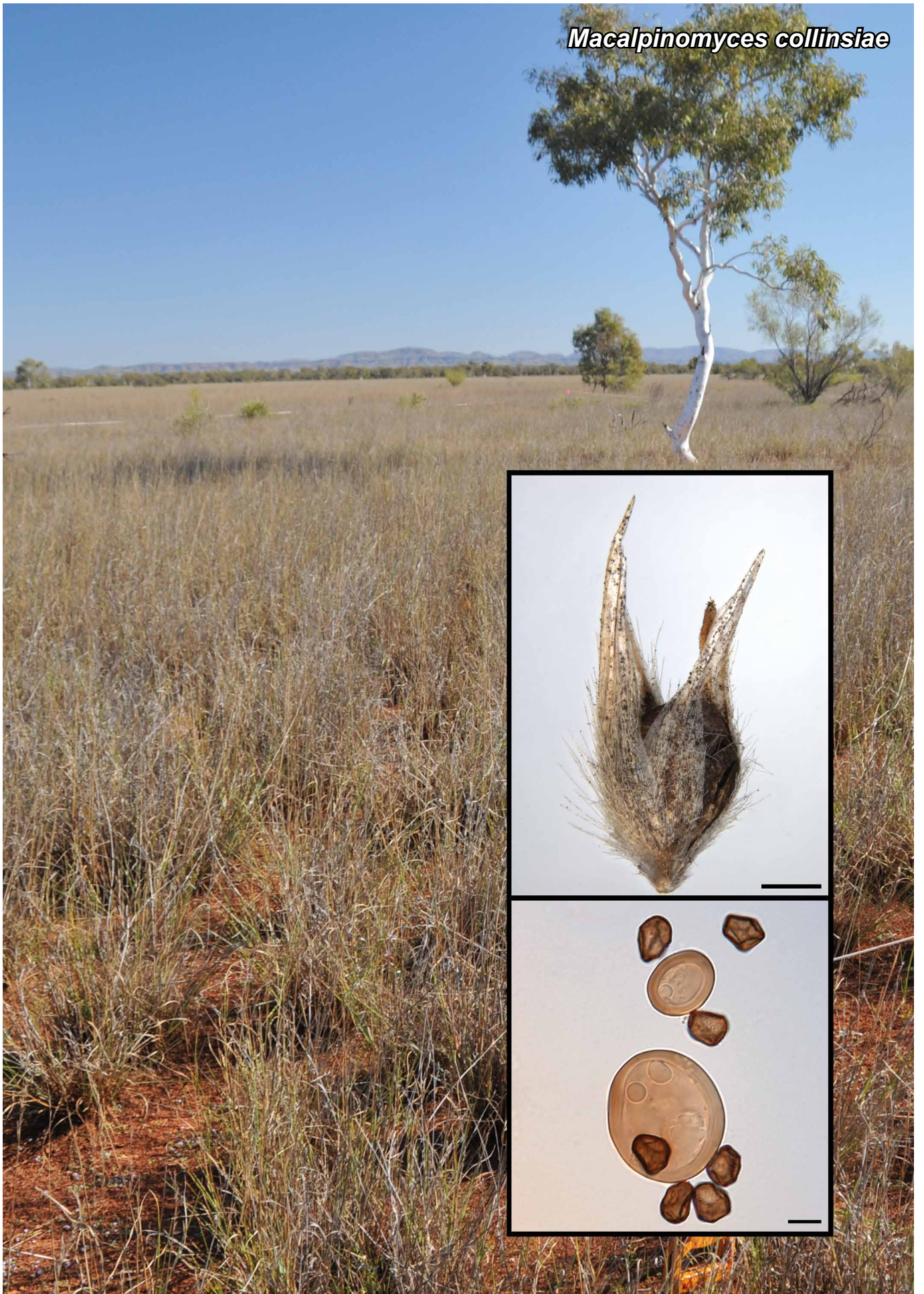


Macalpinomyces collinsiae



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Macalpinomyces collinsiae J. Kruse, M.N. Lyons, McTaggart & R.G. Shivas, *sp. nov.*

Etymology. Named after Dr Margaret Thora Collins, a Western Australian botanist, conservation biologist and mycologist, for her role in the discovery of this fungus.

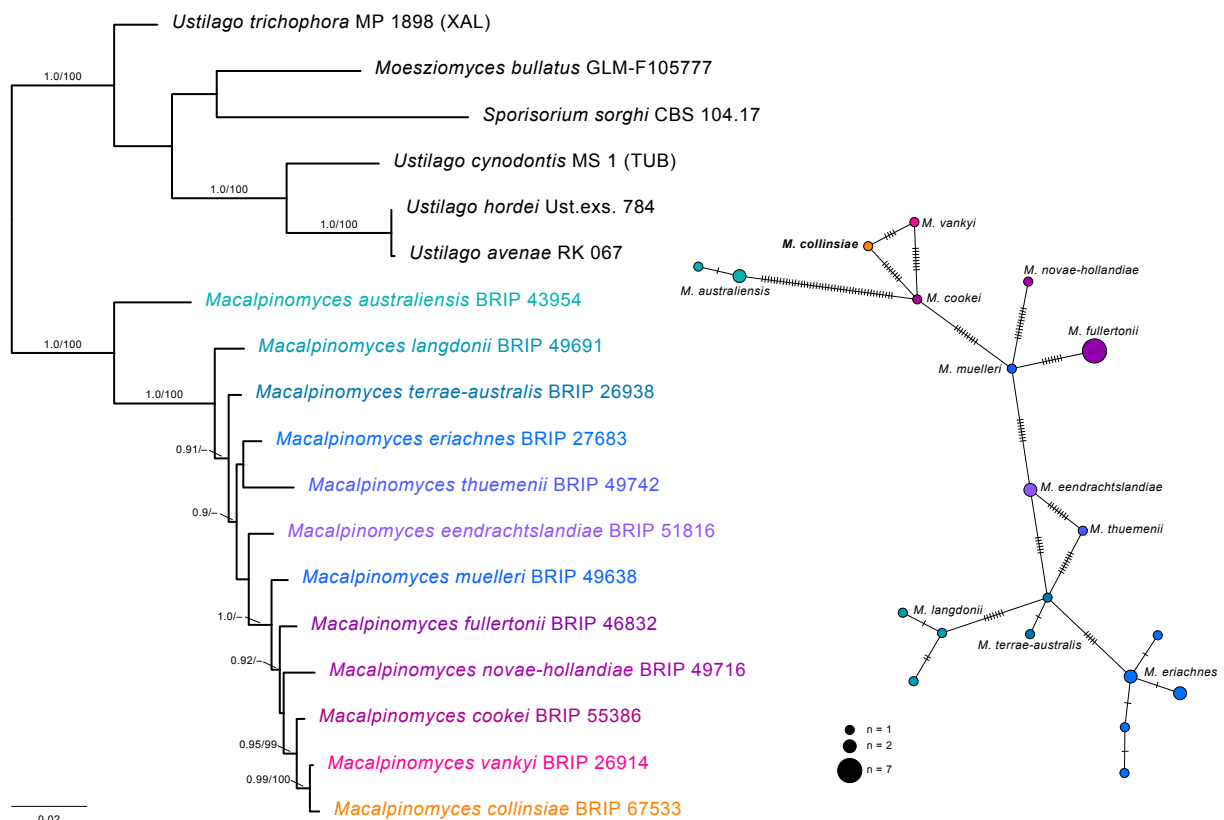
Classification — *Ustilaginaceae*, *Ustilaginales*, *Ustilaginomycetes*.

Sori ovoid, 1.5–2 × 2–3 mm, in all of the ovaries of *Eriachne benthamii*. **Spore mass** blackish brown, semi-agglutinated, comprised of spores and large giant sterile cells. **Spores** reddish brown, polyhedrally irregular, 11–15 × 8–10 µm; wall c. 1 µm wide, smooth. **Sterile cells** pale yellowish brown, globose to broadly ellipsoidal, 19–37 µm diam; wall 3–4 µm wide, smooth.

Typus. AUSTRALIA, Western Australia, Pilbara Region, c. 17.5 km ENE of intersection of Great Northern Highway and Nanutarra-Munjina Road, 15 km WNW of Mulga Downs Outcamp, 1.4 km SSW of Bernie Bore, Mulga Downs Station, on *Eriachne benthamii* (*Poaceae*), 2 Aug. 2015, M.N. Lyons & S.D. Lyons (holotype BRIP 67533; ITS sequence GenBank MN855218, MycoBank MB833910; isotype PERTH 08981019).

Notes — Prior to this study, *Macalpinomyces* contained 11 host-specific species restricted to *Eriachne* (*Poaceae*) in Australasia (Li et al. 2017). *Macalpinomyces collinsiae* is the twelfth species, known only from the type specimen on *E. benthamii* in north-western Australia. All species of *Macalpinomyces* are morphologically similar and can only be reliably separated by host range and molecular phylogenetic analysis.

Based on a mega-BLAST search of species of *Macalpinomyces*, the ITS sequence of *M. collinsiae* differs from the sister species *M. vankyi* (GenBank KX686918; Identities = 730/746 (98 %), 9 gaps (1 %)), and from *M. cookei* (GenBank KX686942; Identities = 732/764 (96 %), 21 gaps (2 %)). The species of *Macalpinomyces* are further illustrated on the Smut Fungi of Australia Lucid Key (Shivas et al. 2014).



Colour illustrations. *Eriachne benthamii* tussock grassland, Mulga Downs Station, Pilbara region of Western Australia (Photo credit: M.N. Lyons). Floret of *Eriachne benthamii* infected with *Macalpinomyces collinsiae*; spores and sterile cells. Scale bars = 1 mm; 10 µm.

Phylogram obtained from a maximum likelihood analysis of the ITS region of rDNA in IQTree v. 1.7 beta (Nguyen et al. 2015) with a model test for each partition (command -m TEST -spp). aRLT values ($\geq 90\%$) (Guindon et al. 2010) and ultrafast bootstrap values ($\geq 95\%$) (Hoang et al. 2018) from 10000 replicates above nodes. Minimum spanning network (Bandelt et al. 1999) sampled from all available ITS sequences of *Macalpinomyces* on GenBank. Hashes in network indicate number of parsimony informative sites in the alignment.

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