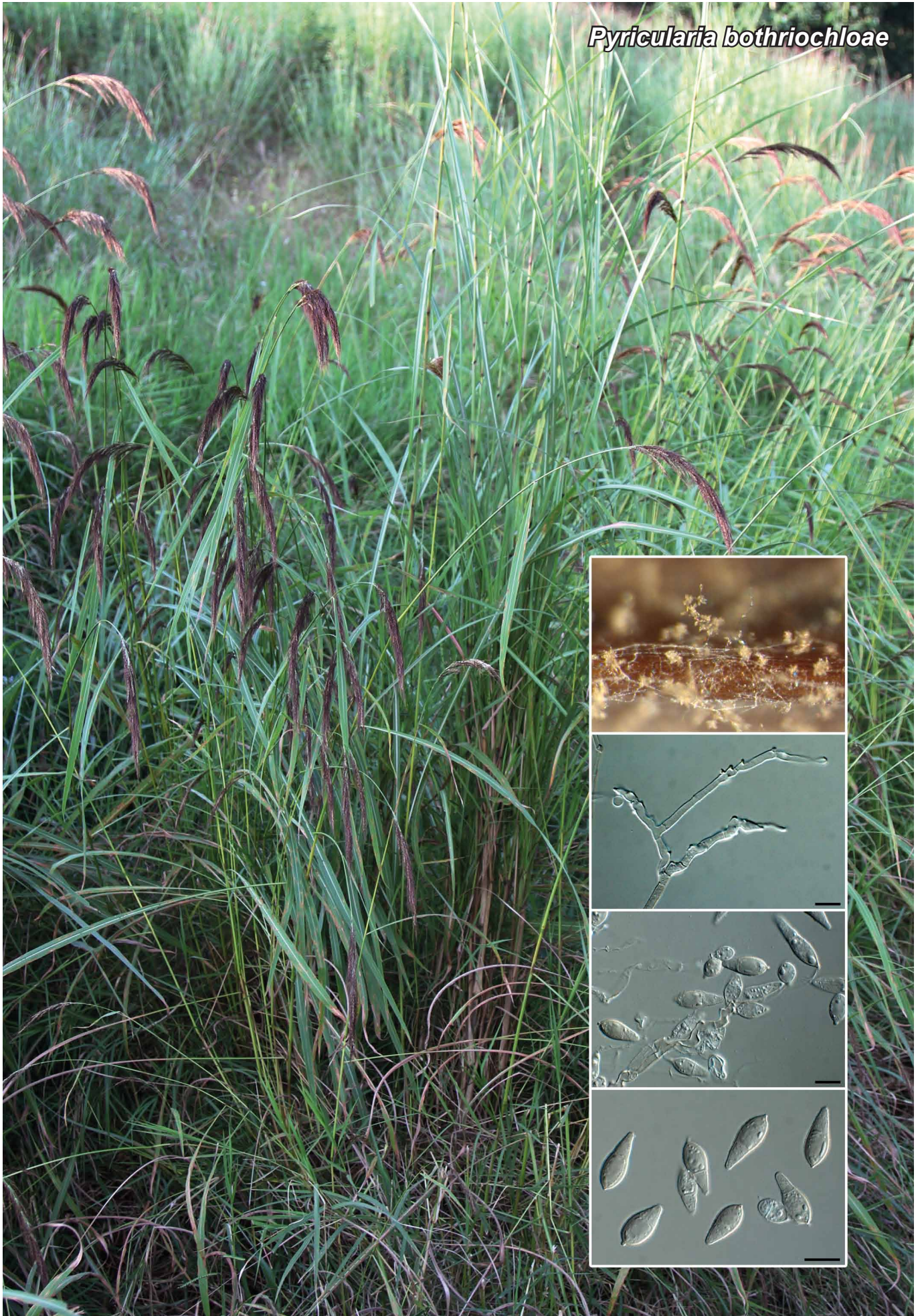


*Pyricularia bothriochloae*



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## *Pyricularia bothriochloae* Crous & Cheew., *sp. nov.*

*Etymology.* Named after the host genus from which it was collected, *Bothriochloa*.

*Leaf spots* angular, pale to medium brown with red-purple margin, up to 4 mm diam. On SNA. *Mycelium* consisting of smooth, hyaline, branched, septate hyphae, 1.5–2 µm diam. *Conidiophores* solitary, erect, straight or curved, branched or not, medium brown, smooth, 90–180 × 3–6 µm, 5–8-septate. *Conidigenous cells* 8–30 × 3–4 µm, integrated, terminal and lateral, pale brown, smooth, forming a rachis with several protruding denticles, phialidic with minute periclinal thickening, 1–1.5 µm long, 1–2 µm diam. *Conidia* solitary, obclavate, pale brown, smooth to finely roughened, guttulate, (18–)19–22(–23) × (6–)7–8(–9) µm; apical cell 6–8 µm long, basal cell 11–14 µm long.

*Culture characteristics* — Colonies covering plates in 2 wk, with moderate aerial mycelium. On OA surface with patches of olivaceous-grey, iron-grey and pale olivaceous-grey; on MEA surface and reverse honey to isabelline; on PDA surface and reverse olivaceous-black.

*Typus.* THAILAND, Royal Project, N18°09'24.8" E98°23'19.6", on leaves of *Bothriochloa bladhii* (*Poaceae*), 29 Oct. 2012, P.W. Crous (holotype CBS H-21436, culture ex-type CPC 21650, 21651 = CBS 136427, ITS sequence GenBank KF777186, LSU sequence GenBank KF777238, MycoBank MB805841).

*Notes* — *Pyricularia bothriochloa* represents a novel species of *Pyricularia* on *Bothriochloa bladhii* from Thailand, which does not correspond to any species presently in GenBank, or in our own unpublished DNA sequence database.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Dactylaria higginsii* (GenBank DQ341512; Identities = 861/875 (98 %), Gaps = 1/875 (0 %)), *Utrechtiana cibiessia* (GenBank JF951176; Identities = 883/909 (97 %), no gaps) and *Pyricularia borealis* (GenBank DQ341511; Identities = 833/860 (97 %), no gaps). Closest hits using the ITS sequence had highest similarity to *Magnaporthe oryzae* (GenBank JQ747492; Identities = 641/703 (91 %), Gaps = 17/703 (2 %)), *Dactylaria junci* (GenBank AY265320; Identities = 496/546 (91 %), Gaps = 15/546 (2 %)) and *Dactylaria higginsii* (GenBank AB274438; Identities = 420/464 (91 %), Gaps = 15/464 (3 %)).

*Colour illustrations.* *Bothriochloa bladhii* growing in Thailand; colony sporulating on PNA; conidiophores and conidia. Scale bars = 10 µm.

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