

Article



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Deniquelata barringtoniae gen. et sp. nov., associated with leaf spots of Barringtonia asiatica

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Abstract

Deniquelata barringtoniae gen. et sp. nov. (Montagnulaceae) forms numerous ascomata on distinct zonate leaf spots of Barringtonia asiatica (Lecythidaceae). We isolated this taxon and sequenced the 18S and 28S nrDNA. The result of phylogenetic analysis based on 18S and 28S nrDNA sequence data indicate that the genus belongs in the family Montagnulaceae, Dothideomycetes, Ascomycota. The ascomata are immersed, dark brown to black, with bitunicate asci and brown, muriform ascospores. Deniquelata is distinguished from the other genera in Montagnulaceae based on its short, broad, furcate and pedicellate asci, verruculose ascospores with short narrow pseudoparaphyses with parasitic naturee and this is also supported by molecular data. A new genus and species is therefore introduced to accommodate this taxon. We used isolates of this species to show via pathogenicity testing that the taxon is able to cause leaf spots when leaves are pin pricked.

Key words: Dothideomycetes, foliar pathogen, Montagnulaceae, new genus, new species

Introduction

Among the classes of Ascomycota, Dothideomycetes is the largest and most diverse (Kirk et al. 2008, Zhang et al. 2012) and is characterized by bitunicate, usually fissitunicate asci (Schoch et al., 2009). The majority of members in this class are endophytes, epiphytes or saprobes with a small number occurring as lichens and hyperparasites (Kirk et al. 2008, Zhang et al. 2012). Many, especially asexual or mitosporic Dothideomycetes, are agents of plant diseases, causing serious problems to crop plants (Manamgoda et al. 2011, Wikee et al. 2011).

Besides marine and freshwater fungi (Suetrong et al. 2010), there have been a few taxonomic studies of Dothideomycetes of Thailand. Boonmee et al. (2011) illustrated new collections of *Tubeufiaceae*, including a new genus *Chlamydotubeufia* based on dictyochlamydosporous anamorphs and three new species; one each in *Acanthostigma*, *Tubeufia* and *Thaxteriella* based on phylogenetic analysis of rDNA sequence data (Boonmee et al. 2011). Based on combined dataset of 18S and 28S nrDNA sequences, Chomnunti et al. (2011) introduced *Phragmocapnias asiaticus*, *P. longicollus*, *P. penzigii*, *P. siamensis*, *Leptoxyphium cacuminum* and *Capnodium coartatum* in the family *Capnodiaceae* and epitypified the genus *Phragmocapnias* with a new collection of *P. betle*. Liu et al. (2011) reported two new genera, *Fussiroma* and *Neoastrosphaeriella*, in *Aigialaceae*, based on their distinguishing morphology and molecular phylogeny.

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