

*Neodeightoniella phragmiticola*





Fungal Planet 168 – 26 November 2013

***Neodeightoniella* Crous & W.J. Swart, gen. nov.**

*Etymology.* Named after its morphological similarity to the genus *Deightoniella*.

*Foliicolous*, plant pathogenic. *Conidiophores* fasciculate, arising from stromata, amphigenous, associated with weakly developed brown stroma of a few brown cells; fascicles with 3–6 conidiophores. *Conidiophores* erect, brown, unbranched, finely roughened, straight to slightly flexuous, subcylindrical, septate. *Conidiogenous cells* terminal and integrated, subcylindrical, brown, finely roughened; scars terminal and lateral on conidio-

genous cells, darkened, thickened, protruding, tretic with central pore. *Conidia* solitary, pale brown, surface finely roughened, fusoid-ellipsoid, straight or gently curved, 1-septate; apical cell globose, with prominent mucoid cap; basal cell funnel-shaped, widest two thirds from basal hilum, tapering prominently to truncate hilum, thickened, darkened, with central pore.

*Type species.* *Neodeightoniella phragmiticola*.  
Mycobank MB805827.

***Neodeightoniella phragmiticola* Crous & W.J. Swart, sp. nov.**

*Etymology.* Named after the host genus on which it occurs, *Phragmites*.

*Foliicolous*. *Leaf spots* amphigenous, brown to dark brown, ellipsoid, up to 5 µm diam. *Conidiophores* fasciculate, arising from stromata, amphigenous, associated with weakly developed brown stroma of a few brown cells; fascicles with 3–6 conidiophores. *Conidiophores* erect, brown, unbranched, finely roughened, straight to slightly flexuous, subcylindrical, 0–2-septate, 40–70 × 5–10 µm. *Conidiogenous cells* terminal and integrated, subcylindrical, brown, finely roughened, 15–60 × 5–10 µm; scars terminal and lateral on conidiogenous cells, darkened, thickened, protruding, tretic with central pore, 3–4 µm diam. *Conidia* solitary, pale brown, surface finely roughened, fusoid-ellipsoid, straight or gently curved, (33–)34–38(–40) × (15–)16–18(–20) µm, 1-septate; apical cell globose, 10–12 × 14–16 µm, with prominent mucoid cap, 8–15 × 20–25 µm; basal cell funnel-shaped, widest two thirds from basal hilum, 20–27 × 15–20 µm, tapering prominently to truncate hilum, thickened, darkened, 3–4 µm diam, with central pore.

Culture characteristics — After 2 wk at 25 °C reaching 30 mm diam; with moderate aerial mycelium and lobed, smooth margins. On OA and PDA surface dirty white with patches of rosy buff. On MEA surface rosy buff with patches of pale purplish grey, reverse fuscous black in centre, apricot in outer region.

*Typus.* SOUTH AFRICA, Free State, Bultfontein, on leaves of *Phragmites australis* (*Poaceae*), 31 Jan. 2013, W.J. Swart, holotype CBS H-21427, cultures ex-type CPC 22059, 22060 = CBS 136418. Additional collections at same venue but different plants: cultures CPC 22061, 22062; cultures CPC 22057, 22058; ITS sequence GenBank KF777170–KF777172, LSU sequence GenBank KF777223–KF777225, MycoBank MB805828).

*Notes* — *Neodeightoniella* resembles the genus *Deightoniella* (based on *D. africana*, on *Imperata* sp., West Africa), in having pale brown, fusoid-ellipsoid, unequally 1-septate conidia arising from brown conidiophores. It is distinct in that conidiophores do not undergo percurrent rejuvenation (seen as nodal swellings in the type of *Deightoniella*), have prominent apical and lateral conidiogenous loci on the conidiogenous cells, conidia have a prominent mucoid cap, and conidiophores are arranged in fascicles.

*Colour illustrations.* Symptomatic leaves of *Phragmites australis* in Bultfontein, South Africa; conidiophores, conidia with mucoid caps (arrows), and germinating conidia. Scale bars = 10 µm.

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Septoria rumicum* (GenBank KF252034; Identities = 786/792 (99 %), no gaps) and *Passalora fusimaculans* (GenBank KF251817; Identities = 786/792 (99 %), no gaps).

The genus *Deightoniella* presently contains a heterogeneous assemblage of taxa. Crous et al. (2011a) described the genus *Utrechtiana* (based on *U. cibiessia*, pathogenic to *Phragmites australis* in The Netherlands). An earlier name exists for the taxon, namely *D. roumegueri* (on *P. australis* in France) (Constantinescu 1983). This taxon fits *Deightoniella* (based on *D. africana*, occurring on leaves of *Imperata cylindrica* var. *africana*; *Poaceae*) rather well, as conidiophores are solitary, and a reexamination of the type material found the conidiogenous cells to rejuvenate percurrently as in *D. africana* (see Seifert & Gams 2011 for synonymy). Assuming that *D. africana* and *D. roumegueri* are congeneric, *Deightoniella* belongs to the *Magnaporthaceae*.

Another species accommodated in *Deightoniella* is *D. torulosa*, which causes *Deightoniella* black tip, leaf spot and fruit speckle of banana (Ploetz 2003). This species was originally placed in *Deightoniella* as the conidiophores were also observed to rejuvenate internally and percurrently, creating the same nodose swellings as observed in the type, *D. africana*. Phylogenetically, however, *D. torulosa* clusters with isolates of *Corynespora cassicola*, the type species of the genus *Corynespora*. This finding suggests that the species of *Deightoniella* with distoseptate conidia belong elsewhere.

***Corynespora torulosa* (Syd.) Crous, comb. nov.**

*Basionym.* *Brachysporium torulosum* Syd., Hedwigia 49: 83. 1909.  
= *Deightoniella torulosa* (Syd.) M.B. Ellis, Mycol. Pap. 66: 7. 1957.  
= *Helminthosporium torulosum* (Syd.) S.F. Ashby, Trop. Agric. (Trinidad) 10: 6. 1932.  
= *Cercospora musarum* S.F. Ashby, Bull. Dept. Agric. (Kingston) 2: 109. 1913.

*Specimens examined.* BRAZIL, Pará, on *Musa cavendishii* (*Musaceae*), 24 Jan. 1908, C.F. Baker, ex Herb. Sydow, portion of holotype of *Brachysporium torulosum* (9810) in IML. – MEXICO, Colima, Tecmán, on *M. cavendishii*, M. de Jesús Yáñez-Morales, 17 Nov. 2008 (CBS H-21456 epitype designated here 'MBT176329', cultures ex-epitype CPC 15989, 15990 = CBS 136419, ITS sequence GenBank KF777154, LSU sequence GenBank KF777207, MycoBank MB805829).

*Notes* — Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the LSU sequence are *Corynespora smithii* (GenBank GU323201; Identities = 874/882 (99 %), no gaps) and *C. cassicola* (GenBank GU301808; Identities = 811/820 (99 %), Gaps = 4/820 (0 %)).

Pedro W. Crous & Johannes Z. Groenewald, CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@cbs.knaw.nl & e.groenewald@cbs.knaw.nl

Wijnand J. Swart, Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa; e-mail: Swartwj@ufs.ac.za