Magnaporthiopsis species associated with patch diseases of turfgrasses in Australia

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Abstract
Isolates of Magnaporthiopsis (Magnaporthaceae, Magnaporthales) were obtained from turfgrass species with patch disease symptoms in sports fields and golf courses in eastern Australia. Patch disease was characterised by plants with root rot, vascular discoloration and dark, ectotrophic mycelium on the root surfaces. Four new species, Magnaporthiopsis dharug, M. gadigal, M. gumbaynggirr and M. yugambeh, are described based on phylogenetic analysis of concatenated partial DNA sequences of the internal transcribed spacer (ITS) region, RNA polymerase II largest subunit (RPB1) and translation elongation factor 1-alpha (TEF1α). The descriptions of the fungi include morphological characteristics and host associations. Magnaporthiopsis dharug was isolated from diseased roots of Cynodon dactylon (couch grass, Bermudagrass), Festuca rubra ssp. commutata (Chewing’s fescue) and Poa annua (winter grass); M. gadigal from diseased roots of Pennisetum clandestinum (kikuyu grass); M. gumbaynggirr from diseased roots of C. dactylon; and M. yugambeh from diseased roots of P. annua.

Keywords – ectotrophic root-infecting fungi – phylogeny – plant pathogens – Poaceae – taxonomy

Introduction
The Magnaporthales (Sordariomycetes, Ascomycota) comprises five families, Ceratosphaeriaceae, Magnaporthaceae, Ophioceraceae, Pseudohalonectriaceae and Pyriculariaceae (Zhang et al. 2011, Kaublauf et al. 2014, Luo et al. 2014, Feng et al. 2021). Members of Magnaporthaceae and Pyriculariaceae are pathogens or endophytes of monocotyledonous hosts while those of Ceratosphaeriaceae, Ophioceraceae and Pseudohalonectriaceae are saprobes of dead grasses and decaying or submerged wood (Shearer et al. 1999, Luo et al. 2014, 2015, Feng et al. 2021). The Magnaporthaceae are mainly root parasites or pathogens of grasses (Poaceae) and sedges (Cyperaceae) (Luo & Zhang 2013). Magnaporthiopsis (Magnaporthaceae) was established by Luo & Zhang (2013) to accommodate the type species, M. poae (syn. Magnaporthe poae) and two other species, M. incurstans (syn. Gaeumannomyces incurstans) and M. rhizophila (syn. Magnaporthe rhizophila). Since then, a further five new species have been listed in Species Fungorum (2022), namely, M. agrostidis (Crous et al. 2015b), M. cynodontis (Vines et al. 2020), M. maydis (Klaubauf et al. 2014), M. meyeri-festucae (Luo et al. 2017), and M. panicorum (Luo et al. 2014).

In Australia, patch diseases have been reported on Agrostis spp. (bent grass), Cynodon dactylon (couch grass, Bermudagrass), C. dactylon x C. transvaalensis (dwarf and ultradwarf hybrid couch grass).
grass), *Pennisetum clandestinum* (kikuyu grass), *Poa annua* (winter grass) and *Stenotaphrum secundatum* (buffalo grass, St Augustinegrass). Several ectotrophic root-infecting (ERI) fungi (Clarke & Gould 1993) have been shown to cause some of these patch diseases, including *Budhanggurabania cynodonticola* (cause of a severe patch disease in couch grass) (Crous et al. 2015a); *Gaeumannomyces avenae* (cause of take-all disease of hybrid couch grass) (Wong et al. 2000); *Gaeumannomyces wongoonoo* (cause of wongoonoo patch in buffalo grass) (Wong 2002); *Magnaporthiopsis agrostidis* (cause of a patch disease in bent grass) (Crous et al. 2015b); *Phialocephala bamuru* (cause of fairway patch in couch grass and kikuyu grass) (Wong et al. 2015); *Wongia griffinii* (cause of summer decline in *Cynodon* spp. and hybrids) and *W. garrettii* (cause of Adelaide patch in *Cynodon* spp. and hybrids) (Wong et al. 2012, Khemmuk et al. 2016). In the United States, *M. meyeri-festucae* was isolated from diseased roots of *Festuca* spp. and shown to cause a severe patch disease that resembled summer patch (Landschoot & Jackson 1989b, Luo et al. 2017). Vines et al. (2020) showed that *M. cynodontis* had a widespread distribution in southern United States and was the cause of canopy decline in ultradwarf hybrids of Bermudagrass. In North Carolina, Stephens (2021) isolated *M. cynodontis* from ultradwarf turf with take-all root rot symptoms but other ERI fungi, such as *Candidacolonium cynodontis*, *G. gramincola* and *G. graminis*, were also isolated from the root systems. This suite of fungi was thought to form a disease complex. Interestingly, at this site, *G. graminis* was a more severe pathogen than *M. cynodontis*, which was considered moderately pathogenic. To date, *M. cynodontis*, *M. meyeri-festucae* and *M. poae* have not been found in Australia.

There are still many patch diseases of uncertain etiology in turf grasses in Australia. This study describes four novel species of *Magnaporthiopsis* that were associated with patch disease symptoms in several turf grass species from golf courses, experimental turf plots and a sports oval in New South Wales (NSW) and a golf course in Queensland (Qld), Australia.

**Materials & Methods**

**Isolation of fungi from diseased roots**

Diseased grass samples were collected from the margins and centres of dead and dying grass patches at several NSW and Qld sites (Table 1). The root systems were washed free of soil and observed under a stereo microscope for disease symptoms. Roots with vascular discolouration and lesions were selected and cut into 5 mm long pieces, surface-sterilised in equal parts 10% aqueous sodium hypochlorite (0.3% available Cl) and 95% ethanol for 2 min., rinsed twice in sterile distilled water and plated onto ¼ strength potato dextrose agar (¼ PDA) amended with novobiocin (100 mg/L). Plates were incubated in the dark at 25°C for 3–7 d and the most commonly occurring fungal colonies were sub-cultured onto ¼ PDA to obtain pure cultures. Fungal cultures were maintained on ¼ PDA or PDA at 25°C in an incubator and, for longer storage, in sterile water at room temperature (Ellis 1979). The cultures were accessioned in the culture collection at the Queensland Plant Pathology Herbarium (BRIP), Brisbane, Australia (Table 1).

**Morphology and cultural characteristics of the fungi**

The cultural characteristics of the fungi were recorded from colonies on PDA and ¼ PDA. The diameters of the colonies on three replicate PDA plates were measured after 4 days’ incubation at 25°C in the dark.

To induce ascomata, infected root and stem material that had been washed free of soil, were placed in humid chambers and incubated in diffuse daylight at room temperature (~20°C) on a laboratory bench near a window for 12 weeks. Three PDA plates of each of the cultures were also incubated in this way. This method had successfully induced ascomata for some *Magnaporthaceae* and other ERI fungi (Wong 2002, Wong et al. 2012).
Table 1 Collection details and GenBank accession numbers of *Magnaporthiopsis* and *Gaeumannomyces* isolates included in this study.

| Species                              | Strain⁰   | Host                                      | Locality         | GenBank accessions |
|--------------------------------------|-----------|-------------------------------------------|------------------|-------------------|
|                                      |           |                                           |                  | ITS               |
| *Magnaporthiopsis agrostidis*        | BRIP 59300| *Agrostis stolonifera*                    | Little Bay, NSW  | KT364753          |
| *Magnaporthiopsis cynodontis*        | CBS 141700| *Cynodon dactylon* × *C. transvaalensis*  | Humble, Texas, USA | KJ855508          |
| *Magnaporthiopsis dharug*            | BRIP 62303a| *Cynodon dactylon*                        | Manly, NSW       | OM890901          |
|                                      | BRIP 62295a| *Festuca rubra* spp. *commutata*          | Cobbitty, NSW    | OM890902          |
|                                      | BRIP 62304a| *Poa annua*                               | Auburn, NSW      | OM890903          |
| *Magnaporthiopsis gadigal*           | BRIP 63069a| *Pennisetum clandestinum*                 | Darlinghurst, NSW| OM890904          |
| *Magnaporthiopsis gumbaynggirr*      | BRIP 63053a| *Cynodon dactylon*                        | Coffs Harbour, NSW| OM890905          |
| *Magnaporthiopsis incurstans*        | M51       | *Zoysia matrella*                         | Kansas, USA      | JF414846          |
| *Magnaporthiopsis meyeri-festucae*   | M84       |                                           | New Brunswick, New Jersey, USA | KM009160 |
| *Magnaporthiopsis panicorum*         | CBS 137160| *Panicum sp.*                             | New Jersey, USA  | KF689643          |
| *Magnaporthiopsis poae*              | TAP35     | *Agrostis stolonifera*                    | Wilmington, North Carolina, USA | KJ855511 |
| *Magnaporthiopsis rhizophila*        | M22       | Unknown                                   | Unknown          | JF414833          |
| *Magnaporthiopsis yugambeh*          | BRIP 63074a| *Poa annua*                               | Arundel, Qld     | OM890906          |
| Outgroup                             | CBS 187.65| *Avena sativa*                            | The Netherlands  | JX134668          |
| *Gaeumannomyces avenue*              | CBS 235.32| *Oryza sativa*                            | Arkansas, USA    | JX134669          |

| Species                              | Strain⁰   | Host                                      | Locality         | GenBank accessions |
|                                      |           |                                           |                  | RPB1              |
| *Magnaporthiopsis agrostidis*        | BRIP 59300| *Agrostis stolonifera*                    | Little Bay, NSW  | KT364755          |
| *Magnaporthiopsis cynodontis*        | CBS 141700| *Cynodon dactylon* × *C. transvaalensis*  | Humble, Texas, USA | KJ855508         |
| *Magnaporthiopsis dharug*            | BRIP 62303a| *Cynodon dactylon*                        | Manly, NSW       | OM890901          |
|                                      | BRIP 62295a| *Festuca rubra* spp. *commutata*          | Cobbitty, NSW    | OM890902          |
|                                      | BRIP 62304a| *Poa annua*                               | Auburn, NSW      | OM890903          |
| *Magnaporthiopsis gadigal*           | BRIP 63069a| *Pennisetum clandestinum*                 | Darlinghurst, NSW| OM890904          |
| *Magnaporthiopsis gumbaynggirr*      | BRIP 63053a| *Cynodon dactylon*                        | Coffs Harbour, NSW| OM890905          |
| *Magnaporthiopsis incurstans*        | M51       | *Zoysia matrella*                         | Kansas, USA      | JF710440          |
| *Magnaporthiopsis meyeri-festucae*   | M84       |                                           | New Brunswick, New Jersey, USA | KM009184 |
| *Magnaporthiopsis panicorum*         | CBS 137160| *Panicum sp.*                             | New Jersey, USA  | KF689613          |
| *Magnaporthiopsis poae*              | TAP35     | *Agrostis stolonifera*                    | Wilmington, North Carolina, USA | KJ855533 |
| *Magnaporthiopsis rhizophila*        | M22       | Unknown                                   | Unknown          | JF710431          |
| *Magnaporthiopsis yugambeh*          | BRIP 63074a| *Poa annua*                               | Arundel, Qld     | OM890906          |
| Outgroup                             | CBS 187.65| *Avena sativa*                            | The Netherlands  | JX134722          |
| *Gaeumannomyces avenue*              | CBS 235.32| *Oryza sativa*                            | Arkansas, USA    | JX134694          |

1 BRIP, Queensland Plant Pathology Herbarium, Brisbane, Queensland, Australia; CBS, Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands.
2 NSW, New South Wales; Qld, Queensland.

**DNA Extraction, PCR Amplification and Sequencing**

Isolates were grown on PDA for 14 days at room temperature (approx. 25°C). Mycelium was scraped off the PDA cultures and macerated with 0.5 mm glass beads (Daintree Scientific, Australia) in a Tissue Lyser (Qiagen, Australia) for 2 min. Genomic DNA was extracted with the Gentra Puregene DNA Extraction Kit (Qiagen) according to the manufacturer’s instructions. Primers for the amplification and sequencing of the internal transcribed spacer (ITS) region, and partial regions of the RNA polymerase II largest subunit (*RPB1*) and translation elongation factor 1-alpha (*TEF1α*) were the same as in Zhang et al. (2011). The PCR products were purified and sequenced in both directions by Macrogen Inc. (South Korea).
All sequences generated in this study were assembled using Geneious Prime 2022 (Biomatters Ltd) and deposited in GenBank (Table 1). Sequences were aligned with *Magnaporthiopsis* species obtained from GenBank (Table 1) using the MAFFT alignment algorithm (Katoh & Stanley 2013) in Geneious. *Gaeumannomyces avenae* (CBS 187.65) and *G. graminis* (CBS 235.32) were used as the outgroup. Maximum likelihood (ML) analysis was run using the RAxML v. 8.2.11 (Stamatakis 2014) plug-in in Geneious starting from a random tree topology. The nucleotide substitution model used was general time-reversible (GTR) with a gamma-distributed rate variation. The Bayesian analysis was performed using the MrBayes v.3.2.6 (Ronquist & Huelsenbeck 2003) plug-in in Geneious. To remove the need for a priori model testing, the Markov chain Monte Carlo (MCMC) analysis was set to sample across the entire GTR model space with a gamma-distributed rate variation across the nucleotide sites. Five million random trees were generated using the MCMC procedure with four chains. The sample frequency was set at 100 and the temperature of the heated chain was 0.1. “Burn-in” was set at 25%, after which the log-likelihood values were stationary. The alignments and phylogenetic tree were deposited in TreeBASE under accession number S29597. (see Reviewers Access URL below).

http://purl.org/phylo/treebase/phylows/study/TB2:S29597?x-access-code=42d4fe50b3953bbdf5607fecd259928f&format=html

### Results

**Isolation of fungi from diseased roots**

*Magnaporthiopsis* spp. were consistently isolated from the diseased roots of several turfgrass hosts in eastern Australia (Table 1). Phylogenetic analysis showed that the isolates belonged to a monophyletic clade that included the generic type, *M. poae*. *Magnaporthiopsis* sp. (BRIP 63069a) was consistently isolated from the diseased roots of dying kikuyu grass, which occurred in patches on a sports oval at Darlinghurst, NSW, in the summer of 2015. The disease persisted into autumn, after which the symptoms faded in winter, and reappeared the following spring.

Three *Magnaporthiopsis* spp. (BRIP 62303a, BRIP 62304a, BRIP 62295a) were isolated from discoloured roots of couch grass and winter grass at two golf courses as well as from Chewing’s fescue in experimental turf plots at the Plant Breeding Institute, University of Sydney, at Cobbitty, NSW. The vascular discoloration in the roots was characteristic of that caused by ERI fungi. The disease occurred as distinct, roughly circular brown patches, up to 25 cm in diameter, exhibiting chlorotic leaves and necrotic leaves and stems.

*Magnaporthiopsis* sp. (BRIP 63053a) was consistently isolated from diseased roots of couch grass at a golf course at Coffs Harbour, NSW, which had shown patch disease symptoms for several years on fairways. *Magnaporthiopsis* sp. (BRIP 63074a) was isolated from the diseased roots of *P. annua* in a mixed *P. annua*/bent grass golf green at Arundel Hills Country Club, Arundel, Qld. The grass was chlorotic, unthrifty, and dying within patches up to 50 cm in diameter. The roots showed extensive vascular discoloration and colonisation by dark mycelium, typical of infection by ERI fungi.

**Morphology and cultural characteristics of the fungi**

Colonies of the four *Magnaporthiopsis* spp. produced anamorphic structures on ¼ PDA and PDA at 25°C. Ascomata did not form on PDA or infected plant material after incubation in diffuse daylight at room temperature for 12 wk. Colony diam. on PDA after four days’ incubation at 25°C and gross colony characteristics on PDA after four weeks’ incubation at 25°C (Fig. 1) were recorded. Conidial measurements were recorded from 30 random conidia.

**Phylogenetic analysis**

A multilocus sequence analysis based on the ITS region, *RPB1* and *TEF1α* genes was used to infer the relationship of the six BRIP isolates against recognised species in *Magnaporthiopsis* (Table 1). The resultant concatenated alignment consisted of 2318 characters, including alignment...
gaps (RPB1 1–783, TEF1α 784–1762, ITS 1763–2318). The ML consensus tree inferred from the concatenated alignment is presented with bootstrap support values (BS) greater than 70% and Bayesian posterior probabilities (PP) greater than 0.95 (Fig. 2).

Figure 1 – a, b Colony and conidial morphology of M. dharug. c, d M. gadigal. e, f M. gumbaynggirr. g, h M. yugambeh on PDA plates after incubation for 4 weeks at 25°C. Scale bars: a, c, e, g = 1 cm, b, d, f, h = 10 µm.

Figure 2 – Phylogenetic tree based on maximum likelihood analysis of the combined multilocus (RPB1, TEF1α and ITS) alignment. RAxML bootstrap values (bs) greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). Isolates generated from
this study are in bold. Ex-type isolates are marked with \textsuperscript{T}. \textit{Gaeumannomyces avenae} and \textit{G. graminis} were used as the outgroup taxa.

Phylogenetic and morphological analysis supports the establishment of four new species of \textit{Magnaporthiopsis}. The novel species were registered in MycoBank. The species epithets were derived from Indigenous Australian languages.

\textbf{Magnaporthiopsis dharug} P Wong, YP Tan, TL Weese and RG Shivas, sp. nov.  
MycoBank number: MB 843153  
Etymology – The name acknowledges the Dharug people, traditional owners of the country where the fungus was first found.

On PDA, colonies reaching 6.0 cm diam. after 4 days at 25°C in the dark; sparse to moderate greyish white aerial mycelium, colonies tan in colour becoming darker with age and forming greyish-tan mycelial aggregations resembling “crusts” on the agar surface; reverse dark grey in the centre, paler at the margin. Mycelium hyaline becoming dark grey to brown with age; hyphae septate, branched, smooth, 1–3 µm wide, forming mycelial strands and curling back at the margins. \textit{Conidiophores} hyaline, single or branched. \textit{Conidiogenous cells} hyaline, phialidic, straight or curved, 5–30 x 2–4 µm, narrowed at the base. \textit{Conidia} hyaline, ovoid or cylindrical, mostly straight or slightly curved, 6–12 (–14) x 2–4 µm, apex rounded, base acute, asceptate, hyaline, smooth. \textit{Ascomata} not observed in culture or on infected material.

Holotype – AUSTRALIA, New South Wales, Manly, on diseased roots of \textit{Cynodon dactylon}, Jan. 2015, P.T.W. Wong PW15015 (BRIP 62303a, permanently preserved in a metabolically inactive state).

Other specimens examined – AUSTRALIA, New South Wales, Cobbitty, from diseased roots of \textit{Festuca rubra} ssp. \textit{commuta} (Chewing’s fescue cv. Bridgeport), Jan. 2015, J. Kaapro & P.T.W. Wong PW15007 (BRIP 62295a); Auburn, from diseased roots of \textit{Poa annua}, Feb. 2015, J. Kaapro & P.T.W. Wong PW15016 (BRIP 62304a).

Notes – \textit{Magnaporthiopsis dharug} was closely related to \textit{M. poae} in the phylogenetic analysis (Fig. 2). Morphologically \textit{M. dharug} has larger conidia (6–12 (–14) x 2–4 µm) than \textit{M. poae} (3–8 x 1–3 µm). The colonies of \textit{M. dharug} on PDA are dark tan with small greyish-tan superficial crusts (Fig. 1). By contrast, the colonies of \textit{M. poae} are grey or olivaceous brown with thick strands of dark mycelium radiating away from the centre (Landschoot & Jackson 1989b). The colonies of \textit{M. rhizophila}, which is sister to \textit{M. dharug} and \textit{M. poae}, are dark grey to olivaceous black (Scott & Deacon 1983). \textit{Magnaporthiopsis dharug} has not produced ascomata on PDA or infected plant material incubated in alternating diffuse daylight and darkness on a laboratory bench after 3 months. Both \textit{M. poae} and \textit{M. rhizophila} readily produce ascomata in culture and on infected plant material (Landschoot & Jackson 1989b, Scott & Deacon 1983).

\textbf{Magnaporthiopsis gadigal} P Wong, YP Tan, TL Weese and RG Shivas, sp. nov.  
MycoBank number: MB 843154  
Etymology – The name acknowledges the Gadigal people, traditional owners of the country where the fungus was found.

On PDA, colonies reaching 6.5 cm diam. after 4 days at 25°C in the dark; moderately abundant grey aerial mycelium, becoming olivaceous brown with age and forming at first white, becoming dark grey to dark brown crust-like mycelial aggregations on the agar surface in older cultures (> 4 wk); reverse dark grey to black. Mycelium hyaline, becoming dark grey to olivaceous brown with age; hyphae septate, branched, smooth, 2–6 µm wide, forming mycelial strands and curling back at the margins. \textit{Conidiophores} hyaline, single or branched. \textit{Conidiogenous cells} hyaline, phialidic, straight or curved, 5–20 x 2–4 µm, narrowed at the base and tapering at the apex. \textit{Conidia} hyaline, ovoid or cylindrical, mostly straight or slightly curved, 6–10 (–12) x 3–4 µm, apex rounded, base acute, asceptate, hyaline, smooth. \textit{Ascomata} not observed in culture or on infected material.

Holotype – AUSTRALIA, New South Wales, Darlinghurst, from rotted roots of \textit{Pennisetum...
clandestinum, June 2015, P.T.W. Wong PW15128 (BRIP 63069a, permanently preserved in a metabolically inactive state).

Notes – Magnaporthiopsis gadigal was closely related to M. gumbaynggirr and M. incrustans in the phylogenetic analysis (Fig. 2). Magnaporthiopsis gadigal has black colonies with small superficial crust-like mycelial aggregations that are white, becoming dark grey to dark brown in older cultures (Fig. 1), which differentiates it morphologically from other species. Magnaporthiopsis gadigal was isolated from the diseased roots of P. clandestinum, which is not a plant species associated with either M. gumbaynggirr or M. incrustans.

**Magnaporthiopsis gumbaynggirr** P Wong, YP Tan, TL Weese and RG Shivas, sp. nov.

MycoBank number: MB 843155

Etymology – The name acknowledges the Gumbaynggirr people, traditional owners of the country where the fungus was found.

On PDA, colonies reaching 5.5 cm diam. after 4 days at 25°C in the dark; moderately abundant grey aerial mycelium, becoming darker with age and forming grey to black, raised, mycelial aggregations resembling “crusts” on the agar surface, especially at the centre of the colonies; reverse dark grey to black, paler at the margin. Mycelium hyaline becoming dark grey to black with age; hyphae septate, branched, smooth, 1–3 µm wide, forming mycelial strands and curling back at the margins. Conidiophores hyaline, single or branched. Conidiogenous cells hyaline, phialidic, straight or curved, 5–29 x 2–4 µm, narrowed at the base. Conidia hyaline, mostly ovoid or cylindrical, straight or slightly curved, 5–10 x 3–4 µm, apex rounded, base acute, aseptate, hyaline, smooth. Ascomata not observed in culture or on infected material.

Holotype – AUSTRALIA, New South Wales, Coffs Harbour, from diseased roots of *Cynodon dactylon*, June 2015, P.T.W. Wong PW15102, (BRIP 63053a, permanently preserved in a metabolically inactive state).

Notes – Magnaporthiopsis gumbaynggirr was sister to M. incrustans (Landschoot & Jackson 1989a) in the phylogenetic analysis (Fig. 2). Morphologically, M. gumbaynggirr had larger conidia (5–10 x 3–4 µm) than M. incrustans (3–6 x 2–3 µm).

**Magnaporthiopsis yugambeh** P Wong, YP Tan, TL Weese and RG Shivas, sp. nov. Figs 1g, h

MycoBank number: MB 843156

Etymology – The name acknowledges the Yugambeh people, traditional owners of the country where the fungus was found.

On PDA, colonies reaching 4.0 cm diam. after 4 days at 25°C in the dark; moderately abundant grey aerial mycelium, becoming darker with age and forming small, whitish grey to dark grey mycelial aggregations resembling “crusts” on the agar surface; reverse dark grey to black, paler at the margin. Mycelium hyaline becoming dark grey to black with age; hyphae septate, branched, smooth, 1–3 µm wide, forming mycelial strands and curling back at the margins. Conidiophores hyaline, single or branched. Conidiogenous cells hyaline, phialidic, straight or curved, 5–25 x 2–4 µm, narrowed at the base. Conidia hyaline, mostly ovoid or cylindrical, straight or slightly curved, 6–10 (–12) x 2–4 µm, apex rounded, base acute, aseptate, hyaline, smooth. Microconidia hyaline, aseptate, smooth, filiform, rounded at the apex and narrowed towards the base, curved to lunate, 4–6 x 1 µm, aggregated in slimy heads. Ascomata not observed in culture or on infected material.

Holotype – AUSTRALIA, Queensland, Arundel, from diseased roots of *Poa annua*, August 2015, P.T.W. Wong PW15135, (BRIP 63074a, permanently preserved in a metabolically inactive state).

Notes – Magnaporthiopsis yugambeh was sister to M. cynodontis (Vines et al. 2020) in the phylogenetic analysis. Morphologically, the conidia of these two species are similar in size, i.e. M. yugambeh (6–12 x 3–4 µm) and M. cynodontis (7–13 x 2–6.5 µm). However, M. yugambeh produces narrow lunate microconidia (4–6 x 1 µm), which have not been reported for
M. cynodontis. These lunate microconidia resemble those produced by M. agrostidis (Crous et al. 2015b).

Discussion

All known species of Magnaporthiopsis are root-inhabiting fungi or root-infecting pathogens of grasses and cereals. Magnaporthiopsis gadigal, M. dharug, M. gumbaynggirr and M. yugambeh were consistently isolated from the roots of grasses exhibiting patch disease symptoms (Clarke & Gould 1993, Smiley et al. 2005) in eastern Australia. The pathogenicity of these fungi has yet to be demonstrated experimentally by Koch’s postulates.

Multi-gene phylogenetic analysis is the only reliable way to separate species of Magnaporthiopsis as there are few distinctive morphological or colony characteristics. With a few exceptions, such as M. meyeri-festucae, M. incrustans and M. poae, which have smaller conidia, most species of Magnaporthiopsis cannot be separated by the shape and size of conidigenous cells and conidia. Other useful phenotypic characteristics include narrow lunate microconidia (M. agrostidis and M. yugambeh) and colony colour on PDA, which is dark tan in M. dharug, and dark green in M. panicorum and M. rhizophila. This contrasts with the dark grey or black colonies generally seen in the other species of Magnaporthiopsis.

Several Magnaporthiopsis species cause severe patch diseases of grasses and cereals, e.g., M. poae (Smiley et al. 2005), M. maydis (Samra et al. 1963) and M. meyeri-festucae (Luo et al. 2017) but there is increasing evidence that some Magnaporthiopsis spp. are only moderately pathogenic (Vines et al. 2020). For example, M. agrostidis has been shown to cause a patch disease of bent grass with only symptoms of chlorotic and purple leaves in host plants predisposed by nutritional stress. The aboveground patch symptoms disappear after the application of a complete fertilizer, although the root systems continue to show browning and vascular discoloration. It is noteworthy that M. dharug, M. poae and M. rhizophila occur on the diseased roots of cool-season grasses (Poa and Festuca spp.) (Landschoot & Jackson 1989b), and that M. dharug has also been isolated from the diseased roots of C. dactylon, a warm-season grass.

Some patch diseases may be disease complexes caused by several fungal pathogens of varying pathogenicity. For example, in the southern USA, M. cynodontis is associated with canopy decline of ultradwarf Bermudagrass hybrids from which other fungal pathogens, G. graminis and G. nanograminis, have been isolated (Vines et al. 2020). Environmental conditions and management practices may cause one or other of the pathogens to become dominant. In Australia, summer decline of dwarf hybrid couch in golf greens appears to be a disease complex, as several pathogens have been isolated, including G. graminis, W. griffinii and other undescribed ERI fungi (Stirling 2000, Wong et al. 2012). The exact roles and relative importance of these fungi in causing summer decline in dwarf couch hybrids have not been established.

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