Mycologia Iranica 2025, Vol. 12 (No. 2): 59–68 JIrMS

Original Article

Juglanconis appendiculata and *Melanconiella chrysomelanconium*, two new records of diaporthalean fungi from Iran

Mehdi Mehrabi[1] Bita Asgari[2] ✉

[1]*Assistant Prof., Department of Horticultural Science and Landscape Design, Shirvan Faculty of Agriculture, University of Bojnord, Bojnord, Iran*
[2]*Research Assistant Prof., Department of Botany, Iranian Research Institute of Plant Protection, Agricultural Research, Education and Extension Organization (AREEO), Tehran, Iran*

https://doi.org/10.22092/MI.2025.370862.1329

ABSTRACT

Members of *Diaporthales* occur on a broad range of hosts and substrates, such as trees, crops, soil, and even living tissues of animals and humans, and comprise pathogenic, saprobic and endophytic species. This study was carried out to contribute to the knowledge of *Diaporthales* biodiversity in Iran. *Juglanconis appendiculata* from dead branch of *Juglans regia* in East Azerbaijan Province and *Melanconiella chrysomelanconium* from dead branch of *Carpinus betulus* in Golestan Province were identified using morphological characteristics and molecular data. Phylogenetic analysis of the elongation factor 1-alpha (*tef1-α*) gene using maximum likelihood approach strongly supported the placement of two Iranian isolates, i.e., IRAN 2457C (identified as *J. appendiculata*) and IRAN 5294C (identified as *M. chrysomelanconium*), within the *Diaporthales*. Both species are described and illustrated herein based on Iranian material and compared with closely related species. This study represents the first report of *J. appendiculata* and *M. chrysomelanconium* from Iran, providing geographic range extensions of both species.

KEYWORDS

Juglanconidaceae, *Melanconiellaceae*, Mycobiota, New records, Phylogeny, Taxonomy.

INTRODUCTION

The *Diaporthales* (*Ascomycota*, *Sordariomycetes*) was introduced by Nannfeldt (1932) and presently comprises 32 families (Hyde et al. 2024). Diaporthalean fungi share brown to black perithecia immersed in a stroma or the substrate, unitunicate asci often with a conspicuous ring in the apex and ellipsoidal to elongate, non-septate to multi-septate or muriform, hyaline or pale yellow to dark brown ascospores (Barr 1978, Samuels and Blackwell 2001). Members of this order are pathogens, parasites, and endophytes of plants, human-animal pathogens, saprobes and soil inhabitants (Rossman et al. 2007).

The family *Juglanconidaceae* was introduced by Voglmayr et al. (2017) as a monotypic family classified in the *Diaporthales*, and is typified by *Juglanconis* Voglmayr & Jaklitsch. The genus *Juglanconis* is characterized by perithecia immersed in a pseudostromata, oblong or fusoid, octosporous asci with a more or less distinct apical ring, hyaline, ellipsoid, bicellular ascospores with or without blunt or pointed appendages and a melanconium-like asexual morph characterized by acervular conidiomata bearing annellidic conidiogenous cells and brown, subglobose, ellipsoid, elongate pyriform, pip-shaped to fusoid conidia with distinct gelatinous sheath when fresh. This genus currently comprises seven species (Index Fungorum; http://www.index fungorum.org/Names/Names.asp; accessed on 12 October 2025), the type *J. juglandina* (Kunze) Voglmayr & Jaklitsch, along with *J. appendiculata* Voglmayr & Jaklitsch, *J. magnata* F.H.

Received: 28 Sep. 2025 Revised: 19 Oct. 2025 Accepted: 21 Oct. 2025 Published online: 25 Oct. 2025

✉ Corresponding Author: Bita Asgari; Email: bita_asgari@yahoo.com

Published by Iranian Mycological Society (IrMS)—https://mij.areeo.ac.ir

Wang & C.L., *J. mucosporia* F.H. Wang & C.L. Yang and *J. oblonga* (Berk.) Voglmayr & Jaklitsch, all occurring on *Juglans* spp. in Europe, Asia and North America (Voglmayr et al. 2017, Wang et al. 2025), and *J. japonica* Voglmayr & Jaklitsch and *J. pterocaryae* (Kuschke) Voglmayr & Jaklitsch from *Pterocarya* spp. in Europe and Western Asia (Voglmayr et al. 2017, Voglmayr et al. 2019).

Melanconiellaceae, another family of the *Diaporthales*, was introduced by Senanayake et al. (2017) with *Melanconiella* Sacc. as the type genus. Members of this family function both as saprobes and plant pathogens, causing diseases in economically important plant species. Hyde et al. (2024) listed 10 genera under this family. The genus *Melanconiella* was first introduced by Saccardo (1882) to classify species resembling *Melanconis* Tul. & C. Tul., however characterized by dark-colored ascospores. Voglmayr et al. (2012) conducted a review of the genus *Melanconiella* using herbarium specimens as well as recently collected samples. The study examined the morphological and phylogenetic differences between *Melanconiella* and *Melanconis*. *Melanconiella*, with *M. spodiaea* Tul. ex Sacc. as the type species, is characterized by circularly arranged perithecia immersed in a pseudostromata within the substrate, with oblique or lateral ostioles convergent and erumpent through an ectostromatic disc, oblong or fusoid, octosporous asci with a distinct apical ring and hyaline, yellowish or brown, fusoid or ellipsoid, bicellular ascospores with or without short appendages. The melanconium- or discosporina-like asexual morph of *Melanconiella* is characterized by acervuli with light-coloured central column, with annellidic (in melanconium-like) or phialidic (in discosporina-like) conidiation and brown or hyaline, ellipsoid, subglobose, ovoid or oblong conidia with or without distinct hyaline sheath (Voglmayr et al. 2012).

Phylogenetic analyses of the large subunit nuclear ribosomal DNA (LSU rDNA) support the monophyly of the genus *Melanconiella*, confirming its status as a separate genus from *Melanconis* (Voglmayr et al. 2012). Using macro- and microscopic morphology, pure cultures and phylogenetic analyses of the small subunit nuclear ribosomal DNA (SSU rDNA), the internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2 (ITS rDNA) and the large subunit nuclear ribosomal DNA (LSU rDNA), the elongation factor 1-alpha (*tef1-α*) and the RNA polymerase II subunit 2 (*rpb2*) sequences, Voglmayr et al. (2012) accepted 13 species in the genus. Crous et al. (2016) described a new species, *M. syzygii* Crous & M.J. Wingf., isolated from diseased leaves of *Syzygium* species. Du et al. (2017) identified another new species *M. cornuta* C.M. Tian & Z. Du from *Cornus controversa* in Shaanxi Province, China. However, based on phylogenetic analysis of combined sequence data from ITS, LSU, the calmodulin (*cal*), *rpb2*, and *tef1-α*, Fan et al. (2018) proposed *Sheathospora* X.L. Fan to accommodate *Melanconiella cornuta* and described *M. betulicola* X.L. Fan and *M. corylina* X.L. Fan as two new species. Additionally, two more species, *M. camelliae* T.C. Mu & J. Zhi Qiu and *M. loropetali* T.C. Mu & J. Zhi Qiu were added to the genus *Melanconiella* by Mu et al. (2023). However, *M. camelliae* and *M. loropetali* were recently transferred to *Sinodiscula* M.J. Guo & C.L. Hou and *Septomelanconiella* M.C. Samar. & K.D. Hyde, respectively (Zhang et al. 2025).

In the present study, two specimens of *Diaporthales*, *Juglanconis appendiculata* and *Melanconiella chrysomelanconium* Voglmayr & Jaklitsch, were collected from dead branches of *Juglans regia* L. and *Carpinus betulus* L. in East Azerbaijan Province and Golestan Province, respectively. Both species were identified based on morphological characteristics and sequence data of *tef1-α* gene. This study extends the geographic range of both species.

MATERIALS AND METHODS

Sample collection and isolation

Two dead branch specimens bearing fungal fruiting bodies were collected from *Juglans regia* (East Azerbaijan Province) and *Carpinus betulus* (Golestan Province), Iran. Isolates were obtained by collecting ascospores from ascomata immersed in the substrate, transferring the spore suspension to potato dextrose agar (PDA, Merck, Germany), and incubating at dark at room temperature (25 °C) for 24 h. Single germinated ascospores were transferred onto new PDA Petri plates to obtain pure cultures (Senanayake et al. 2020). Herbarium specimens are preserved at the Fungus Reference Collection (IRAN…F) of the Herbarium Ministerii Iranici Agriculturae "IRAN" Iranian Research Institute of Plant Protection (Tehran, Iran), while living cultures are preserved at the Iranian Fungal Culture Collection (IRAN…C) of the "IRAN" Herbarium.

Morphological Characterization

Macroscopic observations were carried out using a Nikon (SMZ-1B) stereo microscope. Colony growth rate and characteristics were determined on PDA incubated at 25 °C. Color names and codes used for descriptions were based on Rayner (1970). Microscopic slides were prepared using distilled water. Free-hand sections of ascomata were prepared and examined using Olympus CX21 light microscope. Photographs were taken using AmScope digital camera (MD500). Dimensions of fungal structures were measured by ImageJ 1.54g software. Photo plates were prepared using Adobe Photoshop CS6 software (Adobe Systems Inc., San Jose, CA, USA).

DNA Extraction, PCR Amplification and Sequencing

The genomic DNA was extracted from fresh mycelia using the method described by Liu et al. (2000). The *tef1-α* gene was amplified using primers EF1728F

(Chaverri and Samuels 2003) and TEF1LLErev (Jaklitsch et al. 2006). A total of 25 µL volume was used for polymerase chain reaction (PCR), including 1 µL of each primer (10 pmol/µL, SinaClon Inc.), 1.0 µL of genomic DNA (30 ng/µL), 2.5 µL of 10× high yield PCR buffer (SinaClon, Iran), 0.3 µL of Taq polymerase (5 units/ µL, SinaClon, Iran), 1 µL of MgCl2 (25 mM), 0.5 µL of dNTPs (10 mM), and 17.7 µL of sterile distilled water. The PCR thermal cycle program and sequencing were followed as mentioned in Mehrabi (2025).

Phylogenetic Analyses

The chromatograms of the obtained sequences were analyzed using FinchTV v. 1.4.0 (Geospiza Inc.). Validated sequences, with an emphasis on type strains and based on the most recent references, were downloaded from GenBank for phylogenetic analysis (Table 1). The alignments were obtained using MAFFT v. 7 at the web server (https://mafft.cbrc.jp/alignment/server/) (Kuraku et al. 2013, Katoh et al. 2019), using default settings. Maximum likelihood (ML) analysis was performed with RAxML (Stamatakis 2006) as implemented in raxmlGUI-2.0.0-

Table 1. Isolates used in the phylogenetic analysis

Taxon	Strain	Origin	GenBank accession numbers (*tef1-α*)	Reference
Gaeumannomyces graminis var. *graminis*	M57	*Stenotaphrum secundatum*, USA	JF710421	Zhang et al. (2011)
Juglanconis appendiculata	D96 (T)	*Juglans nigra*, Austria	KY427208	Voglmayr et al. (2017)
	IRAN 2457C	*Juglans nigra*, Iran	**PX516431**	This study
Juglanconis japonica	ME20	*Pterocarya rhoifolia*, Japan	KY427224	Voglmayr et al. (2017)
Juglanconis juglandina	ME23 (NT)	*Juglans nigra*, Austria	KY427219	Voglmayr et al. (2017)
Juglanconis oblonga	ME14	*Juglans cinerea*, USA	KY427220	Voglmayr et al. (2017)
Juglanconis pterocaryae	D272 (T)	*Pterocarya fraxinifolia*, Austria	MK238332	Voglmayr et al. (2019)
Melanconiella betulicola	CFCC 52482 (T)	*Betula albosinensis*, China	MK096272	Fan et al. (2018)
Melanconiella carpinicola	CBS 131706 (ET)	*Carpinus betulus*, Austria	JQ926373	Voglmayr et al. (2012)
Melanconiella chrysodiscosporina	CBS 125597 (T)	*Carpinus betulus*, Austria	JQ926376	Voglmayr et al. (2012)
Melanconiella chrysomelanconium	CBS 124271 (T)	*Carpinus betulus*, Austria	JQ926385	Voglmayr et al. (2012)
	IRAN 5294C	*Carpinus betulus*, Iran	**PX516432**	This study
Melanconiella chrysorientalis	CBS 131702 (T)	*Carpinus orientalis*, Croatia	JQ926394	Voglmayr et al. (2012)
Melanconiella corylina	CFCC 52484 (T)	*Corylus mandshurica*, China	MK096274	Fan et al. (2018)
Melanconiella decorahensis	CBS 159.26	*Betula* sp., USA	JQ926398	Voglmayr et al. (2012)
Melanconiella elegans	BPI 843574 (T)	*Carpinus caroliniana*, USA	JQ926403	Voglmayr et al. (2012)
Melanconiella ellisii	BPI 878343	*Carpinus caroliniana*, USA	JQ926406	Voglmayr et al. (2012)
Melanconiella flavovirens	MFV	*Corylus avellana*, Austria	JQ926408	Voglmayr et al. (2012)
Melanconiella hyperopta	CBS 132231 (T)	*Carpinus betulus*, Switzerland	JQ926418	Voglmayr et al. (2012)
Melanconiella hyperopta var. *orientalis*	CBS 131705 (T)	*Carpinus orientalis*, Croatia	JQ926421	Voglmayr et al. (2012)
Melanconiella meridionalis	CBS 131704 (T)	*Ostrya carpinifolia*, Austria	JQ926424	Voglmayr et al. (2012)
Melanconiella ostryae	CBS 208.38	*Ostrya virginiana*, USA	JQ926430	Voglmayr et al. (2012)
Melanconiella spodiaea	SPOD	*Carpinus betulus*, USA	JQ926433	Voglmayr et al. (2012)

Sequences with bold numbers are generated in this study; others are from GenBank. (T), ex-type strain; (ET), ex-epitype strain; (NT), ex-neotype strain. BPI, U.S. National Fungus Collections, Beltsville, USA; CFCC, China Forestry Culture Collection Center, China; CBS, Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands; IRAN…C, Iranian Fungal Culture Collection, Iranian Research Institute of Plant Protection, Tehran, Iran; Others are not registered abbreviations.

beta (Edler et al. 2021), using the ML + rapid bootstrap setting and the GTRGAMMA substitution model with 1000 bootstrap replicates. The tree was rooted with *Gaeumannomyces graminis* var. *graminis* (M57). Tree was visualized in FigTree version 1.4.4 (Rambaut 2012). The newly generated sequences were uploaded to GenBank (Table 1).

RESULTS

Phylogenetic Analyses

The phylogenetic analyses included 22 strains in *Juglanconidaceae* and *Melanconiellaceae*, with *Gaeumannomyces graminis* var. *graminis* (M57) as the outgroup (Voglmayr et al. 2017). The final dataset comprised 1493 characters (*tef1-α*: 1–1493bp). The RAxML analysis of the dataset yielded a best-scoring tree with a final ML optimization likelihood value of - 7323.699272 (Fig. 1). The aligned sequences matrix comprised 567 distinct alignment patterns with 17.49% of undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.204987, C = 0.330723, G = 0.249603, T = 0.214686, with substitution rates AC = 0.980195, AG = 2.529286, AT = 0.987582, CG = 1.014431, CT = 4.104103, GT = 1.000000; gamma distribution shape parameter α = 0.305772. Two new isolates, i.e. IRAN 2457C and IRAN 5294C clustered with the ex-type strains of *Juglanconis appendiculata* (D96) and *Melanconiella chrysomelanconium* (CBS 124271), respectively, with 100% support value (Fig. 1).

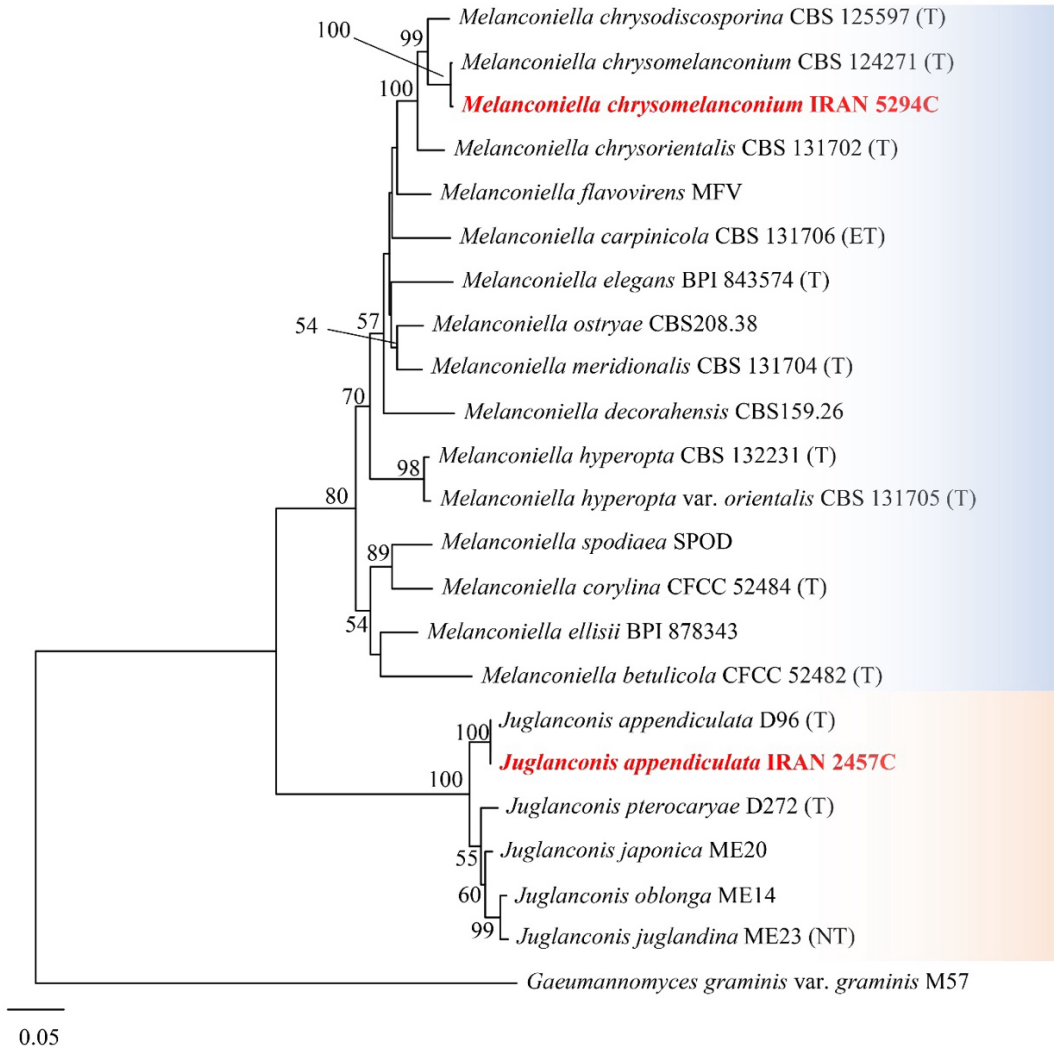

Fig. 1. RAxML tree based on the *tef1-α* gene sequence alignment of *Juglanconis* and *Melanconiella* species. Maximum likelihood bootstrap support values >50% are shown above or below the branches. The scale bar shows the expected number of nucleotide substitutions per site. The newly sequenced isolates are shown in red highlight. The tree is rooted with *Gaeumannomyces graminis* var. *graminis* M57 (*Magnaporthales*). (T), ex-type strain; (ET), ex-epitype strain; (NT), ex-neotype strain.

Taxonomy

Juglanconis appendiculata Voglmayr & Jaklitsch, Persoonia 38: 144 (2017). Fig. 2

Pseudostromata 1–3 mm diam., immersed in the bark of dead branches (ca. 1.7 cm thick), distinct, circular to irregular, slightly erumpent from the surface of substrate. Ectostromatic disc 0.5–1 mm diam., circular or oblong, dark grey, often covered by densely arranged ostioles, pulvinate. Central column brownish grey. Entostroma indistinct. Ostioles 3–13 per disc, 30–70 µm diam. (n = 34), plane or slightly papillate, black. Perithecia 380–500 × 400–560 µm ($\bar{x}$ = 420 × 500 µm, n = 10), flask-shaped to spherical, arranged circularly or irregularly. Peridium 20–40 µm thick, consisting of several layers of brown, (0) 1-septate cells of *textura angularis*. Paraphyses deliquescent at maturity. Asci 90–130 × 17–21 µm ($\bar{x}$ = 115 × 19 µm, n = 15), containing 8 biseriate ascospores, fusoid, with distinct apical ring. Ascospores 20–29 × 8–11.8 µm ($\bar{x}$ = 24 × 10 µm, n = 20), hyaline, ellipsoid or broadly fusoid, symmetric to slightly asymmetric, distinctly constricted at the septum, without appendages, (0)1 septate, cells monomorphic to dimorphic, with rounded to subacute ends. Asexual morph: Conidiomata acervular, 0.5–1 mm diam., black, scattered or occasionally confluent, with central or eccentric stromatic column, at maturity covered by black discharged conidial masses. Conidiophores 20–39 × 3–5 µm ($\bar{x}$ = 25 × 4 µm, n = 20), cylindrical, simple or branched at the base, smooth, subhyaline to pale brown. Conidiogenous cells annellidic with distinct annellations. Conidia 17–23 × 9–13 µm ($\bar{x}$ = 20 × 11 µm, n = 20), unicellular, hyaline at first, later becoming brown, with gelatinous sheath, ellipsoidal to pip-shaped, truncate with distinct scar at the base, guttulate, thick-walled, verrucose.

Culture characteristics (25 °C, 30 d): Mycelium composed of branched, septate, smooth, hyaline hyphae, 1–3.5 µm wide. Colonies on PDA attaining 40 mm diam., flat, felty, with moderate aerial mycelium in center, white to buff (45); margins irregular; reverse ochraceous (44).

Specimen examined: IRAN, East Azerbaijan Province, Jolfa, on dead branches of *Juglans regia*, 11 July 2015, M. Mehrabi, IRAN 16720F, IRAN 2457C.

Notes: Morphological characteristics of our isolate (IRAN 2457C) were similar to those of *J. appendiculata* (Voglmayr et al. 2017), but aseptate ascospores were rarely observed and ascospores had no apex appendages. The lack of appendages could be due to the dead ascospores, as shown in Voglmayr et al. (2017). Based on a MegaBlast search of NCBIs GenBank nucleotide database, the closest hit using the *tef1-α* sequence of our isolate was ex-type of *J. appendiculata* (D96, GenBank KY427208) with a similarity of 100% (1007/1007 bp). Likewise, based on phylogenetic analysis of the *tef1-α* sequence data, our isolate clustered with *J. appendiculata* (D96) with high value (100%, Fig. 1). *Juglanconis appendiculata* occurs on dead corticated twigs and branches of *Juglans nigra* L., *J. regia* and *J. sigillata* Dode distributing in Europe (Austria, France, Greece and Spain; Voglmayr et al. 2017) and Asia (China; Wang et al. 2023). During the study of fungal species associated with canker and dieback diseases of walnut trees (*Juglans regia*) in East Azerbaijan Province, Pourfaraj et al. (2019) reported *J. juglandina* based on its asexual morph. This is the first report of another species of *Juglanconis*, *J. appendiculata* from Iran. Wang et al. (2023) reported branch blight on *J. sigillata* caused by *Juglanconis appendiculata* in China. Although our isolate was found on dead branches of *J. regia* as a saprophyte, its pathogenicity needs to be evaluated in the future to enhance our understanding of walnut pathogenic fungi.

Melanconiella chrysomelanconium Voglmayr & Jaklitsch, Fungal Diversity 57(1): 16 (2012). Fig. 3

Pseudostromata 1–2 mm diam., immersed in the bark of dead branches (ca. 0.7 cm thick), distinct, circular, slightly erumpent from the surface of substrate. Ectostromatic disc small, 0.2–0.5 mm diam., circular or oblong, yellow or greyish yellow. Central column yellow, grey or olive. Entostroma inconspicuous or olive. Ostioles 1–8 per disc, 55–90 µm diam. (n = 20), plane or slightly papillate, black. Perithecia 400–600 × 450–700 µm ($\bar{x}$ = 480 × 560 µm, n = 10), flask-shaped to spherical, arranged circularly to the central column. Peridium 30–50 µm thick, consisting of several layers of brown cells of *textura angularis*. Paraphyses deliquescent at maturity. Asci 90–110 × 10–13 µm ($\bar{x}$ = 100 × 11 µm, n = 20), cylindrical, containing 8 uni- or irregularly biseriate ascospores, with distinct apical ring. Ascospores 14–19 × 7–9 µm ($\bar{x}$ = 16.2 × 8.1 µm, n = 20), hyaline, broadly ellipsoidal, 1-septate, distinctly swollen, particularly at the septum, not constricted at the septum, with hyaline cap-like appendages at each end, 1.7–2 µm long, 2–3 µm wide, cells monomorphic, multiguttulate with one large and numerous small guttules per cell, with rounded to truncate ends. Asexual morph: Conidiomata acervular, 0.5–3.5 mm diam., black, scattered or occasionally confluent, with central or eccentric stromatic column, at maturity covered by black discharged conidial masses. Conidiophores 10–30 × 2–5 µm ($\bar{x}$ = 25 × 4 µm, n = 20), hyaline to light brown, smooth, cylindrical, simple, rarely branched at the base. Conidiogenous cells annellidic with distinct annellations. Conidia 10–15 × 7–9 µm ($\bar{x}$ = 12.6 × 8.5 µm, n = 20), unicellular, hyaline at first, then becoming brown, with gelatinous sheath, ellipsoidal to pip-shaped, truncate with distinct scar at the base, densely multi-guttulate, thick-walled, smooth.

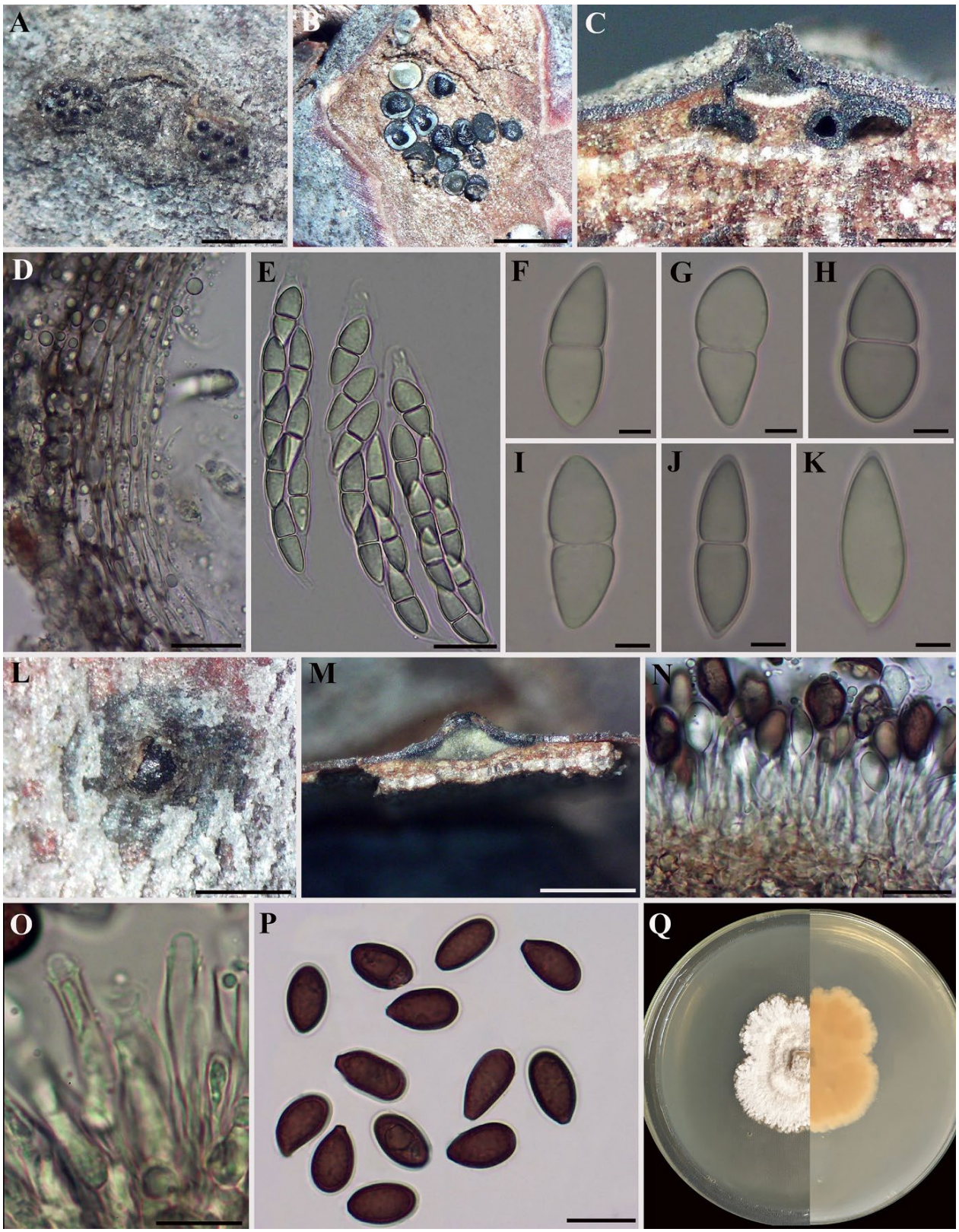

Fig. 2. *Juglanconis appendiculata* (IRAN 16720F). (A) ectostromatic discs and ostioles on dead branch of *Juglans regia*, (B) pseudostroma in transverse section, (C) pseudostroma in vertical section, (D) peridium, (E) asci, (F–K) ascospores, (L) conidioma in surface view, (M) conidioma in vertical section, (N, O) conidiophores (annellides) with conidia, (P) conidia, (Q) colony morphology on PDA from above (left) and below (right). Scale bars: (A, B) 1 mm, (C, L, M) 500 µm, (D, E, N, P) 20 µm, (O) 10 µm, (F–K) 5 µm.

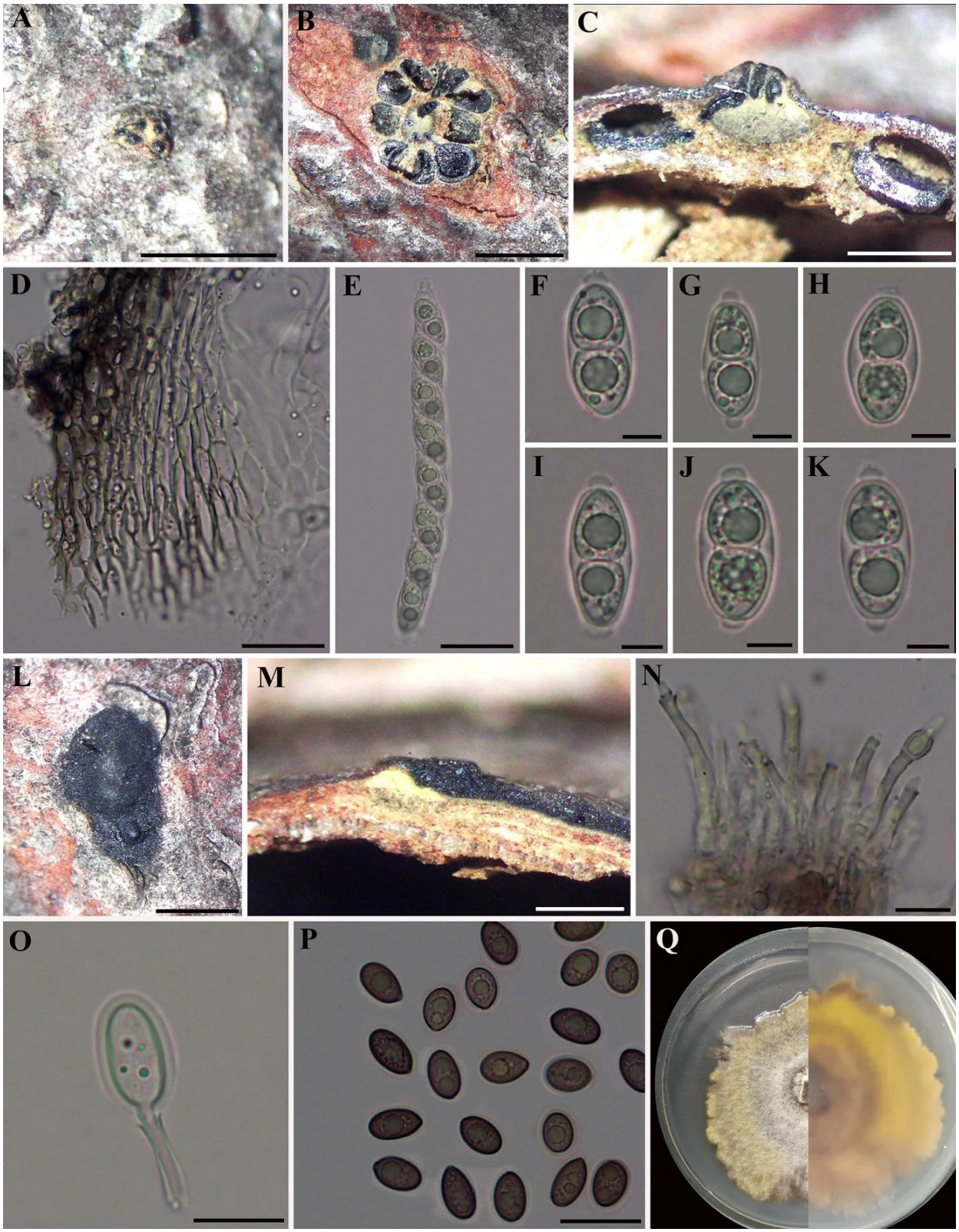

Fig. 3. *Melanconiella chrysomelanconium* (IRAN 18641F). (A) ectostromatic discs and ostioles on dead branch of *Carpinus orientalis*, (B) pseudostroma in transverse section, (C) pseudostroma in vertical section, (D) peridium, (E) ascus, (F–K) ascospores, (L) conidioma in surface view, (M) conidioma in vertical section, (N, O) conidiophores (annellides) with conidia, (P) conidia, (Q) colony morphology on PDA from above (left) and below (right). Scale bars: (A, B) 1 mm, (C, L, M) 500 µm, (D, E, N, P) 20 µm, (O) 10 µm, (F–K) 5 µm.

Culture characteristics (25 °C, 30 d): Mycelium composed of branched, septate, smooth, subhyaline hyphae, 1.5–4 µm wide. Colonies on PDA attaining 57 mm diam., flat, cottony, with moderate aerial mycelium, smoke grey (105) in the center, straw (46) in margin, margin irregular, reverse cinnamon (62) in center, pale luteous (11) in margin.

Specimen examined: IRAN, Golestan Province, Golestan National Park, 37˚22′11.06″ N, 55˚59′11.31″ E, on dead branches of *Carpinus betulus*, 19 June 2024, M. Mehrabi, IRAN 18641F, IRAN 5294C.

Notes: *Melanconiella chrysomelanconium* was described by Voglmayr et al. (2012) on the basis of material from Austria. Based on both morphology and sequence analysis of the *tef1-α* gene (Fig. 1), the occurrence of *M. chrysomelanconium* in Iran is confirmed. Also, based on a MegaBlast search of NCBIs GenBank nucleotide database, the closest hit using the *tef1-α* sequence of our isolate was *M. chrysomelanconium* (MEUK, GenBank JQ926387) with a similarity of 99% (1008/1010). Phylogenetically, *M. chrysodiscosporina*, *M. chrysomelanconium* and *M. chrysorientalis* were grouped on a 100% supported branch (Fig.1). *Melanconiella chrysomelanconium* is similar to *M. chrysodiscosporina* and *M. chrysorientalis* in the ascospores' size, shape and appendages. However, it differs mainly by dark brown conidia (hyaline in both *M. chrysodiscosporina* and *M. chrysorientalis*), and *tef1-α* sequences (6% and 5% difference with *M. chrysodiscosporina* and *M. chrysorientalis*, respectively) (Voglmayr et al. 2012).

Melanconiella has been shown to be confined to the host family *Betulaceae*, and all species are found to be highly host-specific, mostly confined to a single host species (Voglmayr et al. 2012). *Melanconiella chrysomelanconium* has been reported only on *Carpinus betulus* in Europe (Austria, Spain and United Kingdom; Voglmayr et al. 2012). This is the first report of this species from Asia.

ACKNOWLEDGMENT

We are grateful to Ms Fatemeh Shadmehri (Shirvan Faculty of Agriculture, Bojnord, Iran) for technical assistance.

AUTHOR CONTRIBUTION

Experiments, data analysis, and original draft preparation were conducted by M. Mehrabi. B. Asgari carried out the review and editing of the manuscript. All authors read and approved the final manuscript.

DATA AVAILABILITY

All sequence data generated in this study (Table 1) are available at GenBank (https://www.ncbi.nlm.nih.gov/). Requests for materials should be addressed to B. Asgari.

DECLARATION

The authors declare that there is no conflict of interest.

FUNDING

Not applicable.

ETHICS APPROVAL

Not applicable.

REFERENCES

Barr ME. 1978. The *Diaporthales* in North America with emphasis on *Gnomonia* and its segregates. Mycologia Memoirs. 7: 1-232. https://doi.org/10.1002/fedr.19800910313.

Chaverri P, Samuels GJ. 2003. *Hypocrea*/*Trichoderma* (*Ascomycota*, *Hypocreales*, *Hypocreaceae*): species with green ascospores. Studies in Mycology. 48: 1-116

Crous PW, Wingfield MJ, Burgess TI, Hardy GE, Crane C, … et al. 2016. Fungal planet description sheets: 469–557. Persoonia. 37: 218-403. https://doi.org/10.3767/ 003158516X694499.

Du Z, Fan XL, Yang Q, Tian CM. 2017. Host and geographic range extensions of *Melanconiella*, with a new species *M. cornuta* in China. Phytotaxa. 327: 252-260. https://doi.org/10.11646/phytotaxa.327.3.4.

Edler D, Klein J, Antonelli A, Silvestro D. 2021. raxmlGUI 2.0: A graphical interface and toolkit for phylogenetic analyses using RAxML. Methods in Ecology and Evolution. 12: 373-377. https://doi.org/10.1111/2041-210X.13512.

Fan X, Du Z, Bezerra JDP, Tian C. 2018. Taxonomic circumscription of melanconis-like fungi causing canker disease in China. MycoKeys. 42: 89-124. https://doi.org/10.3897/mycokeys.42.29634.

Hyde KD, Noorabadi MT, Thiyagaraja V, He MQ, Johnston PR, … et al. 2024. The 2024 Outline of Fungi and fungus-like taxa. Mycosphere. 15: 5146-6239. https://doi.org/10.5943/mycosphere/15/1/25.

Jaklitsch WM, Komon M, Kubicek CP, Druzhinina IS. 2006. *Hypocrea voglmayrii* sp. nov. from the Austrian Alps represents a new phylogenetic clade in *Hypocrea*/*Trichoderma*. Mycologia. 97: 1365-1378. https://doi.org/10.3852/mycologia.97.6.1365.

Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: Multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics. 20: 1160-1166. https://doi.org/10.1093/bib/bbx108.

Kuraku S, Zmasek CM, Nishimura O, Katoh K. 2013. aLeaves facilitates on-demand exploration of metazoan gene family trees on MAFFT sequence alignment server with enhanced interactivity. Nucleic Acids Research. 41: W22-W28. https://doi.org/10.1093/nar/gkt389.

Liu D, Coloe S, Baird R, Pedersen J. 2000. Rapid mini-preparation of fungal DNA for PCR. Journal of

Clinical Microbiology. 38: 471. https://doi.org/10.1128/jcm.38.1.471-471.2000.

Mehrabi M. 2025. Morphological and molecular data reveal *Albicollum khorasanicum*, sp. nov., from Iran. Sydowia. 78: 57-64. https://doi.org/10.12905/0380.sydowia78-2026-0057.

Mu T, Chen J, Zhao Z, Zhang W, Stephenson SL, … et al. 2023. Morphological and phylogenetic analyzes reveal two new species of *Melanconiella* from Fujian Province, China. Frontiers in Microbiology. 14: 1229705. https://doi.org/10.3389/fmicb.2023.1229705.

Nannfeldt JA. 1932. Studien über die Morphologie und Systematik der nichlichenisierten inoperculaten Discomyceten. Nova Acta Regiae Societatis Scientiarum Upsaliensis Series. 4(8): 1-368.

Pourfaraj A, Arzanlou M, Abed-Ashtiani F. 2019. *Juglanconis juglandina* a new record for the mycobiota of Iran. Mycologia Iranica. 6(2): 119-123. https://doi.org/10.22043/mi.2020.121260.

Rambaut A. 2012. FigTree version 1.4.0. Available from: http://tree.bio.ed.ac.uk/software/figtree/ (accessed 15 May 2024).

Rayner RW. 1970. A mycological colour chart. CMI and British Mycological Society, Kew.

Rossman AY, Farr DF, Castlebury LA. 2007. A review of the phylogeny and biology of the *Diaporthales*. Mycoscience. 48: 135-144. https://doi.org/10.1007/S10267-007-0347-7.

Saccardo PA. 1882. Sylloge Pyrenomycetum, Vol. I. Sylloge Fungorum. 1: 1-768.

Samuels GJ, Blackwell M. 2001. *Pyrenomycetes* – fungi with perithecia. In: McLaughlin, D., McLaughlin, E. (eds), The Mycota VII Part A. Systematics and Evolution. Springer-Verlag, Berlin, 221-255.

Senanayake IC, Crous PW, Groenewald JZ, Maharachchikumbura SSN, Jeewon R, … et al. 2017. Families of *Diaporthales* based on morphological and phylogenetic evidence. Studies in Mycology. 86: 217-296. https://doi.org/10.1016/j.simyco.2017.07.003.

Senanayake IC, Rathnayake AR, Marasinghe DS, Calabon MS, Gentekaki E, … et al. 2020. Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. Mycosphere. 11: 2678-2754. https://doi.org/10.5943/mycosphere/11/1/20.

Stamatakis E. 2006. RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics. 22: 2688-2690. https://doi.org/10.1093/bioinformatics/btl446.

Voglmayr H, Castlebury LA, Jaklitsch WM. 2017. *Juglanconis* gen. nov. on *Juglandaceae*, and the new family *Juglanconidaceae* (*Diaporthales*). Persoonia. 38: 136-155. https://doi.org/10.3767/003158517X694768.

Voglmayr H, Jaklitsch WM, Mohammadi H, Chakusary MK. 2019. The genus *Juglanconis* (*Diaporthales*) on *Pterocarya*. Mycological Progress. 18: 425-37. https://doi.org/10.1007/s11557-018-01464-0.

Voglmayr H, Rossman AY, Castlebury LA, Jaklitsch WM. 2012. Multigene phylogeny and taxonomy of the genus *Melanconiella* (*Diaporthales*). Fungal Diversity. 57: 1-44. https://doi.org/10.1007/s13225-012-0175-8.

Wang F, Zeng Q, Liu C, Xu X, Zhu T, … et al. 2023. Branch blight of *Juglans sigillata* caused by *Juglanconis appendiculata* in China. Plant Disease. 107(1): 224. https://doi.org/10.1094/PDIS-04-22-0782-PDN.

Wang FH, Xu XL, Zeng Q, Liu LJ, Liu F, … et al. 2025. Microfungi associated with walnut trees in southwestern China. Mycosphere. 16(1): 2002-2258. https://doi.org/10.5943/mycosphere/16/1/12.

Zhang N, Zhao S, Shen Q. 2011. A six-gene phylogeny reveals the evolution of mode of infection in the rice blast fungus and allied species. Mycologia. 103(6): 1267-1276. https://doi.org/10.3852/11-022.

Zhang ZX, Shang YX, Liu QY, Li DH, Yin CZ, … et al. 2025. Deciphering the evolutionary and taxonomic complexity of *Diaporthales* (*Sordariomycetes*, *Ascomycota*) through integrated phylogenomic and divergence time estimation. Fungal Diversity. 132: 1-125. https://doi.org/10.1007/s13225-025-00551-4.

گونه های *Juglanconis appendiculata* و *Melanconiella chrysomelanconium*، دو گزارش جدید از قارچ‌های متعلق به راسته *Diaporthales* از ایران

مهدی محرابی[۱]، بیتا عسگری[۲]✉

[۱] استادیار، گروه علوم باغبانی و فضای سبز، دانشکده کشاورزی شیروان، دانشگاه بجنورد، بجنورد، ایران
[۲] استادیار پژوهش، بخش تحقیقات رستنی‌ها، موسسه تحقیقات گیاه‌پزشکی کشور، سازمان تحقیقات، آموزش و ترویج کشاورزی، تهران، ایران

چکیده

اعضای راسته *Diaporthales* روی طیف وسیعی از میزبان‌ها و بسترها مانند درختان و محصولات کشاورزی، خاک و حتی بافت‌های زنده حیوانات و انسان‌ها یافت می‌شوند و شامل گونه‌های بیماری‌زا، پوده‌زی و اندوفیت هستند. این مطالعه به منظور افزایش دانش از تنوع زیستی قارچ‌های متعلق به راسته *Diaporthales* در ایران انجام شد.گونه *Juglanconis appendiculata* از شاخه مرده *Juglans regia* در استان آذربایجان شرقی و *Melanconiella chrysomelanconium* از شاخه مرده *Carpinus betulus* در استان گلستان با استفاده از ویژگی‌های ریخت‌شناختی و داده‌های مولکولی شناسایی شد. بررسی روابط تبارزایی بر اساس ژن فاکتور طویل‌سازی ۱-آلفا (*tef1-α*) با استفاده از آنالیز بیشینه درست نمایی، از قرارگیری دو جدایه ایرانی شامل IRAN 2457C (شناسایی شده بعنوان *Juglanconis appendiculata*) و IRAN 5294C (شناسایی شده بعنوان *Melanconiella chrysomelanconium*) در راسته *Diaporthales* به طور کامل حمایت کرد. در این مقاله، تصاویر و توصیف هر دو گونه شناسایی شده بر اساس بررسی نمونه‌های ایرانی و همچنین نتایج مقایسه آن‌ها با گونه‌های نزدیک ارایه می‌شود. این مطالعه نخستین گزارش از دو گونه *J. appendiculata* و *M. chrysomelanconium* در ایران است و گسترش دامنه جغرافیایی هر دو گونه را نشان می‌دهد.

کلمات کلیدی: تاکسونومی، تبارزایی، جوگلانکونیداسه، مایکوبیوتا، گزارش جدید، ملانکونیلاسه.

مکاتبه کننده: بیتا عسگری bita_asgari@yahoo.com

تاریخ دریافت: ۱۴۰۴/۰۷/۰۶، تاریخ بازنگری: ۱۴۰۴/۰۷/۲۷، تاریخ پذیرش: ۱۴۰۴/۰۷/۲۹، تاریخ انتشار برخط: ۱۴۰۴/۰۸/۰۳