Fungal Planet 1832 MB 857763

Helicogermslita australiensis B. Raphael, M.J. Lynch, E.J. Whiteside & Dearnaley, ***sp. nov.***

Etymology: Named "*australiensis*" as it is the first species of the genus to be discovered in Australia.

Classification: *Xylariaceae*, *Xylariales*, *Sordariomycetes*.

Ascomata solitary, 1–4 mm diam., brown to black with white mycelial sheath; wall of 3–6 layers of pale brown textura angularis, superficial on substrate surface. *Paraphyses* intermingled among asci, hyphae-like, hyaline, smooth, septate, (3.3–)–3.7–4.7(–5.2) µm diam. *Asci* 8-spored, unitunicate, cylindrical, pedicellate, apically, rounded, (147.2–)152.9–168.0(–170.2) × (12.5–)14.5–16.1(–17.5) µm, with amyloid reaction of apical ring to Melzer's reagent. *Ascospores* overlapping uniseriate, hyaline when immature, brown to dark brown when mature, spiral germ slit extending over the full length, (20.8–)21.5–24.3(–26.5) × (8.7–)9.3–10.5(–11.2) µm. *Conidiomata* solitary, 1–4 mm diam., brown to black with white mycelial sheath; wall of 3–6 layers of white to pale brown textura angularis. *Conidiophores* lining inner cavity, hyaline, rough, subcylindrical with slight apical taper, (13.8–)14.0–14.6(–14.9) × (2.3–)2.6–3.4(–3.6) µm. *Conidiogenous cells* hyaline, smooth, cylindrical, terminal, (6.2–)6.4–8.2(–10.06) × (2.24–)2.4–3.4(–3.8) *µm, phialidic. Conidia* solitary, aseptate, hyaline, smooth, obovate to fusiform, (6.4–)6.8–7.2(–8.0) × (2.2–)2.4–3.4(–3.8) µm.

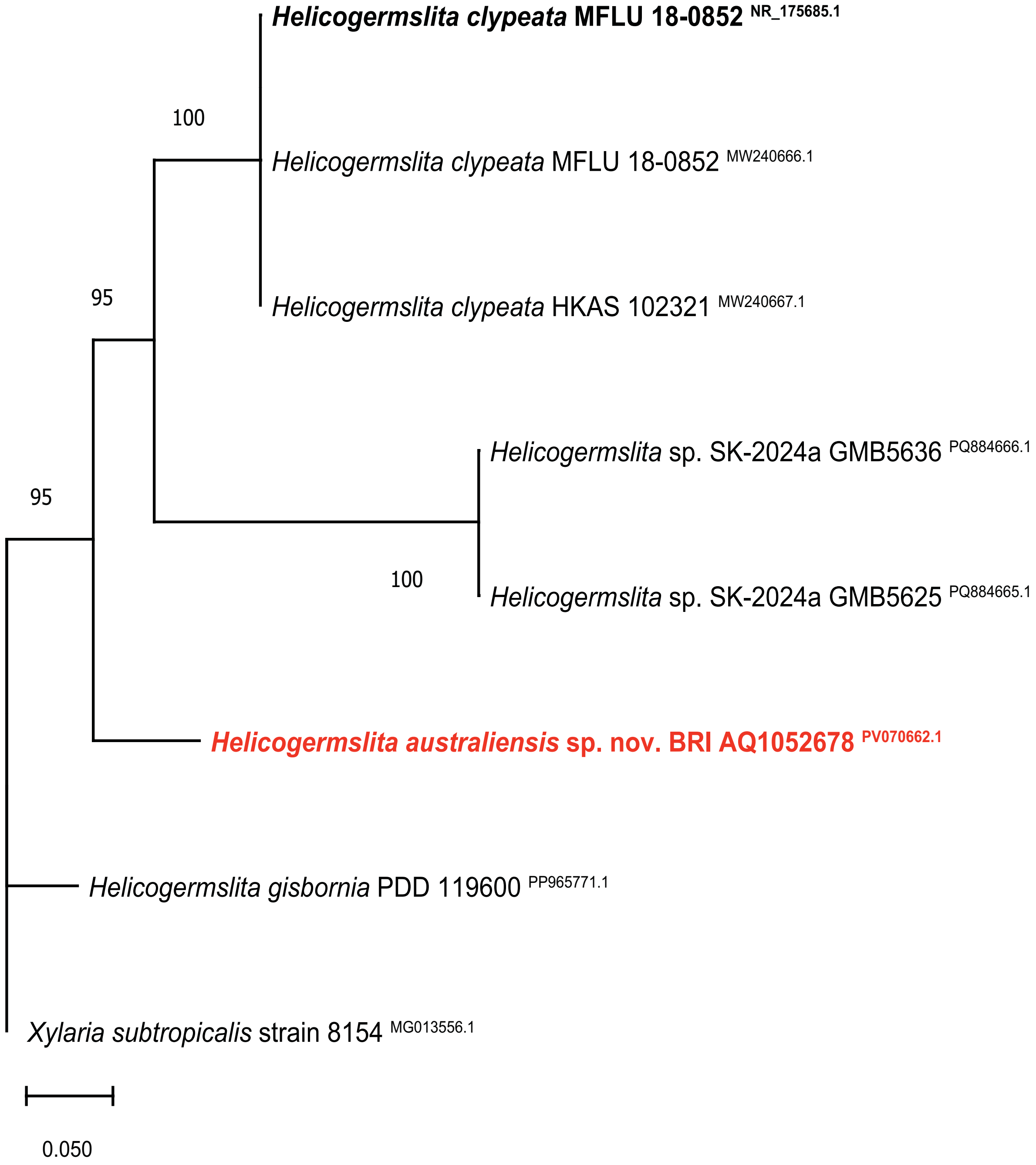
Culture characteristics: Colonies flat, spreading, with sparse to moderate aerial mycelium and folded surface, reaching 80 mm diam. after 2 wk at 22 °C in the dark. On potato dextrose agar (PDA), both surface and reverse are white.

Typus: **Australia**, Queensland, Dilkusha Nature Refuge, 26°44'13''S, 152°53'31''E, 3 m a.s.l., isolated as an endophyte from healthy leaves of *Archontophoenix cunninghamiana* (*Arecaceae*), 6 Dec. 2022, *B. Raphael*, BR002 (**holotype** stroma lodged in herbarium BRI AQ1052678, culture ex-type BRI AQ1052678 = AC1.4.1; ITS and LSU sequences GenBank PV070662.1 and PV070663.1).

Notes: *Helicogermslita australiensis* was collected as an endophyte from foliage of *Archontophoenix cunninghamiana*. The genus *Helicogermslita*, was introduced to accommodate species belonging to the *Xylariaceae* that produced ascospores with spiral germ slits (Hawksworth & Lodha 1983). The genus was typified with *H. celastri* (Kale & Kale 1971). *Helicogermslita australiensis* differs from *H. celastri* by having larger ascospores with 1–2 coils as opposed to 2–4. Phylogenetically, *H. australiensis* is also separate from *H. clypeata*, *H. gisbornia*, and another un-named *Helicogermslita* species. Molecular data do not exist for the other species of *Helicogermslita*. *Helicogermslita australiensis* is also morphologically different from *H. clypeata*, as the ascomata of *H. clypeata* are immersed in the substrate. The ascospores of *H. australiensis* are also smaller than those of *H. gisbornia*. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the **ITS** sequence had highest similarity to *Xylaria* sp. YG-2022a (strain KUNCC 22-12535, GenBank OP912879.1; Identities = 370/374, no gaps), *Xylaria* sp. [strain ATT025, GenBank HQ607803.1; Identities = 374/387, five gaps (1 %)], and *Xylariales* sp. [strain TU22, GenBank HE820889.1; Identities = 321/331, one gap (0 %)]. Closest hits using the **LSU** sequence are *Helicogermslita* sp. YG-2024a [strain CCSG11, GenBank PQ036918.1; Identities = 614/619, no gaps (0 %)], *Xylaria curta* [strain 92092022, GenBank PP336519.1; Identities = 614/632, two gaps (0 %)], and *Helicogermslita clypeata* [strain MFLU 18-0852, GenBank NG_081506.1; Identities = 613/631, two gaps (0 %)].

Supplementary material: doi: 10.6084/m9.figshare.28520450 (alignment).

Colour illustrations: *Archontophoenix cunninghamiana* growing at Dilkusha Nature Refuge, Maleny, Queensland, Australia. Colony of *Helicogermslita australiensis* growing on PDA; stroma of *H. australiensis* growing from sterilised grapevine twigs on synthetic nutrient-poor agar; conidia; ascospores; ascus containing 8 ascospores. Scale bars: colony = 1 cm, stroma = 100 µm, and all others = 10 µm.



Maximum Likelihood tree produced from an analysis of nrDNA ITS sequences from *H. australiensis* and related *Helicogermslita* species in GenBank. Phylogenetic analysis was conducted in MEGA v. 11 (Tamura *et al.* 2021) using a ClustalW alignment, Kimura 2 parameters, Gamma distribution with invariant sites and 1000 bootstrap re-samplings were used to build the tree. Bootstrap support values less than 70 % are not shown, and *Xylaria subtropicalis* (*Xylariaceae*) was used as an outgroup to root the tree. The taxon described here is **bold** and in red font. Other type species in the tree are **bold** in black font. Species are also labelled with the accession numbers for the sequences used in the tree.

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