Magnaporthiopsis species associated with patch diseases of turfgrasses in Australia

Wong PTW[1], Tan YP[2,3], Weese TL[2] and Shivas RG[2,3,*]

[1]Plant Breeding Institute, University of Sydney, 107 Cobbitty Road, Cobbitty, NSW 2570, Australia
[2]Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Ecosciences Precinct, Dutton Park, Queensland 4102, Australia
[3]Centre for Crop Health, University of Southern Queensland, Toowoomba, Queensland 4350, Australia

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 discolouration 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*.

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. incrustans* (syn. *Gaeumannomyces incrustans*) 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), *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	Strain[1]	Host	Locality[2]	GenBank accessions		
				ITS	*RPB1*	*TEF1α*
Magnaporthiopsis agrostidis	BRIP 59300	*Agrostis stolonifera*	Little Bay, NSW	KT364753	KT364755	KT364756
Magnaporthiopsis cynodontis	CBS 141700	*Cynodon dactylon × C. transvaalensis*	Humble, Texas, USA	KJ855508	KP268930	KP282714
Magnaporthiopsis dharug	BRIP 62303a	*Cynodon dactylon*	Manly, NSW	**OM890901**		**OM869948**
	BRIP 62295a	*Festuca rubra* spp. commutata	Cobbitty, NSW	**OM890902**	**OM869944**	**OM869949**
	BRIP 62304a	*Poa annua*	Auburn, NSW	**OM890903**	**OM869945**	**OM869950**
Magnaporthiopsis gadigal	BRIP 63069a	*Pennisetum clandestinum*	Darlinghurst, NSW	**OM890904**	**OM869946**	**OM869951**
Magnaporthiopsis gumbaynggirr	BRIP 63053a	*Cynodon dactylon*	Coffs Harbour, NSW	**OM890905**		
Magnaporthiopsis incrustans	M51	*Zoysia matrella*	Kansas, USA	JF414846	JF710440	JF710417
Magnaporthiopsis maydis	M84			KM009160	KM009184	KM009196
Magnaporthiopsis meyeri-festucae	CBS 143324	*Festuca brevipila*	New Brunswick, New Jersey, USA	MF178146	MF178162	MF178167
Magnaporthiopsis panicorum	CBS 137160	*Panicum* sp.	New Jersey, USA	KF689643	KF689613	KF689623
Magnaporthiopsis poae	TAP35	*Agrostis stolonifera*	Wilmington, North Carolina, USA	KJ855511	KP268933	KP282717
Magnaporthiopsis rhizophila	M22	Unknown	Unknown	JF414833	JF710431	JF710407
Magnaporthiopsis yugambeh	BRIP 63074a	*Poa annua*	Arundel, Qld	**OM890906**	**OM869947**	**OM869952**
Outgroup						
Gaeumannomyces avenae	CBS 187.65	*Avena sativa*	The Netherlands	JX134668	JX134722	JX134694
Gaeumannomyces graminis	CBS 235.32	*Oryza sativa*	Arkansas, USA	JX134669	JX134723	JX134695

[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=42d4fe50b3953bbdf5607ecec259928f&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 discolouration 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 discolouration 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, *TEF1*α 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).
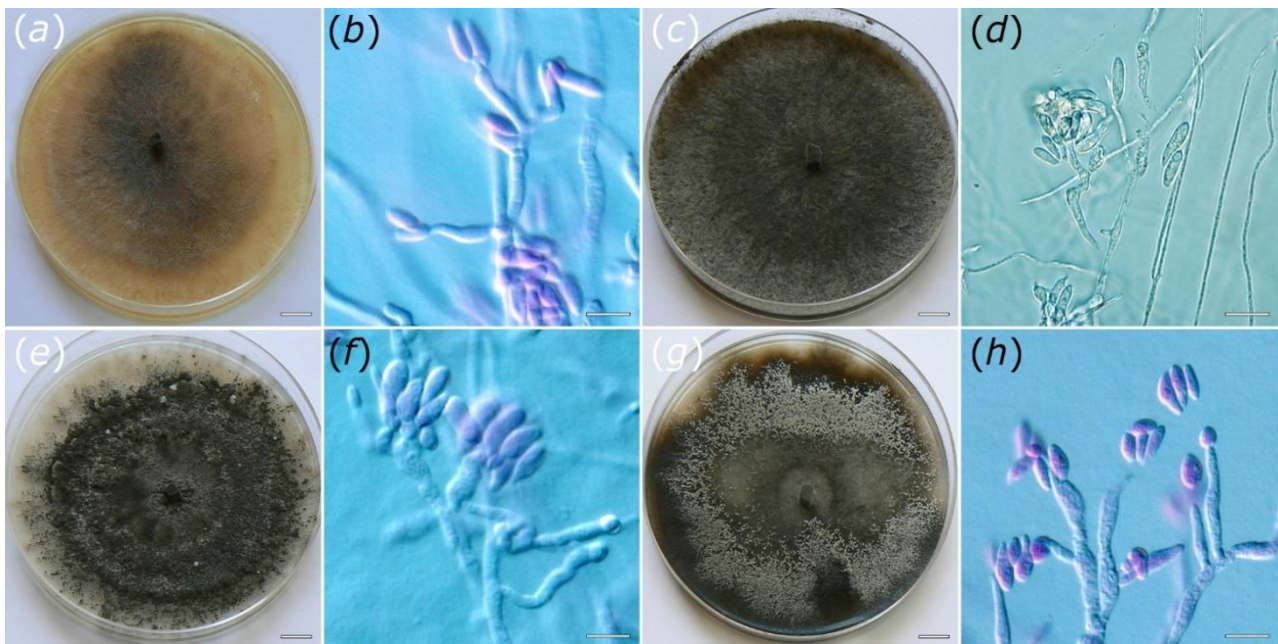

Figure 1 – a, b Colony and conidial morphology of *M. dharug*. c, d *M. gadigal*. e, f *M. gumbaynggirr*. g, h *M. yugambeh* on PDA plates after incubation for 4 weeks at 25°C. Scale bars: a, c, e, g = 1 cm, b, d, f, h = 10 µm.
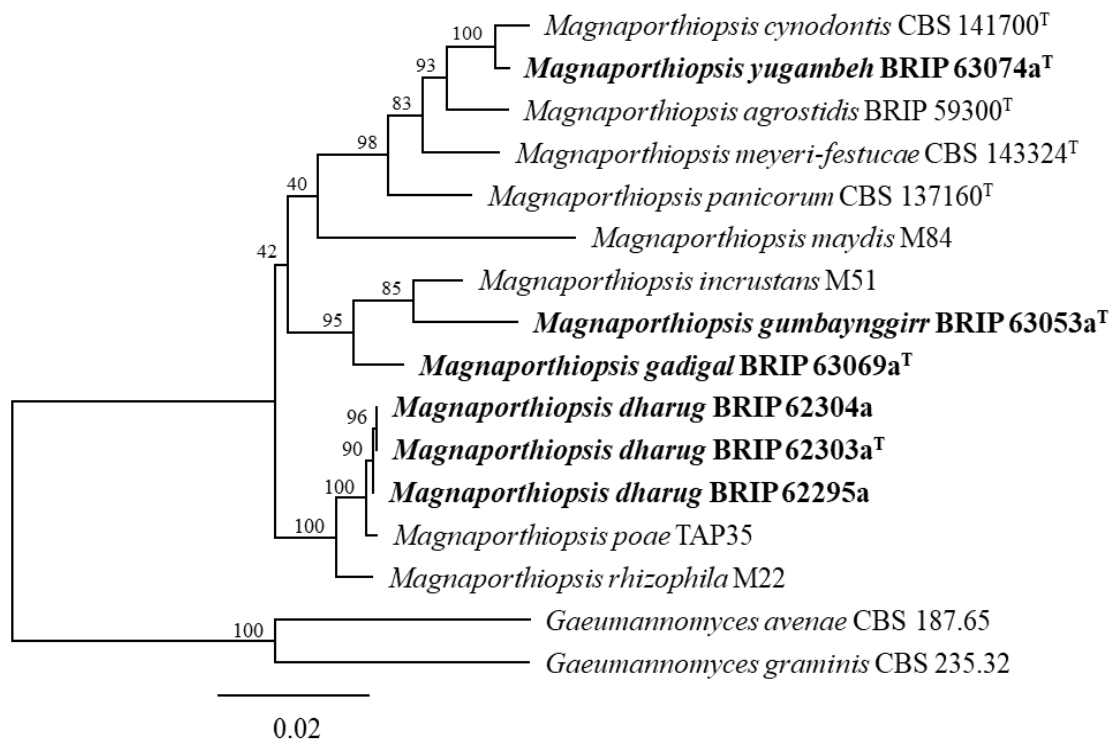

Figure 2 – Phylogenetic tree based on maximum likelihood analysis of the combined multilocus (*RPB1*, *TEF1*α and ITS) alignment. RAxML bootstrap values (bs) greater than 70% and Bayesian posterior probabilities (pp) greater than 0.95 are given at the nodes (bs/pp). Isolates generated from

this study are in bold. Ex-type isolates are marked with [T]. *Gaeumannomyces avenae* and *G. graminis* were used as the outgroup taxa.

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

Magnaporthiopsis dharug P Wong, YP Tan, TL Weese and RG Shivas, sp. nov.   Fig. 1a, b
   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. *Conidiophores* hyaline, single or branched. *Conidiogenous cells* hyaline, phialidic, straight or curved, 5–30 x 2–4 µm, narrowed at the base. *Conidia* hyaline, ovoid or cylindrical, mostly straight or slightly curved, 6–12 (–14) x 2–4 µm, apex rounded, base acute, aseptate, hyaline, smooth. *Ascomata* not observed in culture or on infected material.
   Holotype – AUSTRALIA, New South Wales, Manly, on diseased roots of *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 *Festuca rubra* ssp. *commuta* (Chewing's fescue cv. Bridgeport), Jan. 2015, *J. Kaapro & P.T.W. Wong PW15007* (BRIP 62295a); Auburn, from diseased roots of *Poa annua*, Feb. 2015, *J. Kaapro & P.T.W. Wong PW15016* (BRIP 62304a).
   Notes – *Magnaporthiopsis dharug* was closely related to *M. poae* in the phylogenetic analysis (Fig. 2). Morphologically *M. dharug* has larger conidia (6–12 – (14) x 2–4 µm) than *M. poae* (3–8 x 1–3 µm). The colonies of *M. dharug* on PDA are dark tan with small greyish-tan superficial crusts (Fig. 1). By contrast, the colonies of *M. poae* are grey or olivaceous brown with thick strands of dark mycelium radiating away from the centre (Landschoot & Jackson 1989b). The colonies of *M. rhizophila,* which is sister to *M. dharug* and *M. poae*, are dark grey to olivaceous black (Scott & Deacon 1983). *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 *M. poae* and *M. rhizophila* readily produce ascomata in culture and on infected plant material (Landschoot & Jackson 1989b, Scott & Deacon 1983).

Magnaporthiopsis gadigal P Wong, YP Tan, TL Weese and RG Shivas, sp. nov.   Fig. 1c, d
   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. *Conidiophores* hyaline, single or branched. *Conidiogenous cells* hyaline, phialidic, straight or curved, 5–20 x 2–4 µm, narrowed at the base and tapering at the apex. *Conidia* hyaline, ovoid or cylindrical, mostly straight or slightly curved, 6–10 (–12) 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, Darlinghurst, from rotted roots of *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.

Fig. 1e, f

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, aggregated in slimy heads, 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 conidiogenous 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 discolouration. 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.

Acknowledgements

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