alboniger* (OR081334), *R. alboniger* (OR081333), *R. alboniger* (OP470637), *R. alboniger* (ON166646), *R. alboniger* (MW023095), *R. alboniger* (MK234222), *R. alboniger* (MN752401), *R. alboniger* (MN752400), *R. europaeus* (PQ811038), *R. europaeus* (PP741546), *R. europaeus* (PP741534), *R. europaeus* (PP320577), *R. europaeus* (OR896107), *R. europaeus* (KU355366), *R. europaeus* (KU355365), *R. europaeus* (KU355364), *Hohenbuehelia atrocoerulea* (KU355301)