Generic names in Magnaporthales

Ning Zhang1, Jing Luo1, Amy Y. Rossman2, Takayuki Aoki3, Izumi Chuma4, Pedro W. Crous5, Ralph Dean6, Ronald P. de Vries6,7, Nicole Donofrio8, Kevin D. Hyde9, Marc-Henri Lebrun10, Nicholas J. Talbot11, Didier Tharreau12, Yukio Tosa4, Barbara Valent13, Zonghua Wang14, and Jin-Rong Xu15

1Department of Plant Biology and Pathology, Rutgers University, New Brunswick, NJ 08901, USA; corresponding author e-mail: zhang@aesop.rutgers.edu
2Department of Botany and Plant Pathology, Oregon State University, Corvallis, Oregon 97331, USA
3Genetic Resources Center, National Agriculture and Food Research Organization, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
4Kobe University, 1-1 Rokkodai cho, Nada-ku, Kobe 657-8501, Japan
5CBS-KNAW Fungal Biodiversity Institute, Uppsalaalan 8, 3584 CT Utrecht, The Netherlands
6Department of Plant Pathology, 2510 Thomas Hall, Raleigh, NC 27695, North Carolina State University, USA
7Fungal Molecular Physiology, Utrecht University, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands
8Department of Plant and Soil Sciences, University of Delaware, 531 S. College Ave, 152 Townsend Hall, Newark, DE 19711, USA
9Center of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai, Thailand
10UMR BIOGER, INRA, AgroParisTech, Université Paris-Saclay, 78850 Thiverval-Grignon, France
11University of Exeter, Northcote House, Exeter EX4 4QJ, UK
12UMR BGPI, CIRAD, TA A 54 K, 34398 Montpellier, France
13Department of Plant Pathology, Kansas State University, Manhattan, KS 66506-5502, USA
14Fujian Agriculture and Forestry University, Fuzhou 350002, Fujian, China
15Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907, USA

Abstract: The order Magnaporthales comprises about 200 species and includes the economically and scientifically important rice blast fungus and the take-all pathogen of cereals, as well as saprotrophs and endophytes. Recent advances in phylogenetic analyses of these fungi resulted in taxonomic revisions. In this paper we list the 28 currently accepted genera in Magnaporthales with their type species and available gene and genome resources. The polyphyletic Magnaporthale 1972 is proposed for suppression, and Pyricularia 1880 and Nakataea 1939 are recommended for protection as the generic names for the rice blast fungus and the rice stem rot fungus, respectively. The rationale for the recommended names is also provided. These recommendations are made by the Pyricularia/Magnaporthale Working Group established under the auspices of the International Commission on the Taxonomy of Fungi (ICTF).

Key words: Ascomycota
Magnaporthale
Nakataea
one fungus-one name
pleomorphic fungi
Pyricularia
rice blast
take-all

INTRODUCTION

Magnaporthale (Sordariomycetes, Ascomycota) contains important pathogens of cereals and grasses, including the rice blast fungus Pyricularia oryzae (Magnaporthale oryzae), the take-all pathogen of cereals Gaeumannomyces graminis, the rice stem rot pathogen Nakataea oryzae (Magnaporthale salvinii) and the summer patch pathogen of turf grass Magnaportheopsis poae (Cannon 1994, Thongkantha et al. 2009). To date, about 200 species have been described in Magnaporthales, of which approximately 50 % are pathogens of domesticated and wild monocotyledons.

The rice blast fungus has conidial (asexual) and ascosporic (sexual) morphs and the rice stem rot fungus produces sclerotial (asexual), conidial (asexual) and ascosporic (sexual) morphs. Historically, such pleomorphy added to the difficulty in resolving taxonomic and nomenclatural problems associated with these species.

Recent advancement in gene, transcriptome and genome sequencing of Magnaporthales fungi resulted in robust phylogenies, which correspond well with the pathogenicity, ecology and biology of these species. However, the phylogenies conflict with certain traditional generic concepts based on morphology. Magnaporthale and Gaeumannomyces, for example, were shown to be polyphyletic. Taxonomic revisions have been carried out for some of these taxa in recent publications (Luo & Zhang 2013, Klbaugh et al. 2014, Luo et al. 2015a). In this paper, we list 28 accepted genera in Magnaporthales and provide the rationale for the recommended genera if there is competition.
A list of accepted generic names in Magnaporthales, with the type species, is compiled in Table 1 including references that serve as the basis for recognizing these genera. This follows approval of their usage by the Pyricularia/Magnaporth Working Group, without prejudice. Cases that require action to be approved by the Nomenclature Committee for Fungi (NCF) are indicated by an asterisk in that Table.

RECOMMENDATIONS

(A) = a name typified by an asexual morph, (S) = a name typified by a sexual morph.

Use Nakataea Hara 1939 (A) rather than Magnaportha R.A. Krause & R.K. Webster 1972 (S)

Cattaneo (1876) first named the rice stem rot pathogen as Sclerotium oryzae based on the sclerotal morph. In the same paper he also described Leptosphaeria salvinii, which was later recognized as the sexual morph of the same fungus (Tullis 1933). Hara (1939) named the conidial morph of the species Nakataea sigmoidea. Krause & Webster (1972) then established the new generic name Magnaportha, typified by the ascosporic morph, to accommodate the rice stem rot pathogen as Magnaportha salvinii, as necessitated by the nomenclatural rules then in force. Sclerotium and Leptosphaeria currently belong in Basidiomycota and Dothideomycetes respectively (Xu et al. 2010), and are therefore not applicable to this sordariomycetous species. Nakataea and Magnaportha are congeneric and their type species, Nakataea sigmoidea and Magnaportha salvinii, refer to the same species (Krause & Webster 1972). Subsequent to the ending of the separate naming of morphs of the same fungus species in 2011, under Art. 59.1 of the International Code of Nomenclature for algae, fungi, and plants (ICN; McNeill et al. 2012), Luo et al. (2013) made a new combination for the rice stem rot fungus as Nakataea oryzae, using the oldest legitimate generic name and species epithet. Those authors did not, however, formally propose the rejection or suppression of the later sexually typified names as currently required by Art. 57.2. We note that it is proposed that this requirement be eliminated from the ICN in 2017 (Hawksworth 2015), but it is currently in force.

Use Pyricularia oryzae Cavara 1892 (A) rather than Magnaportha oryzae (Catt.) B.C. Couch 2002 (S)

In 1880, Saccardo established the generic name Pyricularia based on the asexually typified P. grisea on crabgrass. The rice isolates were designated as P. oryzae in 1892 by Cavara, which now is known as the rice blast fungus. Since then, over 50 species have been listed as Pyricularia that cause blast diseases of monocotyledonous plants.

The sexual morph of Pyricularia was first observed in 1970 from laboratory crossing experiments and believed to belong to Magnaportha because of the similarity in ascospore morphology (Hebert 1970, Barr 1977, Couch & Kohn 2002). However, recent phylogenetic and phylogenomic analyses demonstrated that the sexually typified genus Magnaportha was polyphyletic. The rice blast fungus is not congeneric with the type species of Magnaportha, M. salvinii, and the placement of the rice blast fungus in Magnaportha was based on an incorrect morphological identification (Zhang et al. 2011, Luo & Zhang 2013, Luo et al. 2014, Murata et al. 2014, Luo et al. 2015a). This is not a nomenclatural issue because the generic names Magnaportha and Pyricularia are not congeneric and so do not compete for priority.

Pyricularia and Magnaportha are currently both widely used generic names, and the rice blast fungus is an economically and scientifically important species that deserves much caution. The Pyricularia/Magnaporth Working Group has considered the possibility of conserving the name Magnaportha over Pyricularia. However, such conservation would require a change in the type species of the genus Magnaportha, and would cause numerous name changes for those species currently placed in Pyricularia.

The asexually typified generic name Pyricularia is the correct name for the rice blast fungus, which corresponds well with pathogenicity and ecological and evolutionary features. The name Pyricularia oryzae should therefore be used for the rice blast fungus. The synonym Magnaportha oryzae, can nevertheless continue to be mentioned in publications as “Pyricularia oryzae (syn. Magnaportha oryzae)”. This practice will help to bridge a potential gap in the literature and knowledge for this important species.

Use Clasterosporium Schwein. 1832 (A) rather than Clasterosphaeria Sivan. 1984 (S)

The generic name Clasterosphaeria, typified by C. cyperi, was established for the sexual morph of Clasterosporium cyperi and includes only two names. The generic name Clasterosporium based on C. caricinum includes 158 names, many of which have been placed in other genera. Whether or not Clasterosphaeria cyperi is congeneric with Clasterosporium caricinum is not known, although this seems likely given that both occur on Cyperaceae. If this is the case, use of the older, more commonly used generic name Clasterosporium is recommended.

Use Gaeumannomyces Arx & D.L. Olivier 1952 (S) rather than Harpophora Gams 2000 (A)

The generic name Gaeumannomyces, typified by G. graminis, has long been used for the cause of take-all of wheat disease (Walker 1972, 1980). Harpophora was established for philophora-like species that were known to be asexual morphs related to Gaeumannomyces and Magnaportha but did not produce a sexual morph (Gams 2000). With the change to one name, Harpophora based on H. radicicola is to be considered a synonym of Gaeumannomyces, based on phylogeny (Luo et al. 2015b). Given the greater number of species, priority, and numerous reports, we see no reason not to use the first published name, Gaeumannomyces.

ACKNOWLEDGMENTS

This work was partially supported by the National Science Foundation of the United States (grant number DEB 1145174 and DEB 1452971) to Ning Zhang.
| Taxa                          | Type species                                                                 | Number of species | GenBank accession numbers for gene and genome sequence data*  |
|------------------------------|-------------------------------------------------------------------------------|-------------------|---------------------------------------------------------------|
| **MAGNAPORTHACEAE**          |                                                                               |                   |                                                              |
| *Buergenerula* Syd. in Annls mycol. 34: 392. 1936. | *Buergenerula biseptata* (Rostr.) Syd. 1936. *(Metasphaeria biseptata Rostr. 1904).* | 4                 | *Buergenerula spartinae:* transcriptome (SRX798618) (Luo et al. 2015a). |
| *Bussabanomyces* Klaubauf et al. in Stud. Mycol. 79: 100. 2014. | *Bussabanomyces longisporus* (Bussaban) Klaubauf et al. 2014. *(Pyricularia longispora Bussaban 2003).* | 1                 | *Bussabanomyces longisporus:* transcriptome (SRX798619) (Luo et al. 2015a). |
| *Ceratosphaerella* Huhndorf et al. in Mycologia 100: 941. 2008. | *Ceratosphaerella castillensis* (C.L. Sm.) Huhndorf et al. 2008. | 2                 | Ceratosphaerella castillensis: ITS (EU527997), LSU (EU528003) (Huhndorf et al. 2008). |
| *Ceratosphaeria* Niessl in Verh. nat. Ver. Brünn 14: 203. 1876. | *Ceratosphaeria lampadophora* (Berk. & Broome) Niessl 1876. | 34                | Ceratosphaeria lampadophora: ITS (AY761088), LSU (AY346270) (Huhndorf et al. 2008). |
| *Clasterosphorium* Schwein. in Trans. Am. phil. Soc., New Series 4: 300. 1832. | *Clasterosphorium carinicum* Schwein. 1832. | 158               |                                                              |
| *Clavatispora* K.D. Hyde in Mycotaxon 55: 276. 1995. | *Clavatispora muscicola* K.D. Hyde 1995. | 1                 |                                                              |
| *Falciphora* J. Luo & N. Zhang in Mycologia 107: 643. 2015. | *Falciphora oryzae* (Z.L. Yuan et al.) J. Luo & N. Zhang 2015. | 1                 | Falciphora oryzae genome (JNV01000000) (Xu et al. 2014). |
| *Gaemumannomyces* Arx & D.L., Olivier in Trans. Brit. mycol. Soc. 35: 32. 1952. | *Gaemumannomyces graminis var. graminis* (Sacc.) Arx & D.L. Olivier 1952. | 7                 | Gaemumannomyces graminis var. avenae: transcriptome (SRX798620) (Luo et al. 2015a); Gaemumannomyces graminis var. graminis: transcriptome (SRX798621) (Luo et al. 2015a); Gaemumannomyces graminis var. tritici: genome (ADBL00000000) (Okagaki et al. 2015). |
| *Herbampulla* Scheuer & Nograkse in Mycotaxon 47: 419. 1993. | *Herbampulla crassiortis* Scheuer & Nograkse 1993 | 1                 |                                                              |
| *Kohlmyeriopsis* Klaubauf et al. in Stud. Mycol. 79: 101. 2014. | *Kohlmyeriopsis medullaris* (Kohlm., Volkm.-Kohlm. & O.E. Erikss.) Klaubauf et al. 2014. | 1                 | Kohlmyeriopsis medullaris: SSU(FJ176801), ITS(KM484852), LSU(FJ176801), RPB1(KM485069) (Klaubauf et al. 2014). |
| *Magnaporthiopsis* J. Luo & N. Zhang in Mycologia 105: 1021. 2013. | *Magnaporthiopsis poae* (Landsch. & N. Jacks.) J. Luo & N. Zhang 2013. | 5                 | Magnaporthiopsis incurstans: genome (SRX795321), transcriptome (SRX798625) (Luo et al. 2015a); Magnaporthiopsis panicorum: transcriptome (SRX798626) (Luo et al. 2015a); Magnaporthiopsis poae: genome (ADBL01000000) (Okagaki et al. 2015); Magnaporthiopsis rizospha: genome (SRX798599), transcriptome (SRX798627) (Luo et al. 2015a). |
| *Muraeriata* Huhndorf et al. in Mycologia 100: 948. 2008. | *Muraeriata collapsa* Huhndorf, Greif, Mugambi & A.N. Mill. 2008. | 2                 | Muraeriata collapsa: LSU (EU527996) (Huhndorf et al. 2008). |
### Table 1. (Continued).

| Taxa | Type species | Number of species | GenBank accession numbers for gene and genome sequence data** |
|------|--------------|-------------------|-------------------------------------------------------------|
| *Nakataea* Hará, Diseases Rice Plant, 2nd ed.: 185. 1939.  
= Magnaporthe R.A. Krause & R.K. Webster in Mycologia 64: 110. 1972. | *Nakataea oryzae* (Catt.) J. Luo & N. Zhang 2013. | 7 | *Nakataea oryzae*: genome (SRX798605), transcriptome (SRX798628) (Luo et al. 2015a). |
| **Omnidemptus** P.F. Cannon & Alcorn in Mycologia 51: 483. 1994. | **Omnidemptus affinis** P.F. Cannon & Alcorn 1994. | 1 | **Omnidemptus affinis**: transcriptome (SRX798629) (Luo et al. 2015a). |
| *Pseudophialophora* J. Luo & N. Zhang in Mycologia 106: 581. 2014. | *Pseudophialophora eragrostis* J. Luo & N. Zhang 2014. | 8 | *Pseudophialophora eragrostis*: transcriptome (SRX798634) (Luo et al. 2015a);  
*Pseudophialophora panicorum*: transcriptome (SRX798635) (Luo et al. 2015a);  
*Pseudophialophora schizachyrii*: transcriptome (SRX798637) (Luo et al. 2015a). |
| *Pyriculariopsis* M.B. Ellis, Demat. Hyphom.: 206. 1971. | *Pyriculariopsis parasitica* (Sacc. & Berl.) M.B. Ellis 1971. | 1 | *Pyriculariopsis parasitica*: LSU(DQ341514) (Klaubauf et al. 2014). |
| **Slopeiomyces** Klaubauf et al. in Stud. Mycol. 79: 102. 2014. | **Slopeiomyces cylindrosporus** (D. Hornby et al.) Klaubauf et al. 2014. | 1 | **Slopeiomyces cylindrosporus**: transcriptome (SRX798639) (Luo et al. 2015a). |
| **ophioceraceae** | **Ophioceras** Sacc., Syll. Fung. 2: 358. 1883. | 33 | **Ophioceras dolichostomum**: genome (SRX798611) (Luo et al. 2015a);  
**Ophioceras commune**: transcriptome (SRX798630) (Luo et al. 2015a);  
**Ophioceras leptosporum**: transcriptome (SRX798632) (Luo et al. 2015a). |
| **Pseudohalonectria** Minoura & T. Muroi in Trans. Mycol. Soc. Japan 19: 132. 1978. | **Pseudohalonectria lignicola** Minoura & T. Muroi 1978. | 13 | **Pseudohalonectria lignicola**: genome (SRX798616), transcriptome (SRX798633) (Luo et al. 2015a). |
| **pyriculariaceae** | **Bambusicularia** Klaubauf et al. in Stud. Mycol. 79: 104. 2014. | 1 | **Bambusicularia brunnea**: ITS(KM484830), LSU(KM484948), ACT(AB274449), CAL(AB274482), RPB1(KM485043) (Klaubauf et al. 2014). |
| | **Barretomyces** Klaubauf et al. in Stud. Mycol. 79: 104. 2014. | 1 | **Barretomyces calathaeae**: ITS(KM484831), LSU(KM484950), ACT(KM485162), CAL(KM485231), RPB1(KM485045) (Klaubauf et al. 2014). |
| | **Deightoniella** S. Hughes in Mycol. Pap. 48: 27. 1952. | 20 | **Deightoniella africana**: S. Hughes 1952. |
| | **Macgarvieomyces** Klaubauf et al. in Stud. Mycol. 79: 106. 2014. | 2 | **Macgarvieomyces borealis**: SSU(DQ341511), ITS(KM484854), LSU(DQ341511), ACT(KM485170), CAL(KM485239), MCM7(KM009174), RPB1(KM485070), TEF1(KM009198) (Klaubauf et al. 2014, Luo et al. 2015a);  
**Macgarvieomyces juncicola**: transcriptome sequenced (SRX798624) (Luo et al. 2015a). |
| | **Neopyricularia** Klaubauf et al. in Stud. Mycol. 79: 108. 2014. | 1 | **Neopyricularia commelinicola**: SSU(KM009211), ITS(FJ850122), LSU(KM484985), ACT(KM485175), CAL(KM485243), MCM7(KM009175), RPB1(KM485087), TEF1(KM009199) (Klaubauf et al. 2014, Luo et al. 2015a). |
| | **Proxipyricularia** Klaubauf et al. in Stud. Mycol. 79: 109. 2014. | 1 | **Proxipyricularia zingiberis**: ITS(KM484869), LSU(KM484986), ACT(AB274448), CAL(KM485244), RPB1(KM485088) (Klaubauf et al. 2014). |
**Table 1.** (Continued.)

| Taxa                        | Type species                          | Number of species | GenBank accession numbers for gene and genome sequence data** |
|-----------------------------|---------------------------------------|-------------------|-------------------------------------------------------------|
| *Pseudopyricularia* Klaubauf et al. in Stud. Mycol. 79: 109. 2014. | *Pseudopyricularia kyllingiae* Klaubauf et al. 2014. | 3 | *Pseudopyricularia kyllingiae*: ITS(KM484876), LSU(KM484992), ACT(AB274451), CAL(AB274484), RPB1(KM485096) (Klaubauf et al. 2014). |
| *Pyricularia* Sacc. in Michelia 2: 20. 1880. | *Pyricularia grisea* Sacc. 1880. | 55 | *Pyricularia grisea*: transcriptome (SRX798638) (Luo et al. 2015a); genome (PRJEB7653 at http://genome.jouy.inra.fr/gemsi) |
| *Xenopyricularia* Klaubauf et al. in Stud. Mycol. 79: 116. 2014. | *Xenopyricularia zizaniiolina* (Hashioka) Klaubauf et al. 2014. | 1 | *Xenopyricularia zizaniiolina*: transcriptome (SRX798640) (Luo et al. 2015a). |

** Unpublished genome data are not listed.

**REFERENCES**

Barr ME (1977) *Magnaporth, Telimerella, and Hyponecia* (*Physoporellaceae*). Mycologia 69: 952–966.

Cannon PF (1994) The newly recognized family *Magnaportheaceae* and its interrelationships. *Systema Ascomycetum* 13:25–42.

Cattanéo A (1876) Sulla *Sclerotium oryzae*, nuovo parasità vegetale, che ha devastato nel corrente anno molto risaie di Lombardia e del Novaresi. *Rendic. R. Lombard., Milano*, 2 ser. 9: 801–807.

Couch BC, Kohn LM (2002) A multilocus gene genealogy concordant with host preference indicates segregation of a new species, *Magnaporth oryzae*, from *M. grisea*. *Mycologia* 94: 683–693.

Dean RA, Talbot NJ, Ebbole DJ, Farman ML, Mitchell TK, et al. (2005) The genome sequence of the rice blast fungus *Magnaporth grisea*. *Nature* 434: 980–986.

Gams W (2000) *Phialophora* and some similar morphologically little-differentiated anamorphs of divergent ascomycetes. *Studies in Mycology* 45: 187–199.

Hara, K (1939) The Diseases of the Rice-plant. 2nd edn. Gifu: Japanese Society for Fungi.

Hebert TT (1970) The perfect stage of *Pyricularia grisea*. *Phytopathology* 61: 83–87.

Huhndorf SM, Greif M, Mugambi GK, Miller AN (2008) Two new genera in the *Magnaporthaceae*, a new addition to *Ceratosphaeria* and two new species of *Lentomitella*. *Mycologia* 100: 940–955.

Klaubauf S, Tharreau D, Fournier E, Groenewald JZ, Crous PW, et al. (2014) Resolving the polyphyletic nature of *Pyricularia* (*Pyriculariaceae*). *Studies in Mycology* 79: 85–120.

Krause RA, Webster RK (1972) The morphology, taxonomy, and sexuality of the rice stem rot fungus, *Magnaporthe salvinii* (Ceratosphaeria salvinii). *Mycologia* 64: 103–114.

Luo J, Qiu H, Cai G, Wagner NE, Bhattacharya D, et al. (2015a) Phylogenomic analysis uncovers the evolutionary history of nutrition and infection mode in rice blast fungus and other *Magnaporthales*. *Scientific Reports* 5: 9448.

Luo J, Walsh E, Zhang N (2015b) Toward monophyletic generic concepts in *Magnaporthales*: species with *Harpophora* asexual states. *Mycologia* 107: 641–646.

Luo J, Zhang N (2013) *Magnaporphiopsis*, a new genus in *Magnaporthaceae* (*Ascomycota*). *Mycologia* 105: 1019–1029.

McNeill J, Barrie FF, Buck WR, Demoulin V, Greuter W, et al. (2012) International code of nomenclature for algae, fungi, and plants (*Melbourne Code*). [Regnum Vegetabile no. 154.] Königstein: Koeltz Scientific Books.

Murata N, Aoki T, Kusaba M, Tosa Y, Chuma I (2014) Various species of *Pyricularia* constitute a robust clade distinct from *Magnaporthe salvinii* and its relatives in *Magnaporthaceae*. *Journal of General Plant Pathology* 80: 66–72.

Okagaki LH, Nunes CC, Sailsbery J, Clay B, Brown D, et al. (2015) Genome sequences of three phytopathogenic species of the *Magnaporthaceae* family of fungi. G3 (*Bethesda*) 5: 2539–2545.

Thongkantha S, Jeewon R, Vijaykrishna D, Lumyong S, et al. (2009) Molecular phylogeny of *Magnaporthaceae* (*Sordariomycetes*) with a new species *Ophioceras chiangdaoense* from *Dracaena loureiroi* in Thailand. *Fungal Diversity* 34:157–173.

Tullis EC (1933) *Leptosphaeria salvinii*, the ascigerous stage of *Helmithosporium sigmoideum* and *Sclerotium oryzae*. *Mycologia* 25: 944–955.

Walker J (1972) Type studies on *Gaeumannomyces graminis* and related fungi. *Transactions of the British Mycological Society* 58: 427–457.

Walker J (1980) *Gaeumannomyces*, *Linocarpus*, *Ophiobolus* and several genera of scleocospored ascomycetes and *Phialophora* conidial states, with a note on hypophodia. *Mycotaxon* 11:1–129

Xu XH, Su ZZ, Wang C, Kubicek CP, Feng XX, et al. (2014) The rice endophyte *Harpophora oryzae* genome reveals evolution from a pathogen to a mutualistic endophyte. *Scientific Reports* 4: 5783.

Xu Z, Harrington TC, Gleason ML, Batzer JC (2010) Phylogenetic placement of plant pathogenic *Sclerotium* species among teleomorph genera. *Mycologia* 102: 337–346.

Zhang N, Zhao S, Shen Q (2011) A six-gene phylogeny reveals the evolution of mode of infection in the rice blast fungus and allied species. *Mycologia* 103: 1267–1276.


Author/s:
Zhang, N; Luo, J; Rossman, AY; Aoki, T; Chuma, I; Crous, PW; Dean, R; de Vries, RP;
Donofrio, N; Hyde, KD; Lebrun, M-H; Talbot, NJ; Tharreau, D; Tosa, Y; Valent, B; Wang, Z;
Xu, J-R

Title:
Generic names in Magnaporthales

Date:
2016-06-01

Citation:
Zhang, N., Luo, J., Rossman, A. Y., Aoki, T., Chuma, I., Crous, P. W., Dean, R., de Vries, R. P.,
Donofrio, N., Hyde, K. D., Lebrun, M. -H., Talbot, N. J., Tharreau, D., Tosa, Y., Valent, B.,
Wang, Z. & Xu, J. -R. (2016). Generic names in Magnaporthales. IMA FUNGUS, 7 (1),
pp.155-159. https://doi.org/10.5598/imafungus.2016.07.01.09.

Persistent Link:
http://hdl.handle.net/11343/258220

File Description:
Published version

License:
CC BY-NC-ND