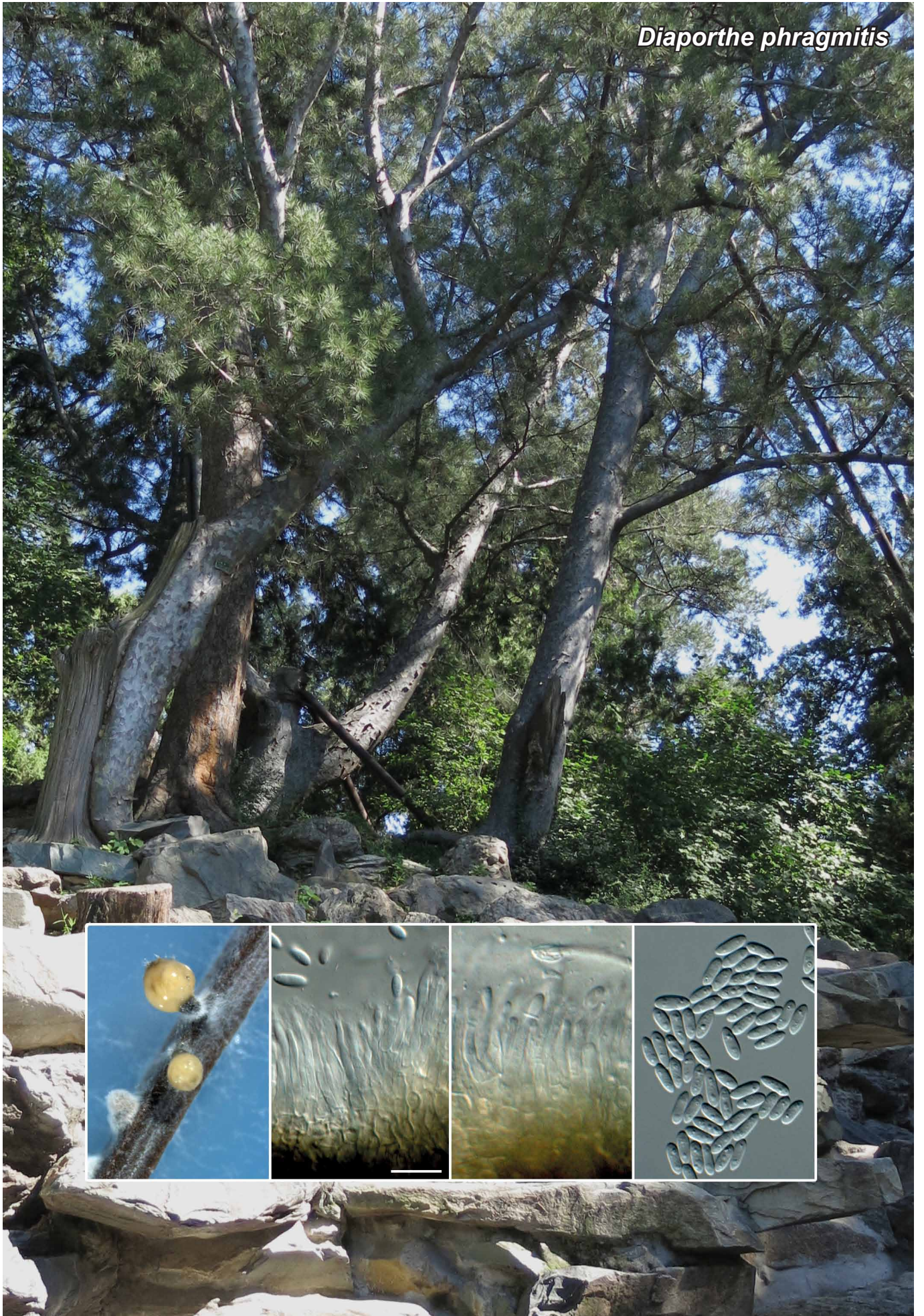


Diaporthe phragmitis



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Diaporthe phragmitis Crous, sp. nov.

Etymology. Name reflects the host genus *Phragmites*, from which the species was isolated.

Sporulating on PNA. *Conidiomata* pycnidial, globose, up to 250 µm diam, black, erumpent, exuding creamy conidial droplets from central ostioles; walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–3-septate, rarely branched, densely aggregated, cylindrical, straight to sinuous, 20–30 × 3–4 µm. *Conidiogenous cells* 10–17 × 2–2.5 µm, phialidic, cylindrical, terminal and intercalary, with slight apical taper, 1–1.5 µm diam, with visible periclinal thickening; collarete prominently flared, up to 3 µm long. *Paraphyses* not observed. *Alpha conidia* aseptate, hyaline, smooth, multi- or bi-guttulate, fusoid to ellipsoid, tapering towards both ends, straight apex subobtuse, base subtruncate, (6–)7–8(–8.5) × (2–)2.5(–3) µm. *Gamma* and *beta conidia* not observed.

Culture characteristics — Colonies covering dish after 2 wk at 25 °C in the dark. On MEA flat, spreading with moderate aerial mycelium and lobed, feathery margins; surface dirty white, reverse apricot. On OA and PDA dirty white.

Typus. CHINA, Beijing, Fragrant Hill, N39°59'18.4" E116°11'25", on *Phragmites australis* (*Poaceae*), 31 Aug. 2013, P.W. Crous & Y. Zhang (holotype CBS H-21979, culture ex-type CPC 23607 = CBS 138897; ITS sequence GenBank KP004445, LSU sequence GenBank KP004473, HIS sequence GenBank KP004503, TUB sequence GenBank KP004507, MycoBank MB810588).

Notes — *Diaporthe phragmitis* was isolated as endophyte from leaves of *Phragmites australis*. Phylogenetically, it is similar to species such as *P. cotoneastri*, *P. juglandica* and *P. vaccinii* based on DNA sequence data of the ITS gene, but can be distinguished from these taxa based on other loci (Lombard et al. 2014).

ITS. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis vaccinii* (GenBank KJ739481; Identities = 561/567 (99 %), no gaps), *Phomopsis juglandina* (GenBank KC242236; Identities = 530/536 (99 %), Gaps = 1/536 (0 %)) and *Diaporthe cotoneastri* (GenBank KJ609015; Identities = 564/572 (99 %), Gaps = 2/572 (0 %)).

LSU. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe eres* (GenBank AF362565; Identities = 794/794 (100 %), no gaps), *Diaporthe maytenicola* (GenBank KF777210; Identities = 793/794 (99 %), no gaps) and *Phomopsis vaccinii* (GenBank AF439630; Identities = 793/794 (99 %), no gaps).

HIS. Closest hits using the HIS sequence had highest similarity to numerous sequences of *Diaporthe eres* (e.g. GenBank KJ420886; Identities = 319/319 (100 %), no gaps), as well as hits with *Diaporthe* cf. *nobilis* (GenBank KC343635; Identities = 319/319 (100 %), no gaps) and *Diaporthe nitschkei* (GenBank KJ420875; Identities = 317/319 (99 %), no gaps).

TUB. Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe* 'sp. YY-2013' (an unpublished species from jujube in China; GenBank KF600610; Identities = 773/785 (98 %), Gaps = 1/785 (0 %)), *Diaporthe* cf. *nobilis* (GenBank KC344115; Identities = 692/697 (99 %), no gaps) and *Diaporthe bicincta* (GenBank KC344102; Identities = 688/697 (99 %), no gaps).

Colour illustrations. Fragrant Hill, Beijing; conidiomata, conidiophores and conidia. Scale bar = 10 µm.

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