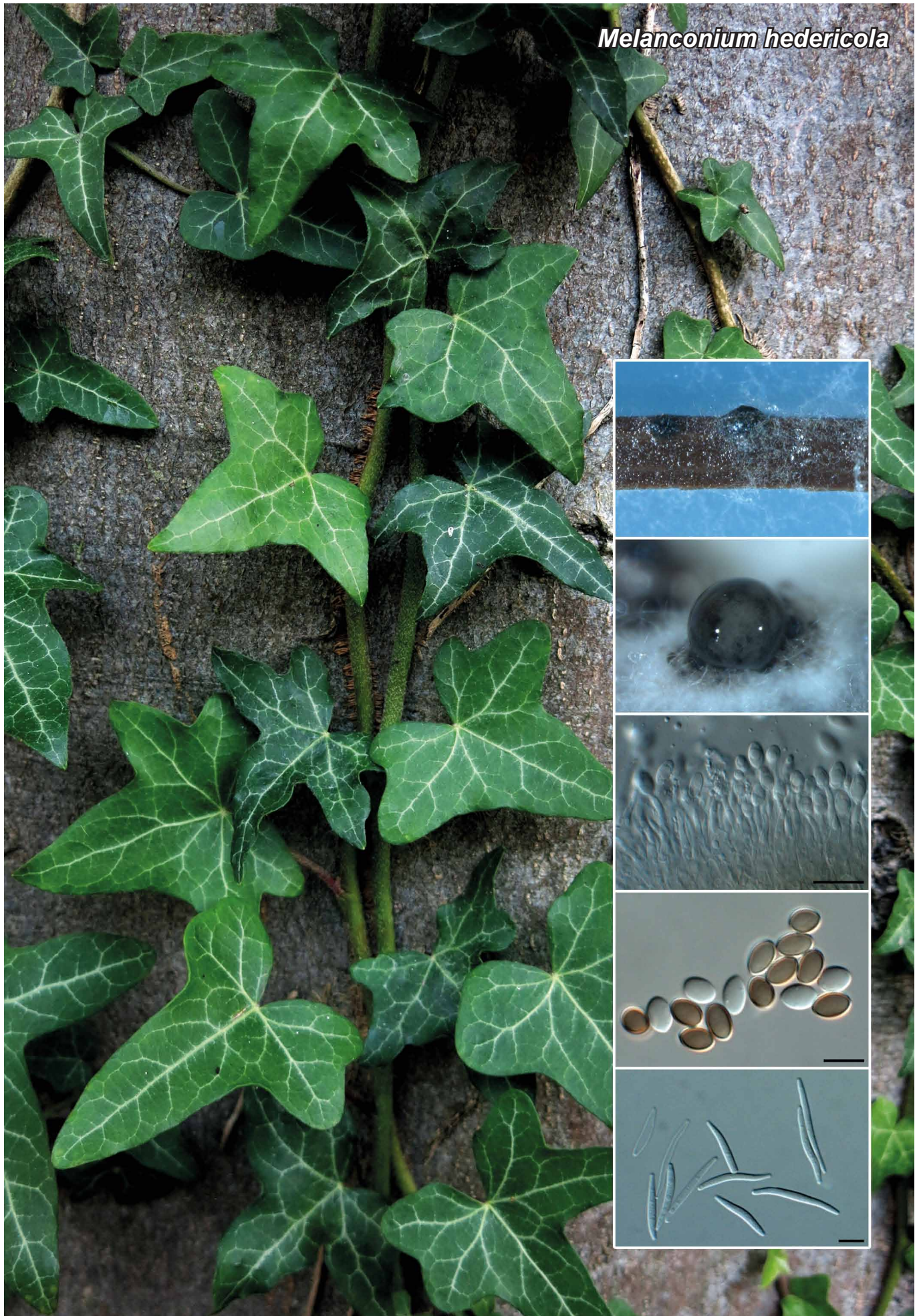


Melanconium hedericola



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***Melanconium hedericola* Crous & R.K. Schumach., sp. nov.**

Etymology. Name reflects the host genus *Hedera*, from which this species was isolated.

Conidiomata pycnidial single or in densely crowded groups under loosened bark, superficial on a black stromatic layer which continues as a black stromatic line deep in the wood, \pm pyriform with flattened base, black, rough, soft, distinctly thick, ostium central and indistinct; periphyses not seen, with a few setae on the outer site of the peridium. *Setae* 1-celled, stiff, pointed, basally enlarged and flattened, brown, thick-walled, smooth, eguttulate, up to 26 μm long. *Peridium* multi-layered, consisting of a red-brown *textura epidermoidea* (outer layer) and hyaline *textura angularis-prismatica* (inner layer), cells thick-walled, smooth and eguttulate. Sporulating on PNA. *Conidiomata* pycnidial, globose, up to 600 μm diam, black, immersed, exuding creamy conidial droplets from central ostioles, or developing 1–4 black necks on OA (not on PNA); walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–2-septate, branched below, densely aggregated, cylindrical, straight to sinuous, 20–40 \times 3–4 μm . *Conidiogenous cells* 10–17 \times 2–3 μm , phialidic, cylindrical, terminal and intercalary, with slight apical taper, 2 μm diam, with visible periclinal thickening; collarete flared, up to 5 μm long. *Paraphyses* not observed. *Alpha conidia* (6–)7(–8) \times (3.5–)4(–4.5) μm , aseptate, hyaline, smooth, ellipsoid with large central guttule, becoming brown with age. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, guttulate, apex bluntly rounded, base truncate, tapering from the middle towards the base, (17–)18–20(–25) \times 2.5(–3) μm .

Culture characteristics — Colonies flat, spreading, covering the dish after 2 wk at 25 °C in the dark, with sparse aerial mycelium. On MEA, PDA and OA surface umber with patches of dirty white and iron-grey; reverse umber with patches of dirty white and iron-grey.

Typus. SPAIN, Sarasibar (Navarra), on branch of *Hedera helix* (*Araliaceae*), 26 Jan. 2014, S. Garcia (holotype CBS H-21995, culture ex-type CPC 24278 = CBS 138863; ITS sequence GenBank KP004461, LSU sequence GenBank KP004489, HIS sequence GenBank KP004505, TUB sequence GenBank KP004510, MycoBank MB810607).

Colour illustrations. *Hedera helix* growing along a tree trunk; conidiomata on PNA and OA, conidiogenous cells, alpha and beta conidia. Scale bars = 10 μm .

Notes — Although *Melanconium hedericola* clusters within the genus *Diaporthe*, the LSU region lacks resolution within the *Diaporthales*. We have thus chosen to describe it in *Melanconium* based on the ellipsoid alpha conidia that turn brown with age, and their characteristic large, central guttules (Sutton 1980). However, *Melanconium* is known to not have species with beta conidia, which suggests that *M. hedericola* might represent an unknown genus within this complex. Further studies and collections are required before this question can be resolved. Previously published taxa on *Hedera* include *Coniothyrium hederiae* and its possible synonym, *Melanconium hederiae*, which have similar alpha conidia (6–8 \times 4.5–6 μm), but that lack beta conidia.

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis columnaris* (GenBank FN394688; Identities = 528/541 (98 %), Gaps = 2/541 (0 %)), *Diaporthe endophytica* (GenBank AB899789; Identities = 566/583 (97 %), Gaps = 7/583 (1 %)) and *Diaporthe phaseolorum* (GenBank JQ936148; Identities = 565/583 (97 %), Gaps = 7/583 (1 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Phomopsis columnaris* (GenBank AF439627; Identities = 834/840 (99 %), no gaps), *Diaporthe ambigua* (GenBank JQ862833; Identities = 821/828 (99 %), no gaps) and *Phomopsis sclerotoides* (GenBank AF439628; Identities = 831/840 (99 %), no gaps).

HIS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the HIS sequence are *Diaporthe longispora* (GenBank KC343619; Identities = 360/378 (95 %), Gaps = 5/378 (1 %)), *Diaporthe sclerotoides* (GenBank KC343678; Identities = 359/381 (94 %), Gaps = 4/381 (1 %)) and *Diaporthe* 'sp. 4' (GenBank KC343690; Identities = 356/378 (94 %), Gaps = 5/378 (1 %)).

TUB. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe longispora* (GenBank KC344103; Identities = 398/420 (95 %), Gaps = 2/420 (0 %)), *Diaporthe sclerotoides* (GenBank KC344161; Identities = 391/416 (94 %), Gaps = 2/416 (0 %)) and *Diaporthe scabra* (GenBank HQ450372; Identities = 418/450 (93 %), Gaps = 2/450 (0 %)).

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