



Fungal Planet 1141 – 19 December 2020

***Neodothiora* Crous, G.C. Adams & Winton, gen. nov.**

Etymology. Name refers to its superficial resemblance of the genus *Dothiora*.

Classification — *Dothioraceae*, *Dothideales*, *Dothideomycetes*.

Conidiomata solitary, erumpent, brown, subglobose, pycnidial, with central ostiole, exuding a crystalline mucoid conidial cirrus; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity,

hyaline, smooth, ampulliform, proliferating percurrently. *Conidiogenous cells* also occurring solitary on superficial hyphae, subcylindrical, hyaline, smooth, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, ellipsoid, apex subobtuse, tapering to truncate apex.

Type species. *Neodothiora populina* Crous, G.C. Adams & Winton. MycoBank MB837857.

***Neodothiora populina* Crous, G.C. Adams & Winton, sp. nov.**

Etymology. Name refers to the host genus *Populus* from which it was isolated.

On PNA: *Conidiomata* solitary, erumpent, brown, subglobose, pycnidial, with central ostiole, 130–180 µm diam, exuding a crystalline mucoid conidial cirrus; wall of 6–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells lining the inner cavity, hyaline, smooth, ampulliform, proliferating percurrently, 5–7 × 4–6 µm. *Conidiogenous cells* also occurring solitary on superficial hyphae, ampulliform to subcylindrical, hyaline, smooth, 5–10 × 2–5 µm, proliferating percurrently at apex. *Conidia* solitary, hyaline, smooth, aseptate, guttulate, ellipsoid, apex subobtuse, tapering to truncate apex, 5–6(–7) × 2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and feathery, uneven margin, covering dish after 2 wk at 25 °C. On MEA surface mucoid, saffron, reverse saffron with patches of umber; on PDA surface and reverse umber, margin black; on OA surface umber.

Typus. USA, Alaska, -148.7762872 64.63940972, on stem cankers of *Populus tremuloides* (*Salicaceae*), 24 June 2018, G. Adams & L.M. Winton (holotype CBS H-24556, culture ex-type CPC 39399 = CBS 147087, ITS, LSU, *tef1* and *tub2* sequences GenBank MW175365.1, MW175405.1, MW173127.1 and MW173142.1, MycoBank MB837858).

Additional materials examined. USA, Alaska, -148.7672229 64.64259316, on stems of *P. tremuloides*, 25 June 2018, G. Adams & L.M. Winton, CPC 39397 = CBS 147085, ITS sequence GenBank MW175366.1; USA, Alaska, -148.3288146 64.73376442, on stems of *P. tremuloides*, 19 June 2018, G. Adams & L.M. Winton, CPC 39398 = CBS 147086, ITS sequence GenBank MW175367.1; Alaska, Bonanza Creek Experimental Forest, -148.33106 64.73243, on stems of *P. tremuloides*, 15. Sept. 2020, L.M. Winton, Univ. of Alaska Herbarium (ALA) H1280665, H1280672; *ibid.*, on stems of *P. tremuloides*, Jan. 2020, L.M. Winton, H1280666–H1280671.

Notes — *Neodothiora* is reminiscent of the genus *Dothiora*, having *Dothichiza* and hormonema-like morphs in culture (Crous & Groenewald 2016, 2017). However, it clusters apart from the type species, *D. pyrenophora*, and thus a new genus is herewith introduced to accommodate this pathogen, which is associated with severe cankers of *Populus tremuloides* in Alaska. In field inoculations, conidiomata developed on the tree

Colour illustrations. Stem canker on *Populus tremuloides*. Conidiomata on PNA; conidiomata on SNA; conidiogenous cells; conidiogenous cells giving rise to conidia; conidia. Scale bars: conidiomata = 150 µm, all others = 10 µm.

bark around points of inoculation, which resembled those that developed in culture (on agar and on PNA).

Based on a megablast search of NCBI's GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to 'Uncultured fungus' (strain UPSC_A12_12, GenBank GU564975.1; Identities = 525/527 (99 %), one gap (0 %)), *Scleroconidioma sphagnicola* (strain JJ-18-24, GenBank MK880096.1; Identities = 563/591 (95 %), 13 gaps (2 %)), *Rhizosphaera macrospora* (strain ARSL_071114.1, GenBank

(text continues on Supplementary material page FP1141)

Supplementary material

FP1141-1 The first of 1000 equally most parsimonious trees obtained from the LSU alignment (57 sequences including the outgroup; 809 characters including alignment gaps analysed: 566 constant, 122 variable and parsimony-uninformative and 121 parsimony-informative) using PAUP* v. 4.0b10 (Swofford 2003). Tree statistics: TL = 496, CI = 0.653, RI = 0.813, RC = 0.531. Parsimony bootstrap support values > 74 % and Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and thickened lines represent branches present in the parsimony strict consensus tree. The Bayesian analysis using MrBayes v. 3.2.7a (Ronquist et al. 2012) resulted in a Bayesian consensus phylogram based on 633002 sampled trees and 180 unique site patterns (data not shown). The scale bar represents the number of changes. The taxonomic novelties described in this study are highlighted with **bold** text and coloured blocks. GenBank accession and culture/specimen numbers are indicated behind the species names. The two orders are indicated to the left of the tree at the basal branches. The tree was rooted to *Diaporthe perijuncta* (GenBank NG_059064.1). The alignment and tree were deposited in TreeBASE (Submission ID 27179).

FP1141-2 The first of 414 equally most parsimonious trees obtained from the ITS alignment (50 sequences including the outgroup; 518 characters including alignment gaps analysed: 332 constant, 74 variable and parsimony-uninformative and 112 parsimony-informative) using PAUP* v. 4.0b10 (Swofford 2003). Tree statistics: TL = 377, CI = 0.647, RI = 0.882, RC = 0.571. Parsimony bootstrap support values > 74 % and Bayesian posterior probabilities (PP) > 0.79 are shown at the nodes and thickened lines represent branches present in the parsimony strict consensus tree. The Bayesian analysis using MrBayes v. 3.2.7a (Ronquist et al. 2012) resulted in a Bayesian consensus phylogram based on 161252 sampled trees and 176 unique site patterns (data not shown). The scale bar represents the number of changes. The taxonomic novelties described in this study is highlighted with **bold** text and coloured blocks. GenBank accession and culture/specimen numbers are indicated behind the species names. The tree was rooted to *Dothidea sambuci* (GenBank NR_111220.1). The alignment and tree were deposited in TreeBASE (Submission ID 27179).

Pedro W. Crous & Johannes Z. Groenewald, Westerdijk Fungal Biodiversity Institute, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; e-mail: p.crous@wi.knaw.nl & e.groenewald@wi.knaw.nl
Gerard C. Adams, Department of Plant Pathology, 406D Plant Science Hall, 1875 N. 38th Street, University of Nebraska, Lincoln, NE, USA; e-mail: gadams3@unl.edu
Loretta M. Winton, U.S.D.A. Forest Service, Forest Health Protection, 3700 Airport Way, Fairbanks, AK 99709, USA; e-mail: loretta.winton@usda.gov