



Fungal Planet 1160 – 19 December 2020

Lophotrichus medusoides Calvert, McTaggart & R.G. Shivas, *sp. nov.*

Etymology. Named for the resemblance of ascomata to Medusa of Greek mythology, a Gorgon described as a winged woman with living venomous snakes for hair.

Classification — *Microascaceae*, *Microascales*, *Sordariomycetes*.

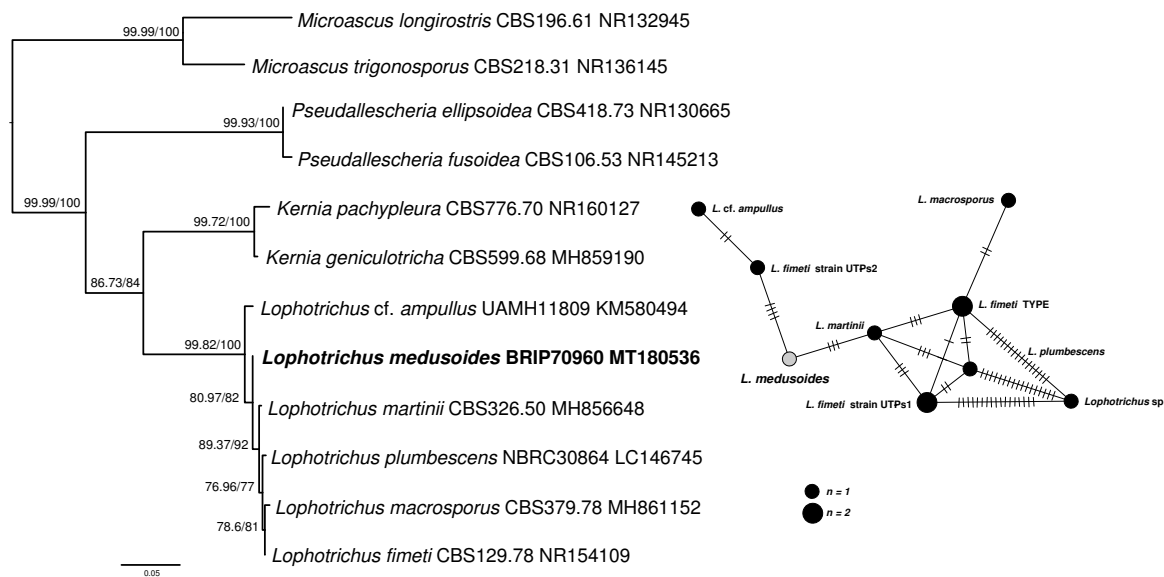
Mycelium on potato-dextrose agar (PDA) smooth, branched, sub-hyaline to pale yellow, hyphae 2–4 µm diam. **Ascomata** perithecial, immersed or partly immersed, globose to subglobose, scattered, 250–400 µm diam, with beaks 120–200 × 30–40 µm, with peridium composed of dark brown *textura angularis*; ascomatal appendages numerous, dark flexuous, up to 1.5 mm long, abundant on the beak, curved and narrowed at the apex. **Asci** evanescent, broadly clavate, 30–36 × 20–24 µm, thin-walled, 8-spored. **Ascospores** ellipsoidal, 7.5–9.5 × 5.5–6.5 µm, apices rounded, yellowish brown, with a germ pore at each end; wall even, 1–1.5 µm wide, smooth, extruded in a mass loosely held by ostiolar appendages.

Culture characteristics — On PDA after 2 wk in the dark at 23 °C colonies 3.5 cm diam, flat, with sparse aerial mycelium, cream white, ascomata concentrated toward margin; with irregular darkened patches after 3 wk; reverse cream white.

Typus. AUSTRALIA, Queensland, Iron Range, Lockhart River Rd, isolated from stem tissue of *Citrus garrawayi* (*Rutaceae*), 19 July 2019, J. Calvert (holotype specimen BRIP 70690, includes the ex-type culture BRIP 70690, ITS and LSU sequences GenBank MT180536 and MT186160, MycoBank MB834991).

Notes — *Lophotrichus medusoides* was isolated as an endophyte from stem tissue of *Citrus garrawayi*, which is an understory tree endemic to tropical rainforests in the Cape York region of northern Queensland. Species of *Lophotrichus* have been described from mammal dung and soil and are morphologically similar to *Microascus*, *Pseudallescheria* and *Kernia* (Sandoval-Denis et al. 2016). Other taxa in the *Microascales* have been reported in association with *Citrus* as either endophytes, e.g., *Scedosporium*, or pathogens, e.g., *Ceratocystis* (De Beer et al. 2014). A phylogenetic analysis of the ITS region showed *Lophotrichus* was monophyletic and that *L. medusoides* shared a most recent common ancestor with coprophilic taxa. It differs in morphology to *L. fimeti*, which lacks beaks on ascomata, to *L. plumbescens*, which has two types of ascomatal hairs, and to *L. martinii*, which has larger ascospores and shorter, wavy ascomatal hairs (Guarro et al. 2012). It differs from *L. indicus*, which has broad ascospores with obtuse ends and ascomata that have abundant terminal hairs (Saxena & Mukerji 1970).

BLASTn results of the ITS sequence of *L. medusoides* indicated similarity to type sequences of *L. fimeti* (NR_154109; Identities = 480/485 (98.97 %), no gaps), and *Enterocarpus grenotii* (NR_159852; Identities = 502/530 (94.72 %), six gaps (1 %)). The LSU sequence shared 1056/1096 (96 %) sequence identities with *Cephalotrichum purpureofuscum* (GenBank MF041789). A network analysis of ITS sequences showed a difference of three parsimony-informative characters between *L. medusoides* and *L. martinii* (GenBank MH856648) and four between *L. medusoides* and *L. fimeti* (GenBank MF161105).



Colour illustrations. Monsoon rainforest in the Iron Range, Cape York Peninsula, Far North Queensland, Australia. Ascomata showing long ascomatal hairs; *textura angularis*; ascospores from ruptured ascomata; 8-spored unitunicate ascus; hyphae. Scale bars = 1 mm (top left), 10 µm (all others).

Mid-point rooted phylogram from a maximum likelihood search using IQ-TREE v. 1.3.11.1 (Nguyen et al. 2015) with 10,000 ultra-fast bootstraps (Minh et al. 2013), 10,000 replicates of an approximate likelihood ratio test (aLRT), and a best-fit model of evolution (command -m TEST). ITS sequences aligned with MAFFT in UGENE v. 1.30.0 (Okonechnikov et al. 2012). The aLRT and UFBootstrap values are indicated at nodes. Minimum spanning network of all available *Lophotrichus* ITS sequences generated using POPART v. 1.7 (Leigh & Bryant 2015); hashes indicate number of parsimony informative characters between taxa.

Jed Calvert, Alistair R. McTaggart, Lília Costa Carvalhais, André Drenth & Roger G. Shivas, Queensland Alliance for Agriculture and Food Innovation (QAAFI), University of Queensland, Ecosciences Precinct, Level 2C East, GPO Box 267, Brisbane 4001, Queensland, Australia; e-mail: J.Calvert@uq.net.au, A.Mctaggart@uq.edu.au, L.Carvalhais@uq.edu.au, A.Drenth@uq.edu.au & R.Shivas@uq.edu.au