Persoonia 33, 2014: 212–289
www.ingentaconnect.com/content/nhn/pimj

RESEARCH ARTICLE

http://dx.doi.org/10.3767/003158514X685680

Fungal Planet description sheets: 281–319

P.W. Crous[1], M.J. Wingfield[2], R.K. Schumacher[3], B.A. Summerell[4], A. Giraldo[5], J. Gené[5], J. Guarro[5], D.N. Wanasinghe[6,7,8], K.D. Hyde[6,7,8], E. Camporesi[9,10], E.B. Gareth Jones[11], K.M. Thambugala[8,12], E.F. Malysheva[13], V.F. Malysheva[13], K. Acharya[14], J. Álvarez[15], P. Alvarado[16], A. Assefa[17], C.W. Barnes[18], J.S. Bartlett[19], R.A. Blanchette[20], T.I. Burgess[21], J.R. Carlavilla[15], M.P.A. Coetzee[22], U. Damm[23], C.A. Decock[24], A. den Breeÿen[25], B. de Vries[26], A.K. Dutta[14], D.G. Holdom[19], S. Rooney-Latham[27], J.L. Manjón[15], S. Marincowitz[22], M. Mirabolfathy[28], G. Moreno[15], C. Nakashima[29], M. Papizadeh[30], S.A. Shahzadeh Fazeli[30], M.A. Amoozegar[30], M.K. Romberg[31], R.G. Shivas[19], J.A. Stalpers[1], B. Stielow[1], M.J.C. Stukely[32], W.J. Swart[33], Y.P. Tan[19], M. van der Bank[34], A.R. Wood[25], Y. Zhang[35], J.Z. Groenewald[1]

Key words

ITS DNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of fungi described in the present study include the following from South Africa: *Alanphillipsia aloeicola* from *Aloe* sp., *Arxiella dolichandrae* from *Dolichandra unguiscati*, *Ganoderma austroafricanum* from *Jacaranda mimosifolia*, *Phacidiella podocarpi* and *Phaeosphaeria podocarpi* from *Podocarpus latifolius*, *Phyllosticta mimusopisicola* from *Mimusops zeyheri* and *Sphaerulina pelargonii* from *Pelargonium* sp. Furthermore, *Barssia maroccana* is described from *Cedrus atlantica* (Morocco), *Codinaea pini* from *Pinus patula* (Uganda), *Crucellisporiopsis marquesiae* from *Marquesia acuminata* (Zambia), *Dinemasporium ipomoeae* from *Ipomoea pes-caprae* (Vietnam), *Diaporthe phragmitis* from *Phragmites australis* (China), *Marasmius vladimirii* from leaf litter (India), *Melanconium hedericola* from *Hedera helix* (Spain), *Pluteus albotomentosus* and *Pluteus extremiorientalis* from a mixed forest (Russia), *Rachicladosporium eucalypti* from *Eucalyptus globulus* (Ethiopia), *Sistotrema epiphyllum* from dead leaves of *Fagus sylvatica* in a forest (The Netherlands), *Stagonospora chrysopyla* from *Scirpus microcarpus* (USA) and *Trichomerium dioscoreae* from *Dioscorea* sp. (Japan). Novel species from Australia include: *Corynespora endiandrae* from *Endiandra introrsa*, *Gonatophragmium triuniae* from *Triunia youngiana*, *Penicillium coccotrypicola* from *Archontophoenix cunninghamiana* and *Phytophthora moyootj* from soil. Novelties from Iran include *Neocamarosporium chichastianum* from soil and *Seimatosporium pistaciae* from *Pistacia vera*. *Xenosonderhenia eucalypti* and *Zasmidium eucalyptigenum* are newly described from *Eucalyptus urophylla* in Indonesia. *Diaporthe acaciarum* and *Roussoella acacia* are newly described from *Acacia tortilis* in Tanzania. New species from Italy include *Comoclathris spartii* from *Spartium junceum* and *Phoma tamaricicola* from *Tamarix gallica*. Novel genera include (*Ascomycetes*): *Acremoniopsis* from forest soil and *Collarina* from water sediments (Spain), *Phellinocrescentia* from a *Phellinus* sp. (French Guiana), *Neobambusicola* from *Strelitzia nicolai* (South Africa), *Neocladophialophora* from *Quercus robur* (Germany), *Neophysalospora* from *Corymbia henryi* (Mozambique) and *Xenophaeosphaeria* from *Grewia* sp. (Tanzania). Morphological and culture characteristics along with ITS DNA barcodes are provided for all taxa.

Article info Received: 1 October 2014; Accepted: 18 October 2014; Published: 24 November 2014.

Acknowledgements Alejandra Giraldo acknowledges support from the Spanish Ministerio de Economía y Competitividad, grant CGL 2011-27185. Ekaterina F. Malysheva & Vera F. Malysheva thank Drs A. Kovalenko and N. Psurtseva (Komarov Botanical Institute) for help in collecting specimens. Financial support was provided by the Russian Foundation for Basic Research (projects 13-04-00838a and 12-04-33018). Gabriel H. Moreno acknowledges financial support from the Spanish grant (project RTA2012-00007-00-00) and to Dr L. Monje and Mr A. Pueblas of the Department of Drawing and Scientific Photography at the Alcalá University for his help in the digital preparation of the photographs, and to Dr J. Rejos, curator of the AH herbarium for his assistance with the specimens examined in the present study. We also thank the technical staff, A. van Iperen (cultures), M. Vermaas (photographic plates), and M. Starink-Willemse (DNA isolation, amplification and sequencing) for their invaluable assistance. Cony Decock acknowledges the financial support received from the Belgian State – Belgian Federal Science Policy through the BCCM research programme and the FNRS / FRFC (convention FRFC 2.4544.10).

HIGHER ORDER CLASSIFICATION OF TAXONOMIC NOVELTIES

ASCOMYCOTA

Dothideomycetes
- ***Acrospermales, Acrospermaceae***
  - *Gonatophragmium triuniae*
- ***Botryosphaeriales, Botryosphaeriaceae***
  - *Alanphillipsia aloeicola*
- ***Botryosphaeriales, Phyllostictaceae***
  - *Phyllosticta mangiferae-indica*
  - *Phyllosticta mimusopisicola*
  - *Phyllosticta rubella*
- ***Capnodiales, Cladosporiaceae***
  - *Rachicladosporium eucalypti*
- ***Capnodiales, Mycosphaerellaceae***
  - *Sphaerulina pelargonii*
  - *Xenosonderhenia eucalypti*
  - *Zasmidium eucalyptigenum*
- ***Incertae sedis***
  - *Arxiella dolichandrae*
- ***Pleosporomycetidae, Pleosporales, Incertae sedis***
  - *Phellinocrescentia guianensis*
- ***Pleosporomycetidae, Pleosporales, Incertae sedis, Corynesporascaceae***
  - *Corynespora endiandrae*
- ***Pleosporomycetidae, Pleosporales, Incertae sedis, Roussoellaceae***
  - *Roussoella acaciae*
- ***Pleosporomycetidae, Pleosporales, Massarineae, Bambusicolaceae***
  - *Neobambusicola strelitziae*
- ***Pleosporomycetidae, Pleosporales, Massarineae, Massarinaceae***
  - *Stagonospora chrysopyla*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Didymellaceae***
  - *Phoma tamaricicola*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae***
  - *Phaeosphaeria podocarpi*
  - *Xenophaeosphaeria grewiae*
- ***Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae***
  - *Comoclathris spartii*
  - *Neocamarosporium chichastianum*

Eurotiomycetes
- ***Chaetothyriomycetidae, Chaetothyriales, Trichomeriaceae***
  - *Trichomerium dioscoreae*
- ***Eurotiomycetidae, Eurotiales, Trichocomaceae***
  - *Penicillium coccotrypicola*
- ***Incertae sedis***
  - *Neocladophialophora quercina*

Lecanoromycetes
- ***Ostropomycetidae, Ostropales, Incertae sedis***
  - *Phacidiella podocarpi*

Leotiomycetes
- ***Helotiales, Hyaloscyphaceae***
  - *Crucellisporiopsis marquesiae*

Pezizomycetes
- ***Pezizomycetidae, Pezizales, Helvellaceae***
  - *Barssia maroccana*

Sordariomycetes
- ***Hypocreomycetidae, Hypocreales, Clavicipitaceae***
  - *Collarina aurantiaca*
- ***Hypocreomycetidae, Hypocreales, Incertae sedis***
  - *Acremoniopsis suttonii*
- ***Hypocreomycetidae, Incertae sedis***
  - *Neophysalospora eucalypti*
- ***Sordariomycetidae, Chaetosphaeriales, Chaetosphaeriaceae***
  - *Codinaea pini*
  - *Dinemasporium ipomoeae*
- ***Sordariomycetidae, Diaporthales, Diaporthaceae***
  - *Diaporthe acaciarum*
  - *Diaporthe phragmitis*
- ***Sordariomycetidae, Diaporthales, Melanconidaceae***
  - *Melanconium hedericola*
- ***Xylariomycetidae, Xylariales, Amphisphaeriaceae***
  - *Seimatosporium pistaciae*

BASIDIOMYCOTA

- ***Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae***
  - *Marasmius vladimirii*
- ***Agaricomycetes, Agaricomycetidae, Agaricales, Pluteaceae***
  - *Pluteus albotomentosus*
  - *Pluteus extremiorientalis*
- ***Agaricomycetes, Agaricomycetidae, Polyporales, Ganodermataceae***
  - *Ganoderma austroafricanum*
- ***Agaricomycetes, Incertae sedis, Cantharellales, Hydnaceae***
  - *Sistotrema epiphyllum*

CHROMISTA

- ***Oomycota, Oomycetes, Pythiales, Pythiaceae***
  - *Phytophthora moyootj*

---

[1] CBS-KNAW Fungal Biodiversity Centre, P.O. Box 85167, 3508 AD Utrecht, The Netherlands; corresponding author e-mail: p.crous@cbs.knaw.nl.

[2] Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, P. Bag X20, Pretoria, 0028, South Africa.

[3] Hölderlinstraße 25, 15517 Fürstenwalde/Spree, Germany.

[4] Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia.

[5] Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV), Sant Llorenç 21, 43201 Reus, Tarragona, Spain.

[6] World Agro forestry Centre East and Central Asia Office, 132 Lanhei Road, Kunming 650201, China.

[7] Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan China.

[8] Institute of Excellence in Fungal Research and School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand.

[9] A.M.B. Gruppo Micologico Forlivese 'Antonio Cicognani', Via Roma 18, Forlì, Italy and A.M.B. Circolo Micologico 'Giovanni Carini', C.P. 314, Brescia, Italy.

[10] Società per gli Studi Naturalisticidella Romagna, C.P. 144, Bagnacavallo (RA), Italy.

[11] Department of Botany and Microbiology, College of Science, King Saudi University, Riyadh, Saudi Arabia.

[12] Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Xiaohe District, Guiyang City, Guizhou Province 550006, People's Republic of China.

[13] Komarov Botanical Institute of the Russian Academy of Sciences, Prof. Popov St. 2, RUS-197376, Saint Petersburg, Russia.

[14] Molecular and Applied Mycology and Plant Pathology Laboratory, Department of Botany, University of Calcutta, 35, Ballygunge Circular Road, Kolkata 700019, West Bengal, India.

[15] Departamento de Ciencias de la Vida (Área de Botánica), Universidad de Alcalá, E-28805 Alcalá de Henares, Spain.

[16] ALVALAB, La Rochela 47, E-39012, Santander, Spain.

[17] Department of Biology, Madawalabu University, P.O. Box 247, Bale Robe, Ethiopia.

[18] Centro de Investigación, Estudios y Desarrollo de Ingeniería (CIEDI), Facultad de Ingenierías y Ciencias Agropecuarias (FICA), Universidad de Las Américas, Calle José Queri s/n entre Av. Granados y Av. Eloy Alfaro, Quito, Ecuador.

[19] Biosecurity Queensland, Ecosciences Precinct, Department of Agriculture, Fisheries and Forestry, Dutton Park 4102, Queensland, Australia.

[20] University of Minnesota, 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA.

[21] Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia.

[22] Department of Genetics, Centre of Excellence in Tree Health Biotechnology (CTHB), Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, P. Bag X20, Pretoria, 0028, South Africa.

[23] Senckenberg Museum of Natural History Görlitz, PF 300 154, 02806 Görlitz, Germany.

[24] Mycothèque de l'Université catholique de Louvain (MUCL, BCCM™), Earth and Life Institute – ELIM – Mycology, Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium.

[25] ARC – Plant Protection Research Institute, P. Bag X5017, Stellenbosch 7599, South Africa.

[26] Roerdomplaan 222, 7905 EL Hoogeveen, The Netherlands.

[27] California Department of Food and Agriculture, 3294 Meadowview Road, Sacramento, CA 95832, USA.

[28] Iranian Research Institute of Plant Protection, Tehran, Iran.

[29] Graduate School of Bioresources, Mie University, 1577 Kurima-machiya, Tsu, Mie 514-8507, Japan.

[30] Iranian Biological Resource Center (IBRC), Academic Center for Education, Culture & Research (ACECR) Tehran, Iran.

[31] USDA APHIS PPQ NIS, 10300 Baltimore Ave, Beltsville, MD 20705, USA.

[32] Science Division, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia.

[33] Department of Plant Sciences, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.

[34] Department of Botany and Plant Biotechnology, University of Johannesburg, P.O. Box 524, Auckland Park, 2006, South Africa.

[35] Institute of Microbiology, Beijing Forestry University, P.O. Box 61, Beijing 100083, PR China.


Crucellisporiopsis marquesiae

Fungal Planet 281 – 24 November 2014

Crucellisporiopsis marquesiae Crous, *sp. nov.*

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

Foliicolous. *Conidiomata* stromatic, scattered to gregarious, erumpent, erect, acervuloid to cup-shaped, up to 400 µm diam; basal stroma up to 100 µm deep, consisting of *textura angularis*, hyaline, thick-walled; excipulum of *textura prismatica* and *textura intricata*; cavity surrounded by sterile hyphae, hyaline, 3–6-septate, with obtuse ends, up to 150 µm long, 2–2.5 µm diam. *Conidiophores* arising from conidiomatal cavity, septate, branched, hyaline, thin- and smooth-walled, branches fertile or ending in obtusely rounded, sterile setae, 10–50 × 2–2.5 µm. *Conidiogenous cells* integrated or discrete, subcylindrical, hyaline, smooth, 8–15 × 2–2.5 µm, with mucoid layer; proliferating inconspicuous percurrently at apex. *Conidia* tetra-radiate, main axis cylindrical, 0–1-septate, cells unequal, base narrow, truncate with marginal frill, hyaline, smooth, 15–20 × 2–2.5 µm, with tubular, unbranched central appendage, 1–3.5 µm long; arms 3(–4), at different apical loci on main axis, separated by septa, attenuated, septate, hyaline, smooth, not constricted at septa, (15–)30–40(–55) × 1.5 µm.

Culture characteristics — Colonies reaching 12 mm diam after 2 wk at 25 °C in the dark, erumpent, with moderate aerial mycelium and even, lobed margin. On MEA, PDA and OA surface dirty white to buff, reverse luteous with patches of buff.

Typus. Zambia, OM 4142, -11.81730 24.36443, on twigs of *Marquesia acuminata* (*Dipterocarpaceae*), 24 Feb. 2013, *M. van der Bank* (holotype CBS H-21977, culture ex-type CPC 22539 = CBS 138895; ITS sequence GenBank KP004443, LSU sequence GenBank KP004471, MycoBank MB810587).

Notes — The genus *Crucellisporiopsis* was treated by Nag Raj (1993), who accepted three species. The genus is characterised by having stromatic, acervuloid conidiomata, hyaline structures with conidiogenous cells giving rise to conidia via inconspicuous percurrent proliferation, and conidia with a subcylindrical central axis with basal appendage, and 4–5 radiate, septate arms. *Crucellisporiopsis marquesiae* can be distinguished from all three species based on its conidia having a basal appendage, and the dimensions of its central axis, and lateral, 3(–4) radiating arms.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Crucellisporium umtamvunae* (GenBank GU291797; Identities = 546/560 (98 %), Gaps = 1/560 (0 %)), *Lachnum varians* (GenBank AB481267; Identities = 465/511 (91 %), Gaps = 8/511 (1 %)) and *Lachnellula tricolor* (GenBank KC464643; Identities = 488/541 (90 %), Gaps = 8/541 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Lachnellula suecica* (GenBank KC492980; Identities = 788/809 (97 %), no gaps), *Lachnellula flavovirens* (GenBank KC492975; Identities = 788/809 (97 %), no gaps) and *Lachnum* cf. *bicolor* (GenBank AY544674; Identities = 788/809 (97 %), no gaps).

Colour illustrations. *Marquesia acuminata* in Zambia; conidiomata, conidiogenous cells and conidia. Scale bars: conidiomata = 400 µm, all others = 10 µm.

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
Michelle van der Bank, Department of Botany and Plant Biotechnology, University of Johannesburg,
P.O. Box 524, Auckland Park, 2006, South Africa; e-mail: mvdbank@uj.ac.za


Alanphillipsia aloeicola

Fungal Planet 282 – 24 November 2014

Alanphillipsia aloeicola Crous, *sp. nov.*

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

Conidiomata pycnidial, erumpent, brown, subglobose, up to 350 µm diam with central ostiole; wall of 6–8 layers of thick-walled, brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 15–25 × 4–6 µm, proliferating several times percurrently at apex. *Paraphyses* intermingled among conidiogenous cells, hyaline, smooth, subcylindrical, unbranched, septate, up to 80 µm long, 4–6 µm diam. *Conidia* solitary, thick-walled, guttulate, initially hyaline, becoming pale brown, finely verruculose, with longitudinal striations (when mature) along the length of its body, (25–)30–35(–42) × (10–)12–14(–17) µm, clavate to subcylindrical, apex obtuse, base truncate, 4–6 µm diam, with marginal frill up to 2 µm long. *Spermatial state* developing in same conidioma. *Spermatophores* tightly aggregated, hyaline, smooth, branched, subcylindrical, 15–25 × 3–4 µm. *Spermatogenous cells* terminal, subcylindrical, 8–12 × 2–3 µm. *Spermatia* hyaline, smooth, subcylindrical, 3–6 × 2 µm.

Culture characteristics — Colonies reaching 40 mm diam after 2 wk at 25 °C in the dark. On MEA flat, spreading with sparse aerial mycelium and lobed, feathery margins; surface olivaceous-grey in centre, outer region dirty white. On OA and PDA olivaceous-grey with a dirty white outer region.

Typus. South Africa, Western Cape province, Clanwilliam, Ramskop, on *Aloe* sp. (*Aloaceae*), Sept. 2013, *M.J. Wingfield* (holotype CBS H-21978, culture ex-type CPC 23674 = CBS 138896; ITS sequence GenBank KP004444, LSU sequence GenBank KP004472, MycoBank MB810590).

Notes — The genus *Alanphillipsia* (*Botryosphaeriaceae*, see Phillips et al. 2013) was recently introduced to accommodate four species that are aplosporella-like in morphology, but have conidia with a hyaline outer layer. Of the three species known from *Aloe*, *A. aloeicola* is most similar to *A. aloetica* in morphology, but distinct in that conidia of *A. aloeicola* (25–)30–35(–42) × (10–)12–14(–17) µm are wider than those of *A. aloetica* (20–)30–33(–35) × (5–)6(–7) µm (Crous et al. 2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Alanphillipsia aloetica* (GenBank KF777139; Identities = 568/571 (99 %), Gaps = 2/571 (0 %)), *Alanphillipsia aloeigena* (GenBank KF777137; Identities = 564/571 (99 %), Gaps = 4/571 (0 %)) and *Alanphillipsia aloes* (GenBank KF777138; Identities = 547/566 (97 %), Gaps = 9/566 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Alanphillipsia aloetica* (GenBank KF777195; Identities = 811/812 (99 %), no gaps), *Alanphillipsia aloeigena* (GenBank KF777193; Identities = 783/784 (99 %), no gaps) and *Alanphillipsia aloes* (GenBank KF777194; Identities = 810/812 (99 %), no gaps).

Colour illustrations. *Aloe* sp. in Clanwilliam; conidiogenous cells with conidia, spermatophores and spermatia. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Diaporthe phragmitis

Fungal Planet 283 – 24 November 2014

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; collarette 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 NCBIs 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 NCBIs 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 NCBIs 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.

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
Ying Zhang, Institute of Microbiology, Beijing Forestry University, P.O. Box 61, Beijing 100083, PR China;
e-mail: yinghku@gmail.com


Dinemasporium ipomoeae

Fungal Planet 284 – 24 November 2014

Dinemasporium ipomoeae Crous, *sp. nov.*

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

Conidiomata stromatic, scattered or aggregated, superficial, pale brown, cupulate, unilocular, globose, up to 250 µm diam, setose with a central crystalline conidial mass on PNA; basal stroma of *textura angularis*, layer 20–30 µm thick. *Setae* of two types. Type A brown to black, simple, subulate with acute apex, unbranched, smooth, thick-walled, up to 6-septate, 50–200 × 5–8 µm, 1 µm wide at acute apex, arising from basal stroma or lateral from excipulum. Type B setate pale brown, flexuous, septate, up to 100 µm long, 1.5–2 µm diam. *Conidiophores* lining the basal stroma, 1–2-septate, sparingly branched, cylindrical, thin-walled, smooth, base pale brown, apex hyaline, 15–20 × 2–3 µm. *Conidiogenous cells* determinate, phialidic with periclinal thickening, hyaline, smooth, subcylindrical, 8–12 × 2–2.5 µm. *Conidia* hyaline, aseptate, thin-walled, smooth, fusoid-ellipsoid, straight, ends acutely rounded, guttulate, (7–)8(–9) × (2.5–)3(–3.5) µm, with three, unbranched, flexuous, centric, tubular appendages at each end, 3–5 µm.

Culture characteristics — Colonies after 2 wk at 25 °C in the dark spreading, flat, with sparse to moderate aerial mycelium and feathery margins. On MEA surface white, reverse white to ochreous. On OA buff. On PDA surface dirty white, reverse buff.

Typus. Vietnam, Can Dao Islands, Con Son, sea shore, on leaves of *Ipomoea pes-caprae* (*Convolvulaceae*), 12 Dec. 2012, *U. Damm* (holotype CBS H-21980, culture ex-type CPC 21885 = CBS 138898; ITS sequence GenBank KP004446, LSU sequence GenBank KP004474, MycoBank MB810589).

Colour illustrations. Scenic tree from Can Dao Islands, Vietnam; conidiomata on CLA, setae, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Dinemasporium* and allied genera were recently treated in separate studies (Crous et al. 2012b, 2014, Hashimoto et al. 2014), in which *Diarimella* and *Stauronema* were reduced to synonymy under *Dinemasporium*. In conidiomata of *Dinemasporium ipomoeae*, dehiscence by a longitudinal raphe was not seen, but the conidial appendages and two types of setae suggest that this is a member of the genus *Diarimella* sensu Sutton (1980). This adds further support to reduce *Diarimella* to synonymy with *Dinemasporium* (Hashimoto et al. 2014). *Dinemasporium ipomoeae* is phylogenetically distinct from other members.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dinemasporium polygonum* (GenBank JQ889276; Identities = 428/445 (96 %), Gaps = 8/445 (1 %)), *Dinemasporium americana* (GenBank JQ889274; Identities = 474/509 (93 %), Gaps = 13/509 (2 %)) and *Dinemasporium strigosum* (GenBank JQ889283; Identities = 521/560 (93 %), Gaps = 16/560 (2 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dinemasporium polygonum* (GenBank JQ889292; Identities = 788/793 (99 %), no gaps), *Dinemasporium morbidum* (GenBank JQ889297; Identities = 786/793 (99 %), no gaps) and *Dinemasporium pseudostrigosum* (GenBank JQ889295; Identities = 786/793 (99 %), no gaps).

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
Ulrike Damm, Senckenberg Museum of Natural History Görlitz, PF 300 154, 02806 Görlitz, Germany;
e-mail: ulrike.damm@senckenberg.de


Phyllosticta mimusopisicola

Fungal Planet 285 – 24 November 2014

Phyllosticta mimusopisicola Crous & W.J. Swart, *sp. nov.*

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

Leaf spots brown, amphigenous, subcircular, associated with leaf margins, up to 2 cm diam. *Conidiomata* pycnidial, solitary, black, erumpent, globose, exuding colourless to opaque conidial masses; *pycnidia* up to 150 µm diam; pycnidial wall of several layers of *textura angularis*, up to 30 µm thick; inner wall of hyaline *textura angularis*. *Ostiole* central, up to 10–20 µm diam. *Conidiophores* subcylindrical to ampulliform, reduced to conidiogenous cells, or with 1–2 supporting cells, at times branched at base, 20–30 × 5–7 µm. *Conidiogenous cells* terminal, subcylindrical, hyaline, smooth, coated in a mucoid layer, 7–15 × 2.5–3 µm; proliferating several times percurrently near apex. *Conidia* 10–11(–12) × (5.5–)6–6.5(–7) µm, solitary, hyaline, aseptate, thin- and smooth-walled, coarsely guttulate, or with a single large central guttule, ellipsoid to obovoid, tapering towards a narrow truncate base, 2.5–3 µm diam, enclosed in a thin, persistent mucoid sheath, 1–2 µm thick and bearing a hyaline, apical mucoid appendage, (8–)17–25(–35) × 1.5(–2) µm, flexible, unbranched, tapering towards an acute tip. *Spermatogonia* resembling conidiomata. *Spermatia* hyaline, smooth, subcylindrical with obtuse apex and truncate base, 7–15 × 1.5–2 µm.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelium, and feathery, lobate margins. On PDA surface greenish black, reverse iron-grey. On OA surface iron-grey. On MEA surface olivaceous-grey in centre, pale olivaceous-grey in outer region, olivaceous-grey underneath.

Typus. South Africa, Limpopo province, Klein Kariba ATKV resort, S24°50'11.6" E28°19'55.6", on leaves of *Mimusops zeyheri* (*Sapotaceae*), 22 Jan. 2013, *P.W. Crous & W.J. Swart* (holotype CBS H-21981, culture ex-type CPC 22063 = CBS 138899; ITS sequence GenBank KP004447, LSU sequence GenBank KP004475, MycoBank MB810591).

Notes — Several species of *Phyllosticta* have been described from *Mimusops*, namely *P. mimusopsidis* Henn., which turned out to be a species of *Phomopsis*, *P. mimusopsidis* Cufino, which appears to be a species of *Phoma*, along with *P. mimusopsidis-elengi* (van der Aa & Vanev 2002). As far as we are aware, *Phyllosticta mimusopisicola* is thus the first true species of *Phyllosticta* reported from *Mimusops.*

In a recent phylogenetic re-evaluation of the genus *Phyllosticta* (Wikee et al. 2013), two nomenclatural errors were made that need to be corrected, namely *P. rubra* Berl. & Voglino (1886) was added to the MycoBank repository after the deposit of *P. rubra* Wikee & Crous (2013), rendering the latter invalid, while the name *P. mangifera-indica* Wikee, Crous, K.D. Hyde & McKenzie was never deposited in MycoBank.

Phyllosticta rubella Wikee & Crous, *nom. nov.* — MycoBank MB810592

≡ *Phyllosticta rubra* Wikee & Crous, Stud. Mycol. 76: 25. 2013 (nom. illegit., Art. 53.1), non *P. rubra* Berl. & Voglino (1886).

Description and illustration: Wikee et al. (2013).

Specimen examined. USA, Missouri, on *Acer rubrum*, July 1999, *G. Carroll* (holotype CBS H-21398, culture ex-type CBS 111635).

Phyllosticta mangiferae-indicae Wikee, Crous, K.D. Hyde & McKenzie, *sp. nov*. — MycoBank MB810593

≡ *Phyllosticta mangifera-indica* Wikee, Crous, K.D. Hyde & McKenzie, Stud. Mycol. 76: 18. 2013 (nom. illegit., Art. 42.1).

Description and illustration: Wikee et al. (2013).

Specimen examined. Thailand, Chiangrai, Nanglae, on healthy leaf of *Mangifera indica*, July 2011, *S. Wikee* (holotype MFU13-0108; ex-type culture CPC 20274 = MFLUCC10-0029 = CBS 136061).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phyllosticta podocarpicola* (GenBank KF206173; Identities = 389/409 (95 %), Gaps = 7/409 (1 %)), *Phyllosticta cornicola* (GenBank KF170307; Identities = 384/409 (94 %), Gaps = 9/409 (2 %)) and *Phyllosticta minima* (GenBank KF766216; Identities = 384/409 (94 %), Gaps = 6/409 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phyllosticta philoprina* (GenBank KF766342; Identities = 762/773 (99 %), no gaps), *Guignardia rhodorae* (GenBank KF206292; Identities = 745/756 (99 %), no gaps) and *Phyllosticta foliorum* (GenBank KF206287; Identities = 745/756 (99 %), no gaps).

Colour illustrations. *Mimusops zeyheri* at the Klein Kariba ATKV resort; conidiomata, conidiophores, conidia and spermatia. Scale bars = 10 µm.

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


Rachicladosporium eucalypti

Fungal Planet 286 – 24 November 2014

Rachicladosporium eucalypti Crous, *sp. nov.*

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

Leaf spots brown, amphigenous, subcircular to irregular, up to 15 mm diam. *Colonies* homothallic, sporulating on OA. *Ascomata* pseudothecial, erumpent, up to 90 µm diam, with central ostiole; wall of 3–6 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate, subsessile, hyaline, smooth, 8-spored, narrowly obovoid, with minute apical chamber, 1 µm diam, 23–40 × 7–12 µm. *Pseudoparaphyses* absent. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, widest in middle of apical cell, tapering towards both ends, constricted at median septum, (10–)11–12 × 3(–3.5) µm; ascospores germinating from both ends, frequently with lateral branches, ascospores becoming distorted, 6–8 µm diam, brown and verruculose.

Culture characteristics — Colonies reaching 12 mm diam after 2 wk at 25 °C in the dark, spreading with moderate aerial mycelium, and even, smooth margins. On MEA surface olivaceous-grey, reverse iron-grey. On PDA surface smoke grey, reverse olivaceous-grey. On OA surface olivaceous-grey.

Typus. Ethiopia, Addis Ababa, Addis Ababa Botanical Garden, N09°05' 16.2" E38°43'4.7", on leaves of *Eucalyptus globulus* (*Myrtaceae*), 24 June 2013, *P.W. Crous & A. Assefa* (holotype CBS H-21982, culture ex-type CPC 23241 = CBS 138900; ITS sequence GenBank KP004448, LSU sequence GenBank KP004476, MycoBank MB810594).

Notes — The genus *Rachicladosporium* was established for taxa associated with leaf spots that are cladosporium-like in morphology, but distinct in that they have conidiophores with an apical rachis, and conidia that are pigmented, occur in chains and have slightly thickened hila (Crous et al. 2007b). *Rachicladosporium eucalypti* is the first species in the genus with a known sexual morph, which is mycosphaerella-like in morphology.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Rachicladosporium alpinum* (GenBank KF309941; Identities = 451/464 (97 %), Gaps = 4/464 (0 %)), *Rachicladosporium inconspicuum* (GenBank KF309939; Identities = 451/464 (97 %), Gaps = 4/464 (0 %)) and *Rachicladosporium pini* (GenBank JF951145; Identities = 564/584 (97 %), Gaps = 3/584 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Rachicladosporium alpinum* (GenBank KF309988; Identities = 705/707 (99 %), no gaps), *Rachicladosporium pini* (GenBank JF951165; Identities = 756/759 (99 %), no gaps) and *Rachicladosporium luculiae* (GenBank EU040237; Identities = 756/759 (99 %), no gaps).

Colour illustrations. *Eucalyptus globulus* leaves at the Addis Ababa Botanical Garden, Ethiopia; ascomata, asci and germinating ascospores. Scale bars = 10 µm.

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
Addisu Assefa, Department of Biology, Madawalabu University, P.O. Box 247, Bale Robe, Ethiopia;
e-mail: addddisu@yahoo.com


Arxiella dolichandrae

Fungal Planet 287 – 24 November 2014

Arxiella dolichandrae Crous, *sp. nov.*

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

Conidiomata sporodochial, forming loose, brown, superficial sporodochia on agar surface, up to 300 µm diam, consisting of brown *textura angularis* to *textura globulosa*, that become fertile at the edges. *Conidiogenous cells* smooth, brown, globose to somewhat elongated, 4–6 µm diam, phialidic, with minute periclinal thickening. *Conidia* solitary, hyaline, smooth, guttulate, reniform, medianly 1-septate, inner plane with apical and basal horn-like appendages following curvature of inner plane, 2–3 µm long; conidia (incl. appendages) 10–11 × 2.5–3 µm, with a slightly raised hilum (0.5 µm diam) at the base where the basal appendage joins the conidium body.

Culture characteristics — Colonies flat, appressed, spreading with sparse aerial mycelium, surface folded with smooth, lobate margin, reaching 3 cm diam after 2 wk at 25 °C in the dark. On MEA surface dirty white, reverse ochreous. On PDA surface dirty white, reverse pale luteous. On OA surface pale luteous.

Typus. South Africa, KwaZulu-Natal, Pietermaritzburg, S29°37'50.95" E30°25'51.67", on leaves of *Dolichandra unguiscati* (*Bignoniaceae*), 24 May 2013, *A. King* (holotype CBS H-21983, culture ex-type CPC 22951 = CBS 138853; ITS sequence GenBank KP004449, LSU sequence GenBank KP004477, MycoBank MB810595).

Notes — The genus *Arxiella* was established for a fungus collected from leaf litter and soil under *Acacia karroo* in South Africa (Papendorf 1967) and presently includes two species. *Arxiella dolichandrae* is distinct from these species by its conidial dimensions (*A. terrestris*, 6–16 × 3–4.5 µm; *A. lunata*, 10–17 × 3–4 µm) (Papendorf 1967, Ruscoe 1970).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Mycoleptodiscus terrestris* (GenBank JN711860; Identities = 363/420 (86 %), Gaps = 17/420 (4 %)), *Polychaeton citri* (GenBank GU214649; Identities = 445/538 (83 %), Gaps = 22/538 (4 %)) and *Leptoxyphium madagascariense* (GenBank GQ303277; Identities = 409/501 (82 %), Gaps = 28/501 (5 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Chlamydotubeufia huaikangplaensis* (GenBank JN865198; Identities = 722/809 (89 %), Gaps = 5/809 (0 %)), *Hysterium vermiforme* (GenBank GQ221897; Identities = 719/810 (89 %), Gaps = 6/810 (0 %)) and *Chlamydotubeufia khunkornensis* (GenBank JN865190; Identities = 720/813 (89 %), Gaps = 11/813 (1 %)).

Colour illustrations. Symptomatic leaves of *Dolichandra unguiscati*; colonies on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Alana den Breeÿen, ARC – Plant Protection Research Institute, P. Bag X5017, Stellenbosch 7599, South Africa;
e-mail: DenBreeyenA@arc.agric.za


Corynespora endiandrae

Fungal Planet 288 – 24 November 2014

Corynespora endiandrae Crous & Summerell, *sp. nov.*

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

Mycelium consisting of hyaline, smooth, branched, septate, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, straight to flexuous, subcylindrical, unbranched, brown, thick-walled, finely roughened, base bulbous, lacking rhizoids, 10–12 µm diam, stipe 200–300 × 5–7 µm, 8–16-septate. *Conidiogenous cells* integrated, terminal and lateral, monotretic, subcylindrical, brown, finely roughened, slightly darkened, 2 µm diam. *Conidia* obclavate, solitary or in short chains (2–3), thick-walled, brown, finely roughened, 3(–4) distoseptate, (35–)37–45(–57) × (7–)8(–9) µm; hila darkened, thickened, 2.5–3.5 µm diam.

Culture characteristics — Colonies reaching 20 mm diam after 2 wk at 25 °C in the dark, with moderate aerial mycelium and smooth, even margins. On MEA, PDA and OA surface and reverse dirty white.

Typus. Australia, New South Wales, Nightcap National Park, S28.33.918 E153.20.228, on leaves of *Endiandra introrsa* (*Lauraceae*), 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21984, culture ex-type CPC 22194 = CBS 138902; ITS sequence GenBank KP004450, LSU sequence GenBank KP004478, MycoBank MB810596).

Notes — Species of *Corynespora* are commonly associated with leaf spots as necrotrophic pathogens. Species have mainly been described based on host association, and the genus is in need of revision. No species have thus far been recorded on *Endiandra*, and based on the key provided by Siboe et al. (1999), *C. endiandrae* appears to represent a novel taxon.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Helminthosporium velutinum* (GenBank JN198435; Identities = 453/505 (90 %), Gaps = 9/505 (1 %)), *Helminthosporium solani* (GenBank KC106739; Identities = 501/560 (89 %), Gaps = 13/560 (2 %)) and *Helminthosporium chlorophorae* (GenBank AF120259; Identities = 422/475 (89 %), Gaps = 16/475 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Corynespora leucadendri* (GenBank KF251654; Identities = 806/819 (98 %), no gaps), *Corynespora olivacea* (GenBank JQ044448; Identities = 806/820 (98 %), Gaps = 1/820 (0 %)) and *Byssothecium circinans* (GenBank GU205217; Identities = 802/819 (98 %), no gaps).

Colour illustrations. Nightcap National Park, Australia; conidiophores and conidia. Scale bars = 10 µm.

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
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au


Gonatophragmium triuniae

Fungal Planet 289 – 24 November 2014

Gonatophragmium triuniae Crous & Summerell, *sp. nov.*

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

Mycelium consisting of hyaline, septate, branched, 2–3 µm diam hyphae. *Conidiophores* solitary, macronematous, erect, arising from superficial hyphae, straight to flexuous, T-cell at base slightly swollen (up to 7 µm diam) or not, stipe 200–280 µm long, 4–5 µm diam at the base, 4–7-septate, brown, smooth, thin-walled, branched in upper part. Primary branches pale brown, verruculose, subcylindrical, aseptate, 25–35 × 3–4 µm, giving rise to 1–2 secondary branches, pale brown, subcylindrical, aseptate, 15–20 × 3–4 µm. Secondary branches giving rise to a conidiogenous region consisting of 3–4 subcylindrical cells, pale brown, finely verruculose to smooth, each cell with an upper fertile region consisting of aggregated denticulate loci, 0.5 µm long, 1 µm diam, darkened and thickened; at times cells also have a fertile lateral branch, 13–20 × 3–3.5 µm. *Conidia* solitary, clavate, pale brown, guttulate, roughened, apex obtuse, lower part attenuating towards truncate base, 1 µm diam; conidia 1-septate, slightly constricted at septum, straight to slightly curved, apical cell 5–6 µm long, basal cell 7–8 µm long, conidia (10–)12–14(–15) × (3.5–)4(–4.5) µm (apical cell rarely developing a second septum); hila 0.5–1 µm diam, somewhat darkened and thickened.

Culture characteristics — Colonies reaching 15 mm diam after 2 wk at 25 °C in the dark, with moderate aerial mycelium and smooth, even margins. On MEA surface ochreous, reverse umber. On PDA surface luteous to buff, with diffuse, luteous pigment, but umber in reverse. On OA surface dirty white with diffuse buff pigment.

Typus. AUSTRALIA, New South Wales, Nightcap National Park, S28.38.413 E153.20.179, on leaves of *Triunia youngiana* (*Proteaceae*), 9 Mar. 2013, *B.A. Summerell* (holotype CBS H-21985, culture ex-type CPC 22191, 22192 = CBS 138901; ITS sequence of CPC 22191, GenBank KP004451, LSU sequence GenBank KP004479, MycoBank MB810597).

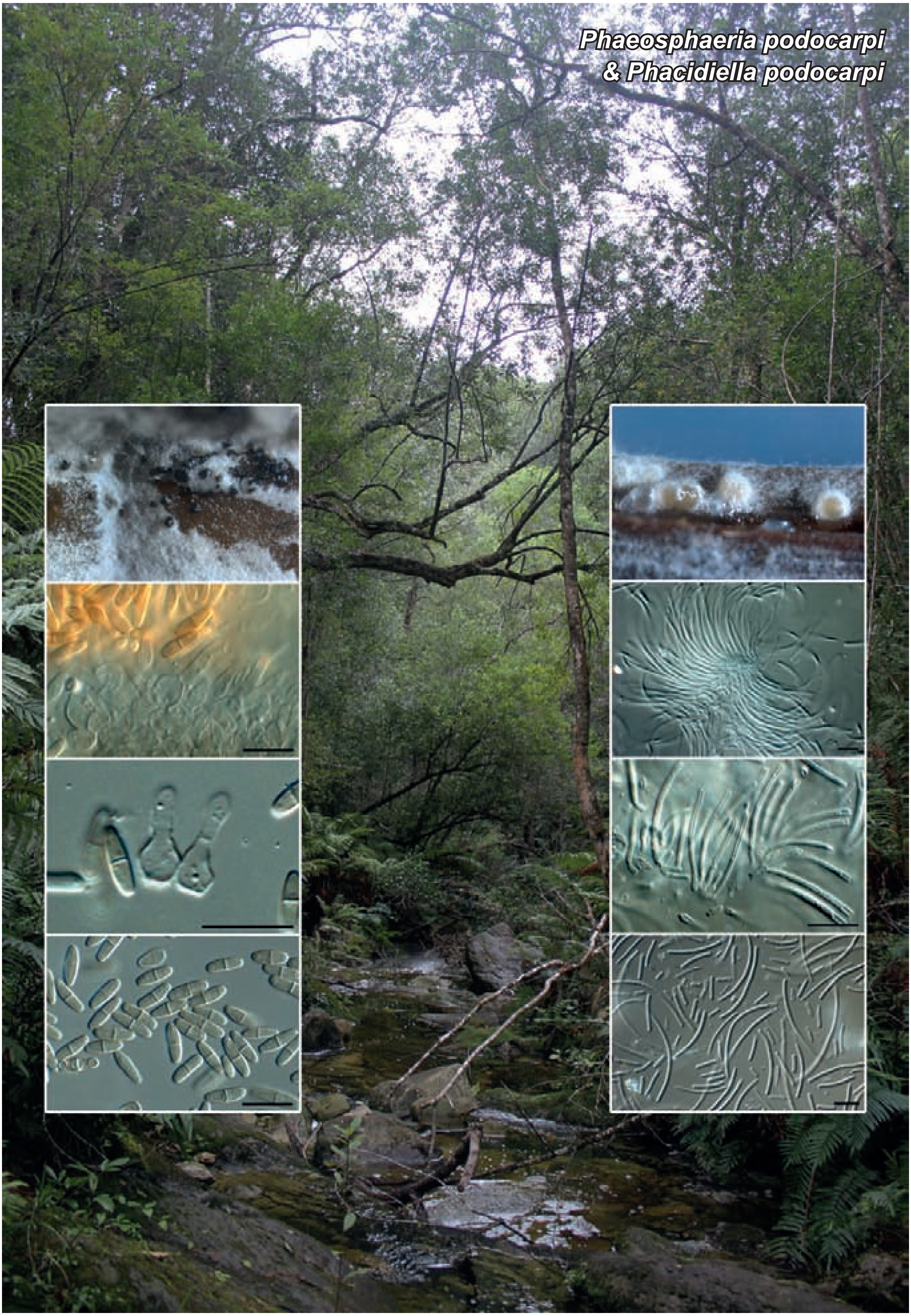
Notes — Species of *Gonatophragmium* are commonly associated with leaf spots on a wide range of hosts (Ellis 1971, 1976, Braun & Hill 2008). Of the approximately 15 species presently known to occur in the genus, *G. triuniae* is easily distinguished based on its small, 1-septate conidia. It is also the only species thus far reported from *Triunia.*

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Arthothelium spectabile* (GenBank AF138814; Identities = 446/469 (95 %), Gaps = 9/469 (1 %)), *Phaeodactylium stadleri* (GenBank HF678526; Identities = 317/369 (86 %), Gaps = 8/369 (2 %)) and *Radulidium subulatum* (GenBank EU041790; Identities = 436/544 (80 %), Gaps = 36/544 (6 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Acrospermum adeanum* (GenBank EU940104; Identities = 758/800 (95 %), no gaps), *Pseudovirgaria grisea* (GenBank JF957610; Identities = 780/827 (94 %), Gaps = 2/827 (0 %)) and *Pseudovirgaria hyperparasitica* (GenBank EU041822; Identities = 780/827 (94 %), Gaps = 2/827 (0 %)).

Colour illustrations. Nightcap National Park, Australia; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Brett A. Summerell, Royal Botanic Gardens and Domain Trust, Mrs. Macquaries Road, Sydney, NSW 2000, Australia;
e-mail: Brett.Summerell@rbgsyd.nsw.gov.au


Phaeosphaeria podocarpi
& Phacidiella podocarpi

Fungal Planet 290 & 291 – 24 November 2014

Phaeosphaeria podocarpi Crous & A.R. Wood, *sp. nov.*

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

Conidiomata pycnidial, erumpent, brown, globose, solitary, up to 300 µm diam, with central ostiole; wall of 4–8 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform, 4–7 × 3–4 µm, phialidic with inconspicuous periclinal thickening at apex. *Paraphyses* intermingled among conidiogenous cells, subcylindrical, hyaline, 1–2-septate, up to 25 µm long, 2–3 µm diam. *Conidia* solitary, red-brown in mass, smooth, fusoid-ellipsoidal, apex obtuse, base truncate, 1–1.5 µm diam, medianly 1-septate, mostly straight, (7–)8–10(–12) × (2–)2.5(–3) µm.

Culture characteristics — Colonies reaching 30 mm diam after 2 wk at 25 °C in the dark, surface folded, with moderate aerial mycelium and even, lobate margins. On MEA surface dirty white, reverse apricot. On OA surface pale olivaceous-grey. On PDA surface pale olivaceous-grey, reverse olivaceous-grey.

Typus. South Africa, Western Cape Province, Knysna, Garden Route National Park, Velbroeksdraai picnic site, Diepwalle Forest, S33°56' E23°09', on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 1 July 2013, *A.R. Wood* (holotype CBS H-21986, culture ex-type CPC 23433 = CBS 138903; ITS sequence GenBank KP004452, LSU sequence GenBank KP004480, ACT sequence GenBank KP004502, TUB sequence GenBank KP004508, MycoBank MB810598).

Notes — The genus *Phaeoseptoria* was shown to be synonymous with *Phaeosphaeria* by Quaedvlieg et al. (2013). Although most of the asexual morphs of *Phaeosphaeria* species have multiseptate conidia, the general morphology of *P. podocarpi* corresponds with other members of the genus. However, there are several unresolved lineages that are phaeosphaeria-like awaiting study. It is thus possible that *P. podocarpi* could still be segregated in a distinct genus based on additional collections and DNA sequence data.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Ascochyta manawaorae* (GenBank GU230751; Identities = 461/478 (96 %), Gaps = 3/478 (0 %)), *Phaeosphaeria poagena* (GenBank KJ869114; Identities = 522/542 (96 %), Gaps = 3/542 (0 %)) and *Parastagonospora nodorum* (GenBank KF512822; Identities = 510/532 (96 %), Gaps = 9/532 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria oryzae* (GenBank KF251689; Identities = 816/816 (100 %), no gaps), *Phaeosphaeriopsis musae* (GenBank DQ885894; Identities = 816/816 (100 %), no gaps) and *Phaeosphaeria papayae* (GenBank KF251690; Identities = 815/815 (100 %), no gaps).

Phacidiella podocarpi Crous & A.R. Wood, *sp. nov.*

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

Conidiomata pycnidial, hyaline to subhyaline on SNA, aggregated in clusters, globose, up to 350 µm diam; wall of 3–6 layers of hyaline *textura intricata*. *Conidiophores* lining the inner cavity, subcylindrical, smooth, hyaline, 1-septate, giving rise to 1–2 conidiogenous cells, 5–8 × 2–2.5 µm. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical to doliiform, proliferating sympodially at apex, 3–6 × 2–2.5 µm. *Conidia* solitary, hyaline, smooth, subcylindrical, flexuous, apex obtuse, base truncate, (45–)50–70(–90) × 2(–2.5) µm, 9–18-septate, disarticulating into phragmospores, cylindrical with truncate ends, 5–6 µm long.

Culture characteristics — Colonies reaching 10 mm diam after 2 wk at 25 °C in the dark, spreading, with fluffy aerial mycelium and feathery margin. On MEA surface and reverse dirty white, with diffuse apricot zone in agar. On OA surface apricot. On PDA surface salmon, reverse dirty white.

Typus. South Africa, Western Cape Province, Knysna, Garden Route National Park, Velbroeksdraai picnic site, Diepwalle Forest, S33°56' E23°09', on leaves of *Podocarpus latifolius* (*Podocarpaceae*), 1 July 2013, *A.R. Wood* (holotype CBS H-21987, culture ex-type CPC 23447 = CBS 138904; ITS sequence GenBank KP004453, LSU sequence GenBank KP004481, MycoBank MB810599).

Colour illustrations. Velbroeksdraai picnic site, Diepwalle Forest, South Africa; *Phaeosphaeria podocarpi* (left column): colonies on OA, conidiogenous cells and conidia; *Phacidiella podocarpi* (right column): conidiomata on PNA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — The genus *Phacidiella* (1884) has been linked to *Pyrenopeziza* (1870) sexual morphs (Sutton 1980). However, *Pyrenopeziza* is also linked to *Cylindrosporium* (1823), while some species of *Cylindrosporium* are linked to *Blumeriella* (1961) (Johnston et al. 1914). Sutton (1980) stated that *Phacidiella* and its generic synonyms are in need of revision, as some have 1-septate conidia (e.g. *Ramulariospora*), and others are aseptate, suggesting that they may not all be congeneric. *Phacidiella podocarpi* is thus best described in the genus *Phacidiella* based on its hyaline, aseptate conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Glomerobolus gelineus* (GenBank DQ247782; Identities = 232/248 (94 %), Gaps = 6/248 (2 %)), *Caloplaca albopruinosa* (GenBank EF093566; Identities = 240/260 (92 %), Gaps = 3/260 (1 %)) and *Umbilicaria mammulata* (GenBank DQ782851; Identities = 243/265 (92 %), Gaps = 5/265 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Stictis radiata* (GenBank AY300864; Identities = 751/783 (96 %), no gaps), *Carestiella socia* (GenBank AY661682; Identities = 790/827 (96 %), Gaps = 3/827 (0 %)) and *Conotrema populorum* (GenBank AY300833; Identities = 780/826 (94 %), Gaps = 4/826 (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
Alan R. Wood, ARC – Plant Protection Research Institute, P. Bag X5017, Stellenbosch 7599, South Africa; e-mail: wooda@arc.agric.za


Phellinocrescentia guianensis

Fungal Planet 292 – 24 November 2014

Phellinocrescentia Crous & Decock, *gen. nov.*

Etymology. L. = *crescit*, growing on, referring to its ecological habit, growing on *Phellinus*.

Conidiomata pycnidial, globose, solitary or aggregated, uni- to multilocular, with central ostiole; wall consisting of 3–6 layers of brown *textura angularis*; outer surface covered in brown, warty hyphae. *Conidiophores* reduced to conidiogenous cells or a supporting cell. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, tightly aggregated, subcylindrical, straight to curved, phialidic with periclinal thickening. *Conidia* aseptate, solitary, hyaline, smooth, guttulate, thin-walled, ellipsoid to tear-drop-shaped.

Type species. *Phellinocrescentia guianensis*.
MycoBank MB810600.

Phellinocrescentia guianensis Crous & Decock, *sp. nov.*

Etymology. Name reflects the locality, French Guiana, where this species was collected.

Conidiomata pycnidial, globose, solitary or aggregated, uni- to multilocular, up to 220 µm diam, with central ostiole; wall consisting of 3–6 layers of brown *textura angularis*, becoming hyaline towards inner centrum; outer surface covered in brown, warty hyphae, 3–4 µm diam. *Conidiophores* reduced to conidiogenous cells or a supporting cell. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, tightly aggregated, subcylindrical, straight to curved, phialidic with periclinal thickening, 5–12 × 1.5 µm. *Conidia* aseptate, solitary, hyaline, smooth, guttulate, thin-walled, ellipsoid to tear-drop-shaped, (2.5–)3(–4) × 1.5 µm.

Culture characteristics — Colonies reaching 7 mm diam after 2 wk at 25 °C in the dark, surface folded, with sparse aerial mycelium and even, lobed margins. On MEA surface a mixture of dirty white and olivaceous-grey, reverse olivaceous-grey. On OA and PDA olivaceous-grey.

Typus. French Guiana, on polypore No. 742 (*Phellinus* sp.), 12 July 2013, *C. Decock* (holotype CBS H-21988, culture ex-type CPC 23600 = CBS 138913; ITS sequence GenBank KP004454, LSU sequence GenBank KP004482, MycoBank MB810601).

Notes — The strain was found growing on the sporocarp of a *Phellinus* sp. and isolated by plating it on malt agar. *Phellinocrescentia guianensis* is phoma-like in morphology, but distinct in having solitary or aggregated, uni- to multilocular conidiomata, and ellipsoid to tear-drop-shaped conidia. It also has a unique ecological habit, growing on basidiocarps of a *Phellinus* sp. It was not possible to assign a genus to this fungus based on phylogenetic inference and the new genus, *Phellinocrescentia*, is introduced to accommodate it.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Didymosphaeria futilis* (GenBank EU552123; Identities = 470/574 (82 %), Gaps = 38/574 (6 %)), *Funbolia dimorpha* (GenBank JF951136; Identities = 362/424 (85 %), Gaps = 15/424 (3 %)) and *Geomyces pannorum* var. *asperulatus* (GenBank AJ938166; Identities = 329/395 (83 %), Gaps = 25/395 (6 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pseudopassalora gouriqua* (GenBank JN712565; Identities = 743/790 (94 %), no gaps), *Heleiosa barbatula* (GenBank GU479787; Identities = 735/793 (93 %), Gaps = 5/793 (0 %)) and *Funbolia dimorpha* (GenBank JF951156; Identities = 729/790 (92 %), Gaps = 1/790 (0 %)).

Colour illustrations. Basidiomata of *Phellinus* sp. on a dead standing tree in French Guiana; conidiomata in agar, warty hyphae, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Cony A. Decock, Mycothèque de l'Université catholique de Louvain (MUCL, BCCM™), Earth and Life Institute – ELIM – Mycology,
Université catholique de Louvain, Croix du Sud 2 bte L7.05.06, B-1348 Louvain-la-Neuve, Belgium;
e-mail: cony.decock@uclouvain.be


Neocamarosporium chichastianum

Fungal Planet 293 – 24 November 2014

Neocamarosporium chichastianum Papizadeh, Crous, Shahzadeh Fazeli & Amoozegar, *sp. nov.*

Etymology. Name reflects the location, Lake Urmia (formerly known as Chichast), from which the species was isolated.

Conidiomata pycnidial, solitary, uniloculate, black, up to 200 µm diam, with 1–3 papillate necks (up to 150 µm diam), with central ostioles 5–10 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, subcylindrical, 7–15 × 4–5 µm, proliferating percurrently at apex. *Paraphyses* intermingled between conidiogenous cells, hyaline, smooth, subcylindrical, 1–2-septate with obtuse ends, up to 35 µm long, 4–5 µm diam. *Conidia* solitary, brown, finely roughened, ellipsoid, widest in middle, apex obtuse, muriformly septate, thick-walled, base truncate, 2–3 µm diam, (11–)15–19(–22) × (6–)8–9(–11) µm; 3 transverse septa, 1–2 oblique or vertical septa.

Culture characteristics — Colonies flat, spreading with sparse aerial mycelia. On OA surface olivaceous-grey. On MEA surface pale olivaceous-grey to olivaceous-grey. Optimum growth occurred at 25 °C, but the fungus grew at 15 °C up to 35 °C. Furthermore, optimum growth was recorded at pH values between 5.5 and 6.5, although it could grow at a broad range of pH values (4–10).

Typus. Iran, Lake Urmia, soil, 2011, *M. Papizadeh & M.R. Soudi* (holotype CBS H-21989, culture ex-type IBRC-M 30126 = CBS 137502; ITS sequence GenBank KP004455, LSU sequence GenBank KP004483, MycoBank MB810602).

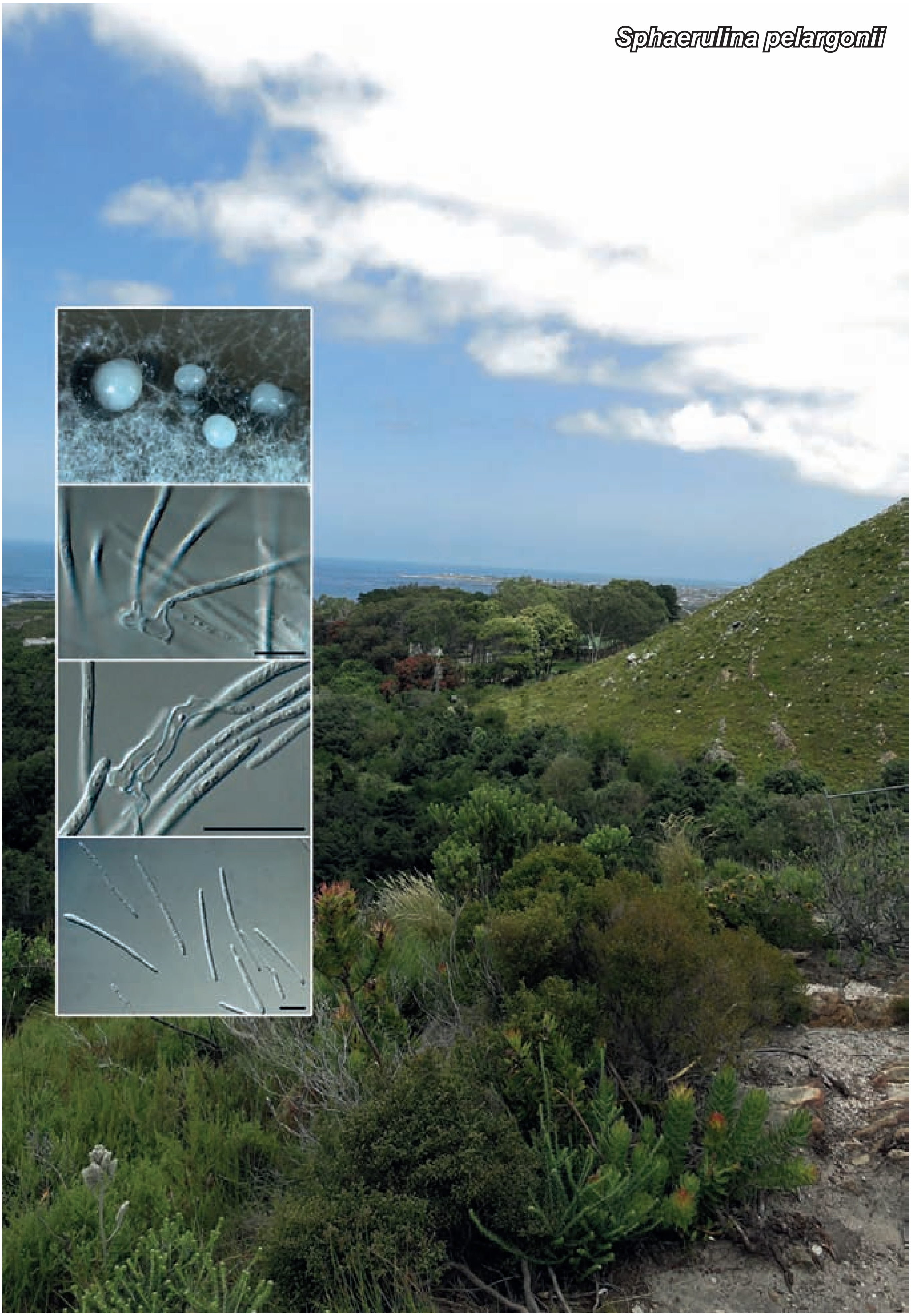
Notes — *Neocamarosporium chichastianum* clusters with *N. goegapense*, the type species of the genus *Neocamarosporium*, which is morphologically similar to the genus *Camarosporium* based on its pycnidial conidiomata, hyaline, percurrently proliferating conidiogenous cells, and brown, muriformly septate conidia (Crous et al. 2014). *Neocamarosporium chichastianum* is the second species described in this genus, and interestingly has paraphyses, which were not observed in *N. goegapense.*

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Neocamarosporium goegapense* (GenBank KJ869163; Identities = 550/579 (95 %), Gaps = 5/579 (0 %)), *Phoma betae* (GenBank KC460811; Identities = 463/493 (94 %), Gaps = 7/493 (1 %)) and *Ascochyta obiones* (GenBank GU230752; Identities = 463/498 (93 %), Gaps = 4/498 (0 %)). Our ITS sequence is 98 % (517/529) identical to the sequence of *Chaetosphaeronema hispidulum* CBS 826.88 in Q-bank (www.q-bank.eu).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Neocamarosporium goegapense* (GenBank KJ869220; Identities = 804/806 (99 %), no gaps), *Chaetosphaeronema hispidulum* (GenBank EU754145; Identities = 848/851 (99 %), no gaps) and *Coniothyrium obiones* (GenBank DQ678054; Identities = 849/853 (99 %), no gaps).

Colour illustrations. Lake Urmia in Iran; conidiomata on OA and PNA, conidiomatal neck, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Moslem Papizadeh, Seyed Abolhassan Shahzadeh Fazeli & Mohammad Ali Amoozegar,
Microorganisms Bank, Iranian Biological Resource Center (IBRC), Academic Center for Education, Culture & Research (ACECR) Tehran, Iran
e-mail: papizadeh@ibrc.ir, fazeli@ibrc.ir & amoozegar@ibrc.ir


Sphaerulina pelargonii

Fungal Planet 294 – 24 November 2014

Sphaerulina pelargonii Crous & M.J. Wingf., *sp. nov.*

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

Sporulating on SNA. *Conidiomata* pycnidial, brown, separate, immersed to erumpent, globose, up to 150 µm diam, exuding a creamy crystalline conidial mass via a central ostiole; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, at times pale brown, smooth, subcylindrical, straight to geniculous-sinuous, 7–15 × 3–5 µm, proliferating sympodially. *Conidia* hyaline, smooth, guttulate, filiform, narrowly obclavate, apex subobtusely rounded, base long obconically truncate, (1–)3–4-septate, (15–)28–45(–60) × 1.5–2(–2.5) µm.

Culture characteristics — Colonies on PDA, MEA and OA spreading with sparse to moderate aerial mycelium, and smooth, lobate margins, reaching 20 mm diam after 2 wk at 25 °C in the dark. On MEA surface olivaceous-grey with apricot sporulation, iron-grey underneath. On PDA surface olivaceous-grey with strands of dirty white mycelium, reverse iron-grey. On OA surface dirty white.

Typus. South Africa, Western Cape Province, Betty's Bay, Harold Porter National Botanical Garden, on leaves of *Pelargonium* sp. (*Geraniaceae*), 15 Jan. 2014, *P.W. Crous & M.J. Wingfield* (holotype CBS H-21990, culture ex-type CPC 24151 = CBS 138857; ITS sequence GenBank KP004456, LSU sequence GenBank KP004484, TEF sequence GenBank KP004506, MycoBank MB810603).

Notes — The genus *Sphaerulina* was shown to have septoria-like asexual morphs by Quaedvlieg et al. (2013), several of which were either endophytes or important plant pathogens. Although *Sphaerulina pelargonii* was associated with small, brown leaf spots on *Pelargonium*, inoculation studies have not been conducted to confirm its pathogenicity. This is the first species of *Sphaerulina* reported on this host. Similar taxa reported from *Pelargonium* include *Septoria pelargonii* (conidia 3–5-septate, 40–60 × 2–2.5 µm), *Septoria canberrica* (conidia 1–3-septate, 12–30(–36) × 1.5–2 µm), *Septoria geranii* (conidia 35–50 × 1 µm) and *Septoria geranii-nodosi* (conidia 50–65 × 2 µm). Species of *Septoria* that are known from culture were recently treated in detail by Verkley et al. (2013).

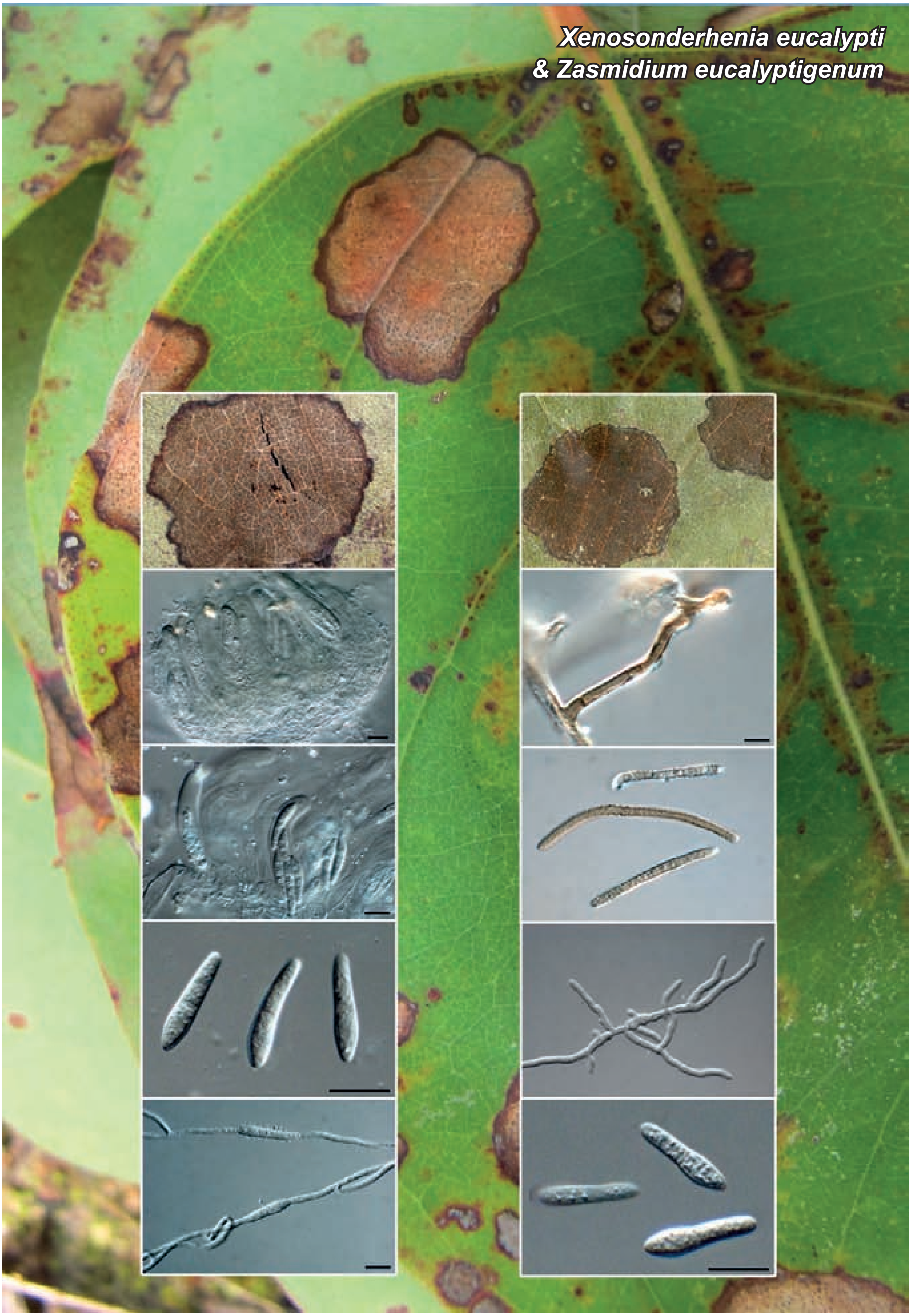
ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Sphaerulina rhododendricola* (GenBank KF777187; Identities = 600/614 (98 %), Gaps = 8/614 (1 %)), *Mycosphaerella ribis* (GenBank EU167588; Identities = 634/649 (98 %), Gaps = 5/649 (0 %)) and *Pseudocercosporella chaenomelis* (GenBank JQ793663; Identities = 573/587 (98 %), Gaps = 8/587 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Sphaerulina rhododendricola* (GenBank KF779493; Identities = 834/836 (99 %), no gaps), *Pseudocercosporella chaenomelis* (GenBank GU253834; Identities = 826/828 (99 %), no gaps) and *Sphaerulina azaleae* (GenBank KF252105; Identities = 823/825 (99 %), no gaps).

TEF. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TEF sequence are *Sphaerulina rhabdoclinis* (GenBank KF253578; Identities = 344/382 (90 %), Gaps = 9/382 (2 %)), *Sphaerulina amelanchier* (GenBank KF253545; Identities = 344/382 (90 %), Gaps = 9/382 (2 %)) and *Sphaerulina menispermi* (GenBank KF253565; Identities = 343/381 (90 %), Gaps = 10/381 (2 %)).

Colour illustrations. Harold Porter National Botanical Garden, Betty's Bay, South Africa; conidiomata on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Xenosonderhenia eucalypti
& Zasmidium eucalyptigenum

Fungal Planet 295 & 296 – 24 November 2014

Xenosonderhenia eucalypti Crous & M.J. Wingf., *sp. nov.*

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

Leaf spots amphigenous, dark brown, 10–20 mm diam, with dark brown border. Co-occurring on leaf spots with *Zasmidium eucalyptigenum*. *Ascomata* hypophyllous, black erumpent, globose, solitary, up to 110 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate, subsessile, hyaline, smooth, 8-spored, obovoid to ellipsoid, aparaphysate, straight to slightly curved, 35–45 × 10–12 µm. *Pseudoparaphyses* absent. *Ascospores* tri- to multiseriate, hyaline, smooth, fusoid-ellipsoid, widest in apical cell, one third from apex, tapering towards both ends, not constricted at median septum, (17–)18–20(–22) × (3–)4 µm; ascospores germinating from both ends, not constricting or distorting, remaining hyaline, 4–5 µm diam; germ tubes developing numerous lateral branches.

Culture characteristics — Colonies spreading, erumpent with moderate aerial mycelium and smooth, lobate margins, reaching 20 mm diam on PDA, MEA and OA after 2 wk at 25 °C in the dark. On MEA surface pale luteus with patches of dirty white, reverse sienna. On OA surface saffron. On PDA surface saffron, reverse pale luteus.

Typus. Mozambique, Forestas de Niassa, leaf spots of *Eucalyptus urophylla* (*Myrtaceae*), 2 Feb. 2014, *M.J. Wingfield* (holotype CBS H-21991, culture ex-type CPC 24247 = CBS 138858; ITS sequence GenBank KP004457, LSU sequence GenBank KP004485, MycoBank MB810604).

Notes — *Xenosonderhenia eucalypti* appears to represent an undescribed genus in the *Mycosphaerellaceae*. It clusters with '*Mycosphaerella*' *elaeocarpi* that lacks an asexual morph and *Xenosonderhenia syzygii*, which lacks a sexual morph (Crous et al. 2012a). Because this taxon is clearly not a species of *Mycosphaerella* s.str., which has *Ramularia* asexual morphs (Verkley et al. 2004, Crous et al. 2009b), we tentatively place it in the genus *Xenosonderhenia*, pending further collections.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Xenosonderhenia syzygii* (GenBank JX069872; Identities = 506/525 (96 %), Gaps = 3/525 (0 %)), *Mycosphaerella elongata* (GenBank EF394833; Identities = 492/520 (95 %), Gaps = 4/520 (0 %)) and *Mycosphaerella elaeocarpi* (GenBank EU040212; Identities = 514/547 (94 %), Gaps = 7/547 (1 %)).

Zasmidium eucalyptigenum Crous & M.J. Wingf., *sp. nov.*

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

Co-occurring on leaf spots with *Xenosonderhenia eucalypti*. *Ascomata* hypophyllous, black erumpent, globose, solitary, up to 100 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Asci* fasciculate, bitunicate, subsessile, hyaline, smooth, 8-spored, obovoid to ellipsoid, aparaphysate, straight to slightly curved, 25–40 × 8–10 µm. *Pseudoparaphyses* absent. *Ascospores* hyaline, smooth, fusoid-ellipsoid, widest in middle of apical cell, tapering towards both ends, constricted at median septum, 13–16 × (2.5–)3.5–4 µm; ascospores germinating from both ends, becoming constricted, but remaining hyaline and smooth, 4–6 µm diam, developing lateral branches. Mycelium brown, verruculose, typical of *Zasmidium* asexual morph. *Conidiophores* brown, verruculose, solitary on superficial hyphae, erect, branched or not, up to 50 µm tall, 3–4 µm diam, 1–3-septate. *Conidiogenous cells* terminal or intercalary, with several thickened, darkened, refractive scars, 1 µm diam. *Conidia* brown, verruculose, straight to curved, solitary or in branched chains, subcylindrical, apex obtuse, base tapering to a truncate hilum, 1–1.5 µm diam, 1–9-septate, 30–120 × (2.5–)3 µm.

Colour illustrations. Leaf spots on *Eucalyptus urophylla*. *Xenosonderhenia eucalypti* (left column): leaf spot, asci with ascospores and germinating ascospores; *Zasmidium eucalyptigenum* (right column): leaf spots, conidiophore and conidia, ascospores and germinating ascospores. Scale bars = 10 µm.

Culture characteristics — Colonies erumpent, spreading, folded, with mucoid exudate and sparse to moderate aerial mycelium, and smooth, lobed margins, reaching 3 cm diam after 2 wk at 25 °C in the dark. Culture is sterile.. On OA surface olivaceous-grey. On MEA surface olivaceous-grey with patches of pale olivaceous-grey. On PDA surface olivaceous-grey with patches of pale olivaceous-grey, iron-grey in reverse.

Typus. Mozambique, Forestas de Niassa, leaf spots of *Eucalyptus urophylla* (*Myrtaceae*), 2 Feb. 2014, *M.J. Wingfield* (holotype CBS H-21992, culture ex-type CPC 24251 = CBS 138860; ITS sequence GenBank KP004458, LSU sequence GenBank KP004486, MycoBank MB810605).

Notes — The genus *Mycosphaerella* is polyphyletic (Crous et al. 2007a), and *Zasmidium* is the oldest name to accommodate stenella-like taxa clustering in the *Mycosphaerellaceae* (Arzanlou et al. 2007). Several species have thus far been described from *Eucalyptus* (Crous et al. 2009a, b, Braun et al. 2010), all of which are phylogenetically distinct from *Z. eucalyptigenum*.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Zasmidium rothmanniae* (GenBank KJ869135; Identities = 461/480 (96 %), Gaps = 7/480 (1 %)), *Periconiella arcuata* (GenBank EU041779; Identities = 427/449 (95 %), Gaps = 6/449 (1 %)) and *Mycosphaerella pseudovespa* (GenBank DQ530216; Identities = 432/457 (95 %), Gaps = 6/457 (1 %)).

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, P. Bag X20, Pretoria, 0028, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za


Diaporthe acaciarum

Fungal Planet 297 – 24 November 2014

Diaporthe acaciarum Crous & M.J. Wingf., *sp. nov.*

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

Sporulating on PNA. *Conidiomata* pycnidial, globose, up to 300 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, 2–3-septate, branched, densely aggregated, cylindrical, straight to sinuous, 20–30 × 2.5–4 µm. *Conidiogenous cells* 15–25 × 2–3 µm, phialidic, cylindrical, terminal and intercalary, with slight apical taper, 1–1.5 µm diam, with visible periclinal thickenening; collarette not flared, up to 2 µm long. *Paraphyses* not observed. *Alpha conidia* (6–)6.5–7(–7.5) × (2–)2.5(–3) µm, aseptate, hyaline, smooth, bi-guttulate, fusoid-ellipsoid, tapering towards both ends, straight apex subobtuse, base subtruncate, 1 µm diam. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, apex acutely rounded, base truncate, tapering from the lower third towards the base, (20–)25–35(–40) × 1.5(–2) µm.

Culture characteristics — Colonies covering the dish after 2 wk at 25 °C in the dark, with sparse to moderate aerial mycelium. On MEA, PDA and OA surface dirty white with patches of grey-olivaceous, reverse dirty white with patches of sienna.

Typus. TANZANIA, Serengeti, on thorns of *Acacia tortilis* (*Fabaceae*), Feb. 2014, *M.J. Wingfield* (holotype CBS H-21994, culture ex-type CPC 24324 = CBS 138862; ITS sequence GenBank KP004460, LSU sequence GenBank KP004488, HIS sequence GenBank KP004504, TUB sequence GenBank KP004509, MycoBank MB810606).

Notes — No *Diaporthe* (incl. *Phomopsis*) species have been described from *Acacia tortilis* (Uecker 1988, Gomes et al. 2013). Phylogenetically, *D. acaciarum* is closely related to several species based on ITS (see below), but it can be distinguished from them based on TUB sequence data.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis chimonanthi* (GenBank KF746059; Identities = 505/513 (98 %), Gaps = 5/513 (0 %)), *Diaporthe helianthi* (GenBank JQ936257; Identities = 546/556 (98 %), Gaps = 1/556 (0 %)) and *Diaporthe infecunda* (GenBank KF939614; Identities = 525/536 (98 %), Gaps = 4/536 (0 %)).

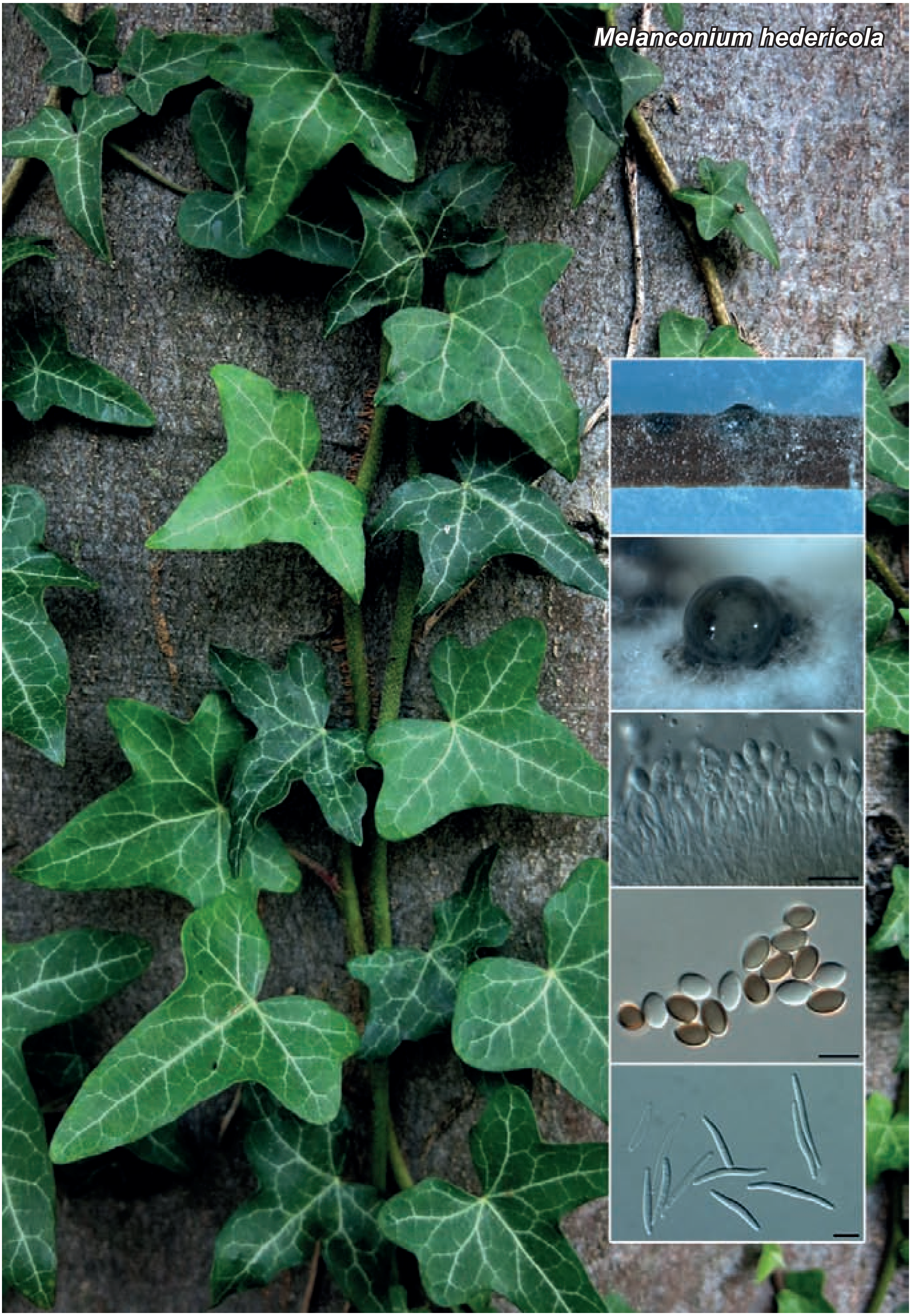
LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Diaporthe leucospermi* (GenBank JN712524; Identities = 836/839 (99 %), no gaps), *Taeniolella alta* (GenBank DQ377938; Identities = 834/839 (99 %), no gaps) and *Diaporthe arctii* (GenBank AF362562; Identities = 831/836 (99 %), no gaps).

HIS. Closest hits using the HIS sequence had highest similarity to *Diaporthe infecunda* (GenBank KC343613; Identities = 359/369 (97 %), Gaps = 1/369 (0 %)), *Diaporthe terebinthifolii* (GenBank KC343702; Identities = 353/371 (95 %), Gaps = 6/371 (1 %)) and *Diaporthe melonis* (GenBank KC343626; Identities = 351/373 (94 %), Gaps = 5/373 (1 %)).

TUB. Closest hits using the TUB sequence had highest similarity to *Diaporthe infecunda* (GenBank KF939619; Identities = 753/783 (96 %), Gaps = 4/783 (0 %)), *Diaporthe beilharziae* (GenBank KF170921; Identities = 743/777 (96 %), Gaps = 1/777 (0 %)) and *Diaporthe terebinthifolii* (GenBank KC344186; Identities = 662/708 (94 %), Gaps = 1/708 (0 %)).

Colour illustrations. Leopard in *Acacia tortilis* tree in the Serengeti, Tanzania; conidiomata on PNA, conidiogenous cells, alpha and beta conidia. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa;
e-mail: mike.wingfield@fabi.up.ac.za


Melanconium hedericola

Fungal Planet 298 – 24 November 2014

Melanconium hedericola Crous & R.K. Schumach., *sp. nov.*

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

Conidiomata pycnidial single or in densely crowded groups under loosened bark, superficial on a black stromatic layer which continues as a black stromatic line deep in the wood, ± pyroid with flattened base, black, rough, soft, distinctly thick, ostiolum central and indistinct; periphyses not seen, with a few setae on the outer site of the peridium. *Setae* 1-celled, stiff, pointed, basally enlarged and flattened, brown, thick-walled, smooth, eguttulate, up to 26 µm long. *Peridium* multi-layered, consisting of a red-brown *textura epidermoidea* (outer layer) and hyaline *textura angularis-prismatica* (inner layer), cells thick-walled, smooth and eguttulate. Sporulating on PNA. *Conidiomata* pycnidial, globose, up to 600 µm diam, black, immersed, exuding creamy conidial droplets from central ostioles, or developing 1–4 black necks on OA (not on PNA); walls consisting of 3–6 layers of medium brown *textura angularis*. *Conidiophores* hyaline, smooth, 1–2-septate, branched below, densely aggregated, cylindrical, straight to sinuous, 20–40 × 3–4 µm. *Conidiogenous cells* 10–17 × 2–3 µm, phialidic, cylindrical, terminal and intercalary, with slight apical taper, 2 µm diam, with visible periclinal thickening; collarette flared, up to 5 µm long. *Paraphyses* not observed. *Alpha conidia* (6–)7(–8) × (3.5–)4(–4.5) µm, aseptate, hyaline, smooth, ellipsoid with large central guttule, becoming brown with age. *Beta conidia* spindle-shaped, aseptate, smooth, hyaline, guttulate, apex bluntly rounded, base truncate, tapering from the middle towards the base, (17–)18–20(–25) × 2.5(–3) µm.

Culture characteristics — Colonies flat, spreading, covering the dish after 2 wk at 25 °C in the dark, with sparse aerial mycelium. On MEA, PDA and OA surface umber with patches of dirty white and iron-grey; reverse umber with patches of dirty white and iron-grey.

Typus. Spain, Sarasibar (Navarra), on branch of *Hedera helix* (*Araliaceae*), 26 Jan. 2014, *S. Garcia* (holotype CBS H-21995, culture ex-type CPC 24278 = CBS 138863; ITS sequence GenBank KP004461, LSU sequence GenBank KP004489, HIS sequence GenBank KP004505, TUB sequence GenBank KP004510, MycoBank MB810607).

Notes — Although *Melanconium hedericola* clusters within the genus *Diaporthe*, the LSU region lacks resolution within the *Diaporthales.* We have thus chosen to describe it in *Menanconium* based on the ellipsoid alpha conidia that turn brown with age, and their characteristic large, central guttules (Sutton 1980). However, *Melanconium* is known to not have species with beta conidia, which suggests that *M. hedericola* might represent an unknown genus within this complex. Further studies and collections are required before this question can be resolved. Previously published taxa on *Hedera* include *Coniothyrium hederae* and its possible synonym, *Melanconium hederae*, which have similar alpha conidia (6–8 × 4.5–6 µm), but that lack beta conidia.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Phomopsis columnaris* (GenBank FN394688; Identities = 528/541 (98 %), Gaps = 2/541 (0 %)), *Diaporthe endophytica* (GenBank AB899789; Identities = 566/583 (97 %), Gaps = 7/583 (1 %)) and *Diaporthe phaseolorum* (GenBank JQ936148; Identities = 565/583 (97 %), Gaps = 7/583 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phomopsis columnaris* (GenBank AF439627; Identities = 834/840 (99 %), no gaps), *Diaporthe ambigua* (GenBank JQ862833; Identities = 821/828 (99 %), no gaps) and *Phomopsis sclerotioides* (GenBank AF439628; Identities = 831/840 (99 %), no gaps).

HIS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the HIS sequence are *Diaporthe longispora* (GenBank KC343619; Identities = 360/378 (95 %), Gaps = 5/378 (1 %)), *Diaporthe sclerotioides* (GenBank KC343678; Identities = 359/381 (94 %), Gaps = 4/381 (1 %)) and *Diaporthe* 'sp. 4' (GenBank KC343690; Identities = 356/378 (94 %), Gaps = 5/378 (1 %)).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the TUB sequence are *Diaporthe longispora* (GenBank KC344103; Identities = 398/420 (95 %), Gaps = 2/420 (0 %)), *Diaporthe sclerotioides* (GenBank KC344161; Identities = 391/416 (94 %), Gaps = 2/416 (0 %)) and *Diaporthe scabra* (GenBank HQ450372; Identities = 418/450 (93 %), Gaps = 2/450 (0 %)).

Colour illustrations. *Hedera helix* growing along a tree trunk; conidiomata on PNA and OA, conidiogenous cells, alpha and beta conidia. Scale bars = 10 µm.

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
René K. Schumacher, Hölderlinstraße 25, 15517 Fürstenwalde/Spree, Germany; e-mail: bolbitius@web.de


Neophysalospora eucalypti

Fungal Planet 299 – 24 November 2014

Neophysalospora Crous & M.J. Wingf., *gen. nov.*

Etymology. Name reflects the fact that the genus is morphologically similar to the genus *Physalospora*.

Endophytic and plant pathogenic. *Ascomata* globose, solitary, brown, immersed, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Asci* cylindrical, hyaline, stipitate, unitunicate with apical mechanism staining in Melzer's reagent, ascospores uniseriate but overlapping, with 8 ascospores per ascus. *Paraphyses* intermingled among asci, hyaline, septate, branched. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, with acutely rounded ends. *Conidiomata* globose, solitary to aggregated, brown, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner conidiomatal wall, subcylindrical, straight to curved, branched, septate, or reduced to conidiogenous cells, hyaline to pale brown, smooth or finely verruculose. *Conidiogenous cells* ampulliform to subcylindrical, hyaline, smooth, terminal or intercalary, phialidic with flared collarette at the apex. *Conidia* solitary, hyaline, smooth, subcylindrical, curved, with obtuse apex and truncate base, thick-walled.

Type species. *Neophysalospora eucalypti*.
MycoBank MB810608.

Neophysalospora eucalypti Crous & M.J. Wingf., *sp. nov.*

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

Associated with brown leaf spots in plantations, and cutting rot in nurseries. *Ascomata* globose, solitary, brown, up to 250 µm diam, with central ostiole, up to 80 µm diam; wall of 2–3 layers of brown *textura angularis*. *Asci* cylindrical, hyaline, stipitate, unitunicate with apical mechanism staining in Melzer's reagent, ascospores uniseriate but overlapping, with 8 ascospores per ascus, 70–100 × 6–8 µm. *Paraphyses* intermingled among asci, hyaline, septate, branched, 2–3 µm diam. *Ascospores* hyaline, smooth, guttulate, fusoid-ellipsoid, widest in middle, tapering to acutely rounded ends, (13–)15–17(–19) × (4–)4.5(–5) µm. Ascospores germinate from one end, remain hyaline, fusoid-ellipsoid, 15–17 × 7 µm. *Conidiomata* globose, solitary to aggregated, brown, up to 200 µm diam, with central ostiole; wall of 2–3 layers of brown *textura angularis*. *Conidiophores* lining the inner conidiomatal wall, subcylindrical, straight to curved, branched, 1–3-septate, or reduced to conidiogenous cells, hyaline to pale brown, smooth or finely verruculose, 10–30 × 2.5–4 µm. *Conidiogenous cells* ampulliform to subcylindrical, hyaline, smooth, terminal or intercalary, 7–12 × 1.5–3 µm, phialidic with flared collarette at the apex, 1.5–2 µm diam. *Conidia* solitary, hyaline, smooth, subcylindrical, curved, with obtuse apex and truncate base, thick-walled, (13–)14–15(–16) × 1.5 µm.

Culture characteristics — Colonies spreading with sparse, appressed aerial mycelium, reaching 6 mm diam after 2 wk at 25 °C in the dark; surface folded with feathery, lobate margin. On MEA surface flesh with patches of saffron, reverse red with patches of coral. On OA surface red with patches of peach and saffron. On PDA surface white, reverse saffron.

Colour illustrations. *Corymbia henryi* leaves in Mozambique; conidiomata on SNA, asci and ascospores, conidiogenous cells, germinating ascospores and conidia. Scale bars = 10 µm.

Typus. MOZAMBIQUE, on leaves of *Corymbia henryi* (*Myrtaceae*), 1 Feb. 2014, *M.J. Wingfield* (holotype CBS H-21996, culture ex-type CPC 24209 = CBS 138864; ITS sequence GenBank KP004462, LSU sequence GenBank KP004490, MycoBank MB810609). – SOUTH AFRICA, Mpumalanga province, Piet Retief, forestry nursery, cutting rot of *Eucalyptus grandis* × *camaldulensis*, 9 Jan. 1989, *P.W. Crous*, CPC 123 = CBS 110740 (ITS, LSU sequence GenBank KP031106, KP031108), CPC 124 = CBS 111123 (ITS, LSU sequence GenBank KP031107, KP031109) (specimen also deposited in IMI, now Kew).

Notes — The genus *Physalospora* (*Hyponectriaceae*) is polyphyletic, and in need of taxonomic revision. *Neophysalospora eucalypti* is reminiscent of *Clypeophysalospora latitans* and to some extent also *Plectosphaera eucalypti* (= *Phyllachora eucalypti*). *Clypeophysalospora latitans* is a saprobe or weak pathogen that is commonly encountered on living eucalypt leaves and leaf litter (Crous et al. 1990). It has a melanised clypeus, and unitunicate asci that strain in Melzer's reagent, and does not produce an asexual morph in culture. *Plectosphaera eucalypti* has black ascomata embedded in the leaf tissue, with a melanised pseudoclypeus, forming circular to irregular colonies on the leaf surface. It has bitunicate asci and ascospores wit a prominent mucoid sheath. Infections are usually visible on only one side of the leaf surface (Pascoe 1990, Park et al. 2000).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Bagadiella lunata* (GenBank GQ303269; Identities = 586/625 (94 %), Gaps = 15/625 (2 %)), *Bagadiella koalae* (GenBank JF951142; Identities = 586/627 (93 %), Gaps = 14/627 (2 %)) and *Bagadiella victoriae* (GenBank JF951141; Identities = 584/627 (93 %), Gaps = 12/627 (1 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Plectosphaera eucalypti* (GenBank DQ923538; Identities = 821/840 (98 %), Gaps = 2/840 (0 %)), *Bagadiella victoriae* (GenBank JF951161; Identities = 815/839 (97 %), no gaps) and *Bagadiella lunata* (GenBank GQ303300; Identities = 815/839 (97 %), no gaps).

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Seimatosporium pistaciae

Fungal Planet 300 – 24 November 2014

Seimatosporium pistaciae Crous & Mirab., *sp. nov.*

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

Foliicolous. *Conidiomata* pycnidioid, separate to gregarious, becoming erumpent, oval to elongate, up to 150 µm diam. *Conidiophores* arising from a central stroma, hyaline, 3–4-septate, branched, subcylindrical, 20–45 × 3–4 µm. *Conidiogenous cells* terminal and intercalary, hyaline, smooth, subcylindrical, straight to somewhat curved, 10–15 × 2–2.5 µm, proliferating inconspicuously percurrently at apex. *Conidia* ellipsoid to fusoid, 3-septate, smooth, not constricted at septa, two median cells medium brown, basal and apical cell hyaline, granular, (15–)17–20(–22) × (4–)4.5(–5) µm, apical cell obtusely rounded with apical appendage single, unbranched, filiform, flexuous, 10–14 µm; basal appendage single, unbranched, filiform, flexuous, excentric, 12–20 µm.

Culture characteristics — Colonies spreading, appressed with moderate aerial mycelium and smooth margin, reaching 7 cm diam after 2 wk at 25 °C in the dark. On MEA surface peach with patches of olivaceous-grey due to sporulation, and diffuse red pigment, reverse similar. On PDA surface dirty white with patches of luteous and olivaceous-grey, reverse salmon with patches of olivaceous-grey. On OA surface salmon with patches of grey-olivaceous.

Typus. Iran, Saveh, on buds of *Pistacia vera* (*Anacardiaceae*), 29 Apr. 2014, *M. Mirabolfathy* (holotype CBS H-21997, culture ex-type CPC 24455 = CBS 138865; CPC 24455 ITS sequence GenBank KP004463, CPC 24455 LSU sequence GenBank KP004491, CPC 24457 ITS sequence GenBank KP004464, CPC 24457 LSU sequence GenBank KP004492, MycoBank MB810610).

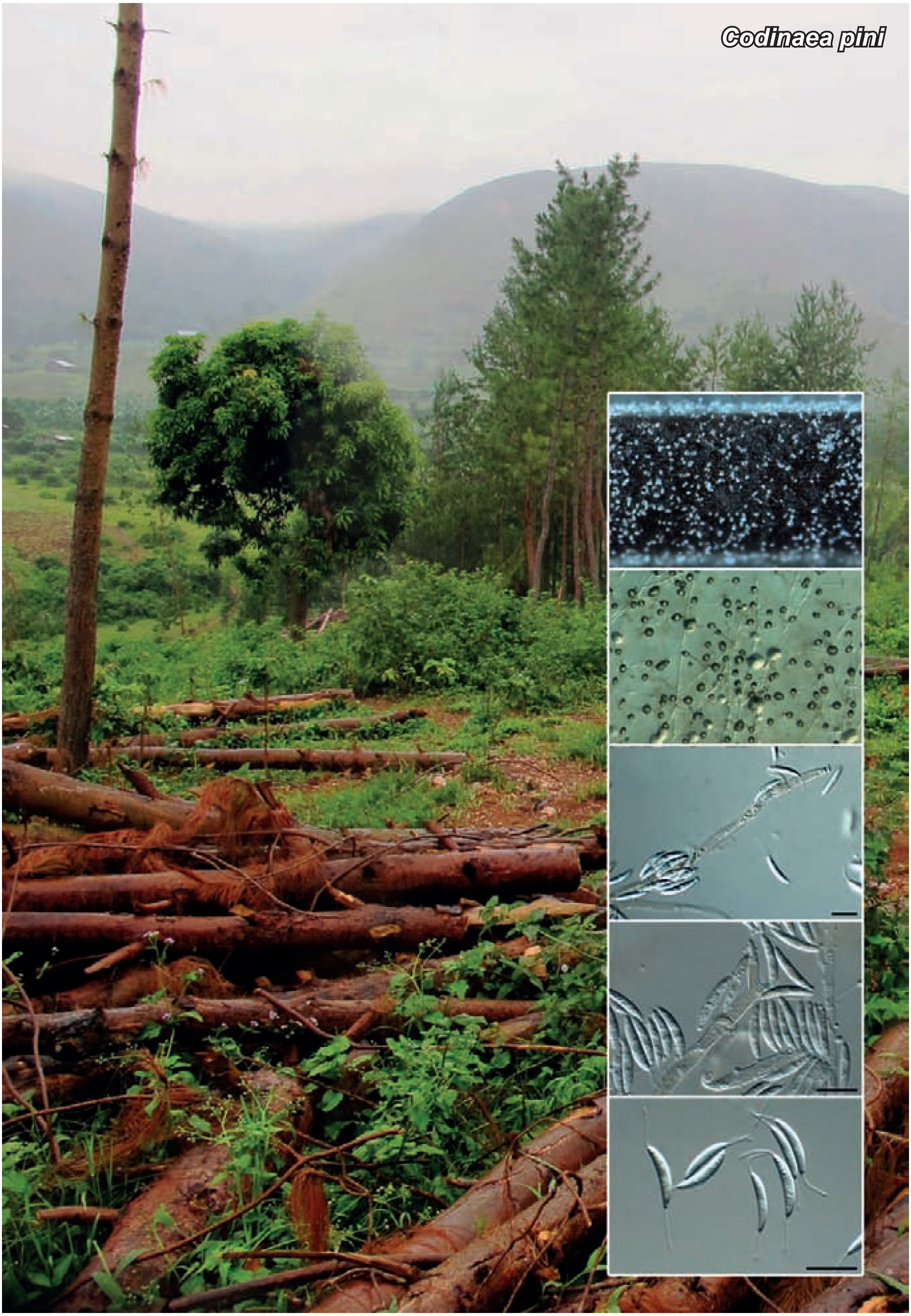
Notes — The genus *Seimatosporium* (1833) is linked to sexual morphs in *Discostroma* (1909). Because the former genus is better established in literature, and represents the older name with many more species, it has preference over *Discostroma*. As far as we are aware, no species of *Seimatosporium* have been described from *Pistacia*. Of the species treated by Nag Raj (1993), *S. pistaciae* morphologically most closely matches *S. lonicerae* (conidia 9–16 × 3.5–5 µm) and *S. rosae* (conidia 12.5–16.5 × 3.5–4 µm), but can be distinguished based on its larger conidial dimensions.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Discostroma fuscellum* (GenBank JF320818; Identities = 559/566 (99 %), Gaps = 2/566 (0 %)), *Seimatosporium parasiticum* (GenBank AB594808; Identities = 542/551 (98 %), no gaps) and *Seimatosporium discosioides* (GenBank AB594800; Identities = 544/555 (98 %), Gaps = 4/555 (0 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Discostroma botan* (GenBank DQ368629; Identities = 826/830 (99 %), no gaps), *Seimatosporium parasiticum* (GenBank AB593741; Identities = 795/799 (99 %), no gaps) and *Discostroma fuscellum* (GenBank AB593726; Identities = 795/799 (99 %), no gaps).

Colour illustrations. *Pistacia vera* trees; conidiomata on PDA, conidiophores and conidia. Scale bars = 10 µm.

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
Mansoureh Mirabolfathy, Iranian Research Institute of Plant Protection, Tehran, Iran;
e-mail: mmirab2000@yahoo.com


Codinaea pini

Fungal Planet 301 – 24 November 2014

Codinaea pini Crous & M.J. Wingf., *sp. nov.*

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

Conidiophores erect, brown, flexuous, finely verruculous, appearing somewhat granular, unbranched, arising from superficial mycelium, mononematous, macronematous, cylindrical, 1–3-septate, 30–100 × 2.5–4 µm. *Conidiogenous cells* terminal, pale to medium brown, mono- to rarely polyphialidic, with one lateral aperture, 25–60 × 3–3.5 µm; collarette funnel-shaped, 3–4 µm diam, 2–3 µm deep, pale brown. *Conidia* (12–)13–15 × (2–)2.5(–3) µm, solitary, aggregating in a globose mucoid mass, hyaline, smooth, granular, fusoid, slightly curved or straight, widest in middle, tapering towards acute apices that give rise to setulae at each end, 8–9(–10) µm.

Culture characteristics — Colonies flat, appressed, spreading, with sparse aerial mycelium and smooth, even, lobate margin, reaching 35 mm diam after 2 wk at 25 °C in the dark. On OA surface iron-grey in centre, crystalline in outer region. On MEA surface olivaceous-grey, pale olivaceous-grey in outer region, olivaceous-grey in reverse. On PDA surface olivaceous-grey in centre, pale olivaceous-grey in outer region; in reverse olivaceous-grey in centre, pale olivaceous-grey in outer region.

Typus. Uganda, on dead needles of *Pinus patula* (*Pinaceae*), Jan. 2014, *M.J. Wingfield* (holotype CBS H-21998, culture ex-type CPC 24400 = CBS 138866; ITS sequence GenBank KP004465, LSU sequence GenBank KP004493, MycoBank MB810611).

Notes — The species is described in the genus *Codinaea* because Réblová & Winka (2000) suggested separating *Codinaea* (setulate conidia) from *Dictyochaeta* (asetulate conidia). Based on the keys provided by Kuthubutheen & Nawawi (1991) and Whitton et al. (2000), *C. pini* appears to be distinct from presently known taxa. Phylogenetically, it is part of the *C. simplex* species complex (Hughes & Kendrick 1968).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Dictyochaeta simplex* (GenBank EF029193; Identities = 472/515 (92 %), Gaps = 21/515 (4 %)), *Pseudolachnella guaviyunis* (GenBank KJ834524; Identities = 493/548 (90 %), Gaps = 27/548 (4 %)) and *Dictyochaeta fertilis* (GenBank AF178540; Identities = 463/507 (91 %), Gaps = 23/507 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Dictyochaeta simplex* (GenBank AF178559; Identities = 827/832 (99 %), Gaps = 1/832 (0 %)), *Rattania setulifera* (GenBank HM171322; Identities = 811/838 (97 %), Gaps = 1/838 (0 %)) and *Pseudolachnella guaviyunis* (GenBank KJ834525; Identities = 803/831 (97 %), Gaps = 1/831 (0 %)).

Colour illustrations. *Pinus patula* plantation in Uganda; colonies sporulating on PNA and SNA, conidiophores and conidia. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Xenophaeosphaeria grewiae

Fungal Planet 302 – 24 November 2014

Xenophaeosphaeria Crous & M.J. Wingf., *gen. nov.*

Etymology. Name reflects a morphological similarity to *Phaeosphaeria*.

Caulicolous. *Ascomata* solitary to gregarious, immersed, opening via a central ostiole, somewhat papillate, globose, brown; wall of 3–4 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, hyphal-like, anastomosing. *Asci* clavate to fusoid-ellipsoid, fasciculate, short-stipitate with apical chamber, bitunicate, ascospores uni- to biseriate, overlapping, 8-spored. *Ascospores* brown, guttulate, smooth, fusoid-ellipsoid, straight, apex obtusely rounded, base subobtusely rounded, medianly euseptate, but each cell contains 2–4 distosepta.

Type species. *Xenophaeosphaeria grewiae.*
MycoBank MB810612.

Xenophaeosphaeria grewiae Crous & M.J. Wingf., *sp. nov.*

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

Caulicolous. *Ascomata* solitary to gregarious, immersed, opening via a central ostiole, up to 100 µm diam, somewhat papillate; ascomata up to 350 µm diam, globose, brown; wall of 3–4 layers of brown *textura angularis*. *Pseudoparaphyses* intermingled among asci, hyaline, smooth, septate, hyphal-like, anastomosing, 3–5 µm diam, frequently constricted at septa. *Asci* clavate to fusoid-ellipsoid, fasciculate, short-stipitate with apical chamber, 3–4 µm diam, bitunicate, ascospores uni- to biseriate, overlapping, 8-spored, 80–120 × 12–15 µm. *Ascospores* brown, guttulate, smooth, fusoid-ellipsoid, straight, apex obtusely rounded, base subobtusely rounded, 1-euseptate, apical cell (12–15 µm) shorter than basal cell (15–20 µm), widest at top of basal cell, but each cell contains 2–4 distosepta, (28–)32–37(–40) × (6–)7(–8) µm.

Culture characteristics — Colonies appressed, spreading with sparse aerial mycelium and smooth, even, lobate margins, reaching 20 mm diam after 2 wk at 25 °C in the dark. On PDA surface greyish sepia with patches of mouse grey, reverse greyish sepia. On MEA surface greyish sepia with patches of dirty white, reverse greyish sepia. On OA surface mouse grey with patches of red in outer zone.

Typus. Tanzania, Masek Lake, on twigs of *Grewia* sp. (*Malvaceae*), Feb. 2014, *M.J. Wingfield* (holotype CBS H-21999, culture ex-type CPC 24398 = CBS 138867; ITS sequence GenBank KP004466, LSU sequence GenBank KP004494, MycoBank MB810613).

Notes — *Xenophaeosphaeria* represents a novel genus in the *Phaeosphaeriaceae* (Zhang et al. 2009, 2012). This resembles genera such as *Neomassariosphaeria* and *Neophaeosphaeria*, but is distinct with regards to the development of its ascospore septation. *Xenophaeosphaeria grewiae* sporulates readily in culture, and is not associated with an asexual morph.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Setophoma vernoniae* (GenBank KJ869141; Identities = 423/481 (88 %), Gaps = 15/481 (3 %)), *Ophiobolus disseminans* (GenBank KM014664; Identities = 424/483 (88 %), Gaps = 15/483 (3 %)) and *Chaetosphaeronema hispidulum* (GenBank KF871469; Identities = 423/483 (88 %), Gaps = 16/483 (3 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeosphaeria juncicola* (GenBank KF251686; Identities = 786/810 (97 %), Gaps = 2/810 (0 %)), *Coniothyrium concentricum* (GenBank EU754152; Identities = 786/810 (97 %), Gaps = 2/810 (0 %)) and *Leptospora rubella* (GenBank DQ195792; Identities = 86/810 (97 %), Gaps = 2/810 (0 %)).

Colour illustrations. *Grewia* sp. in Tanzania; colony sporulating on OA, ostiolar region, asci and ascospores. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Neobambusicola strelitziae

Fungal Planet 303 – 24 November 2014

Neobambusicola Crous & M.J. Wingf., *gen. nov.*

Etymology. Name reflects the morphological similarity with the genus *Bambusicola*.

Conidiomata separate or aggregated, erumpent, globose, dark brown, opening via central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, phialidic, proliferating percurrently at apex, or with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth (becoming olivaceous with age), prominently guttulate, medianly 1-septate, constricted at septum, fusoid-ellipsoid, apex bluntly subobtusely rounded, tapering to a distinctly truncate base, mostly straight, but at times slightly curved. *Microconidial state* occurring in same conidioma. *Microconidiogenous cells* hyaline, smooth, doliiform to subcylindrical, proliferating percurrently at apex. *Microconidia* solitary, hyaline, smooth, guttulate to granular, aseptate, subglobose to subcylindrical, apex obtusely rounded, base truncate.

Type species. *Neobambusicola strelitziae*.
MycoBank MB810614.

Neobambusicola strelitziae Crous & M.J. Wingf., *sp. nov.*

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

Conidiomata separate or aggregated, erumpent, globose, dark brown, up to 200 µm diam, opening via central ostiole; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, subcylindrical to ampulliform, 7–15 × 3–5 µm, phialidic, proliferating percurrently at apex, or with prominent periclinal thickening. *Conidia* solitary, hyaline, smooth (becoming olivaceous with age), prominently guttulate, medianly 1-septate, constricted at septum, fusoid-ellipsoid, apex bluntly subobtusely rounded, tapering to a distinctly truncate base, 2 µm diam, mostly straight, but at times slightly curved, (15–)17–19(–21) × (3–)3.5(–4) µm. *Microconidial state* occurring in same conidioma. *Microconidiogenous cells* hyaline, smooth, doliiform to subcylindrical, 3–6 × 3–5 µm, proliferating percurrently at apex. *Microconidia* solitary, hyaline, smooth, guttulate to granular, aseptate, subglobose to subcylindrical, 3–7 × 3–4 µm, apex obtusely rounded, base truncate, 2–2.5 µm diam.

Culture characteristics — Colonies erumpent with sparse aerial mycelium and smooth, even, lobate margin, reaching 15 mm diam after 2 wk at 25 °C in the dark. On MEA surface dirty white with luteous in centre, reverse rust to red. On OA surface dirty white with diffuse luteous pigment. On PDA surface pale luteous with diffuse luteous pigment, reverse orange with diffuse luteous pigment.

Typus. South Africa, Eastern Cape Province, Haga Haga, on leaves of *Strelitzia nicolai* (*Strelitziaceae*), Dec. 2013, *M.J. Wingfield* (holotype CBS H-22000, culture ex-type CPC 24182 = CBS 138869; ITS sequence GenBank KP004467, LSU sequence GenBank KP004495, MycoBank MB810615).

Colour illustrations. *Strelitzia nicolai* at Haga Haga, Eastern Cape Province, South Africa; colony sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

Notes — *Neobambusicola strelitziae* was isolated from necrotic leaf tissue associated with infections of *Phyllachora strelitziae*. The latter fungus causes well-defined subcircular leaf spots, 3–10 mm diam, with epiphyllous black ascostromata. As these leaf spots get older and enlarge, conidiomata are observed surrounding the ascomata in the dead leaf tissue. Doidge (1942) commented on 2-celled conidia of a potential hyperparasite invading old ascomata of *P. strelitziae*, which we suspect is *Neobambusicola strelitziae*. Further collections are required, however, to resolve the relationship between these two species.

Neobambusicola resembles the genus *Bambusicola* in having reduced conidiophores with percurent proliferation, and conidia that turn pale brown at maturity (Dai et al. 2012, Hyde et al. 2013). However, *Neobambusicola* is distinct in that it does not have pycnothyrial conidiomata, and its conidia are fusoid-ellipsoid, rather than cylindrical.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Microdiplodia hawaiiensis* (GenBank GU361956; Identities = 391/461 (85 %), Gaps = 24/461 (5 %)), *Camarographium koreanum* (GenBank JQ044432; Identities = 413/494 (84 %), Gaps = 28/494 (5 %)) and *Paraconiothyrium hawaiiense* (GenBank KF177681; Identities = 390/461 (85 %), Gaps = 24/461 (5 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Bambusicola irregulispora* (GenBank JX442036; Identities = 783/809 (97 %), Gaps = 3/809 (0 %)), *Bambusicola massarinia* (GenBank JX442037; Identities = 782/808 (97 %), Gaps = 2/808 (0 %)) and *Bambusicola bambusae* (GenBank JX442035; Identities = 785/814 (96 %), Gaps = 3/814 (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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Trichomerium dioscoreae

Fungal Planet 304 – 24 November 2014

Trichomerium dioscoreae Crous & C. Nakash., *sp. nov.*

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

Mycelium consists of olivaceous-brown, septate, branched, smooth, 3–4 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells; conidia arising directly from hyphae. *Conidiogenous loci* inconspicuous, truncate, somewhat erumpent, 1.5–2 µm diam. *Conidia* solitary, pale to medium brown, smooth, consisting of a subcylindrical basal cell, 1–3-septate, 10–20 × 3–5 µm, with truncate hilum, 2 µm diam, giving rise to 2–3 lateral arms from a central cell; arms 1–2-septate, subcylindrical with obtusely rounded ends, 12–25 × 3–6 µm.

Culture characteristics — Colonies erumpent, spreading, surface folded, with sparse to moderate aerial mycelium and even, lobate margins, reaching 35 mm diam after 2 wk at 25 °C in the dark. On MEA, PDA and OA surface iron-grey to fuscous-black, reverse fuscous-black.

Typus. JAPAN, Iwate, Morioka, Koma, on leaves of *Dioscorea* sp. (*Dioscoreaceae*), 10 Sept. 2013, *C. Nakashima* (holotype CBS H-22001, culture ex-type CPC 24259 = CBS 138870; ITS sequence GenBank KP004468, LSU sequence GenBank KP004496, MycoBank MB810616).

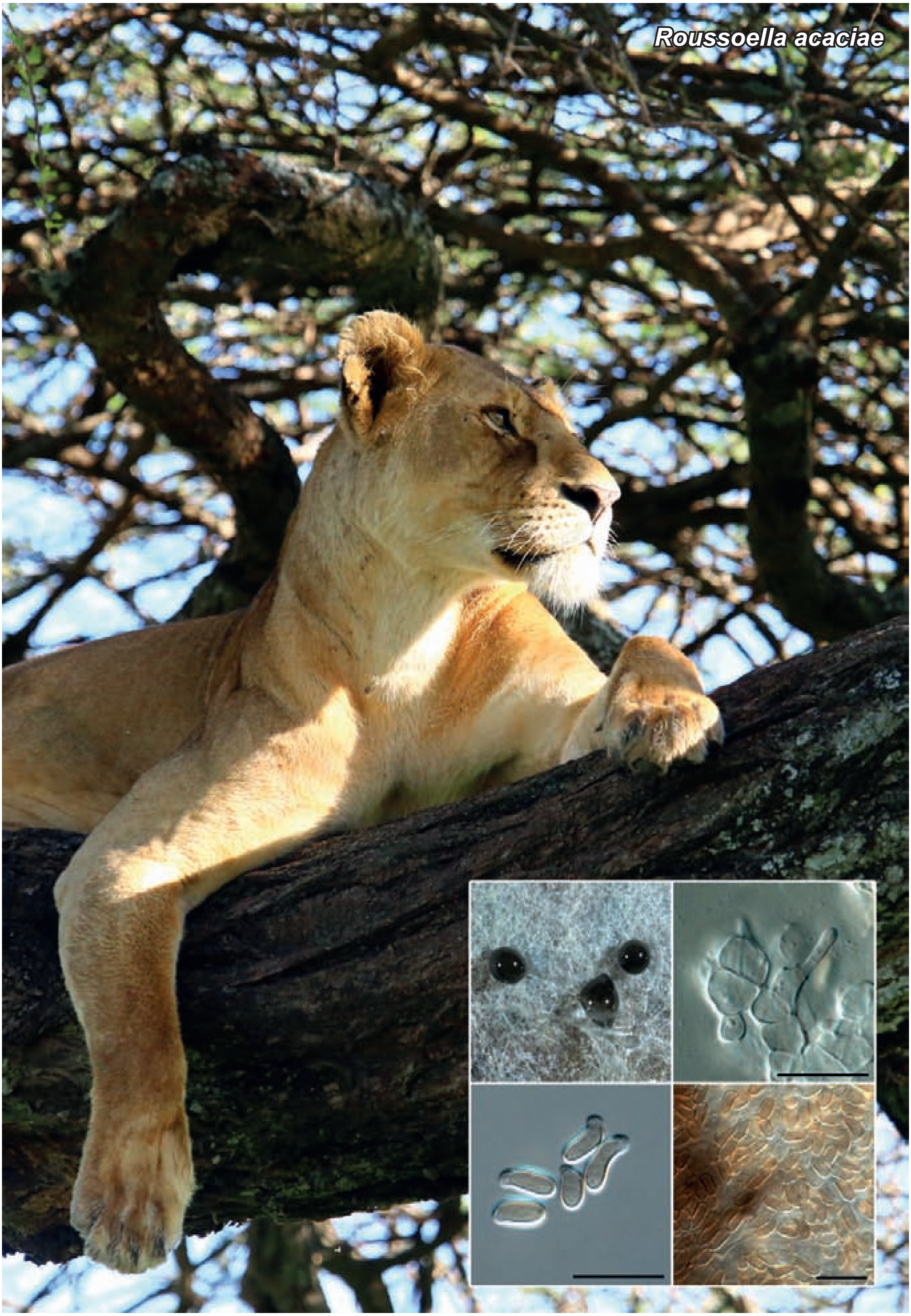
Colour illustrations. Leaf of *Dioscorea* sp. infected with *Distocercospora pachyderma* and co-colonised by *Trichomerium dioscoreae*; conidiogenous loci and conidia. Scale bars = 10 µm.

Notes — The genus *Trichomerium* (1918) was recently studied by Chomnunti et al. (2012), who established the new family, *Trichomeriaceae* to accommodate it. Although these authors focused on the sexual morph, they did note that it possibly had *Tripospermum* (1918) asexual morphs. The present collection of a *Tripospermum* morph that clusters in *Trichomerium*, thus conforms this association.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Trichomerium deniqulatum* (GenBank JX313654; Identities = 627/672 (93 %), Gaps = 20/672 (2 %)), *Trichomerium gleosporum* (GenBank JX313656; Identities = 628/684 (92 %), Gaps = 31/684 (4 %)) and *Trichomerium foliicola* (GenBank JX313655; Identities = 628/684 (92 %), Gaps = 31/684 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Trichomerium foliicola* (GenBank JX313659; Identities = 834/845 (99 %), no gaps), *Trichomerium deniqulatum* (GenBank JX313660; Identities = 828/839 (99 %), no gaps) and *Trichomerium gleosporum* (GenBank JX313662; Identities = 831/843 (99 %), Gaps = 1/843 (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
Chiharu Nakashima, Graduate School of Bioresources, Mie University, 1577 Kurima-machiya,
Tsu, Mie 514-8507, Japan; e-mail: chiharu@bio.mie-u.ac.jp


Roussoella acaciae

Fungal Planet 305 – 24 November 2014

Roussoella acaciae Crous & M.J. Wingf. *sp. nov.*

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

Conidiomata eustromatic, multilocular, separate, globose, immersed, brown, up to 200 µm diam, opening via central ostiole, exuding a brown conidial mass; wall of 3–6 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* lining the inner cavity, hyaline, smooth, ampulliform to doliiform, 3–7 × 5–7 µm, with prominent periclinal thickening at apex, or with tightly aggregated percurrent proliferations at apex. *Conidia* solitary, pale to medium brown, smooth, guttulate, subcylindrical, straight to slightly curved, apex obtuse, base truncate, 2–3 µm diam, mostly central, but at times also displaced laterally, (5–)6–7(–10) × (2–)2.5–3 µm.

Culture characteristics — Colonies flat, spreading, with sparse aerial mycelium and even, smooth margin, reaching 6 mm diam after 2 wk at 25 °C in the dark. On MEA surface olivaceous-grey with patches of pale luteous, reverse sienna in centre, orange in outer region. On OA olivaceous-grey in centre, with dirty white in outer region. On PDA centre olivaceous-grey on surface and reverse.

Typus. Tanzania, Serengeti, on leaves of *Acacia tortilis* (*Fabaceae*), Feb. 2014, *M.J. Wingfield* (holotype CBS H-22002, culture ex-type CPC 24314 = CBS 138873; ITS sequence GenBank KP004469, LSU sequence GenBank KP004497, MycoBank MB810617).

Notes — Members of the genus *Roussoella* (1888) (*Roussoellaceae*; Liu et al. 2014) mostly occur on monocotyledons, thus the occurrence of *R. acaciae* on *Acacia* is unusual. Although we isolated only the *Cytoplea* (1885) asexual morph, which is unknown for most species of *Roussoella*, the fungus on *Acacia* appears to be phylogenetically distinct from other members of the genus. Both the genera *Roussoella* and *Cytoplea* are in need of revision.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Roussoella chiangraina* (GenBank KJ474828; Identities = 360/395 (91 %), Gaps = 17/395 (4 %)), *Roussoella siamensis* (GenBank KJ474837; Identities = 352/387 (91 %), Gaps = 16/387 (4 %)) and *Arthopyrenia salicis* (GenBank KM030296; Identities = 353/390 (91 %), Gaps = 17/390 (4 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Roussoella percutanea* (GenBank KF366449; Identities = 822/841 (98 %), Gaps = 3/841 (0 %)), *Sporidesmium australiense* (GenBank DQ408554; Identities = 827/847 (98 %), Gaps = 2/847 (0 %)) and *Roussoella hysterioides* (GenBank AB524622; Identities = 809/829 (98 %), Gaps = 2/829 (0 %)).

Colour illustrations. Lion resting in an *Acacia tortilis* tree, Serengeti, Tanzania; conidiomata sporulating on OA, conidiogenous cells and conidia. Scale bars = 10 µm.

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
Michael J. Wingfield, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria,
P. Bag X20, Pretoria, 0028, South Africa; e-mail: mike.wingfield@fabi.up.ac.za


Neocladophialophora quercina

Fungal Planet 306 – 24 November 2014

Neocladophialophora Crous & R.K. Schumach., *gen. nov.*

Etymology. Name reflects its morphological similarity to the genus *Cladophialophora*.

Mycelium consisting of hyaline, smooth, septate, branched, hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* erect, subcylindrical, hyaline to subhyaline, mono- to polyphialidic; loci truncate. *Conidia* formed in long, rarely branched basipetal chains consisting of subcylindrical conidia, apical conidium clavate to subglobose, other conidia subcylindrical, 0–1-septate, somewhat constricted at the septum, guttulate to granular, subhyaline; constricted at the truncate hila, somewhat darkened. Older conidia appear pale olivaceous in mass.

Type species. *Neocladophialophora quercina*.
MycoBank MB810618.

Neocladophialophora quercina Crous & R.K. Schumach., *sp. nov.*

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

Mycelium consisting of hyaline, smooth, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* erect, subcylindrical, hyaline to subhyaline, mono- to polyphialidic, 10–30 × 3–4 µm; loci truncate, 1 µm diam. *Conidia* formed in long, rarely branched basipetal chains consisting of subcylindrical conidia (up to 20 per chain), apical conidium clavate to subglobose, other conidia subcylindrical, 0–1-septate, somewhat constricted at the septum, guttulate to granular, subhyaline, (9–)13–15(–17) × (2.5–)3(–5) µm; constricted at the truncate hila, somewhat darkened, 0.5 µm diam. Older conidia appear pale olivaceous in mass.

Culture characteristics — Colonies spreading, appressed, surface folded with sparse aerial mycelium and smooth, lobate margin, reaching 18 mm diam after 2 wk at 25 °C in the dark. On MEA and PDA surface and reverse ochreous. On OA surface pale luteous.

Typus. Germany, on dead twig of *Quercus robur* (*Fagaceae*), 23 Feb. 2014, *R.K. Schumacher* (holotype CBS H-22003, culture ex-type CPC 24426 = CBS 138874; ITS sequence GenBank KP004470, LSU sequence GenBank KP004498, MycoBank MB810619).

Colour illustrations. *Quercus robur* tree; conidiophores and polyphialidic conidiogenous cells giving rise to branched chains of conidia. Scale bars = 10 µm.

Notes — *Neocladophialophora* is morphologically similar to *Cladophialophora*, *Fusicladium* and *Polyscytalidium* (see Crous et al. 2007c, Bench et al. 2012), but different in that conidiophores are hyaline, conidiogenous cells phialidic, and conidia are constricted at their slightly darkened hila. Furthermore, conidia are pigmented in mass, and terminal conidia are frequently clavate to subglobose.

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are *Triscelophorus* cf. *acuminatus* (GenBank KF730836; Identities = 210/235 (89 %), Gaps = 14/235 (5 %)), *Triscelophorus monosporus* (GenBank KF730840; Identities = 184/193 (95 %), Gaps = 1/193 (0 %)) and *Hemibeltrania mitrata* (GenBank EF029228; Identities = 280/351 (80 %), Gaps = 19/351 (5 %)).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Scolecobasidium tropicum* (GenBank KF156102; Identities = 687/786 (87 %), Gaps = 14/786 (1 %)), *Isthmolongispora ampulliformis* (GenBank EU107303; Identities = 707/809 (87 %), Gaps = 8/809 (0 %)) and *Dactylaria humicola* (GenBank EU107304; Identities = 687/793 (87 %), Gaps = 13/793 (1 %)).

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
René K. Schumacher, Hölderlinstraße 25, 15517 Fürstenwalde/Spree, Germany; e-mail: bolbitius@web.de


Barssia maroccana

Fungal Planet 307 – 24 November 2014

Barssia maroccana G. Moreno, Manjón, Carlavilla & P. Alvarado, *sp. nov.*

Etymology. From the Berber *Mur N'Akush* ('land of God'), which is presently known as Morocco, the country where this species was collected.

Hypogenous ascomata 1.7–5.3 × 1.5–2.5 cm (measurements taken from herbarium material), irregularly globose or subglobose to elongated and flattened, more or less broadly lobed, reddish brown to dark reddish brown, sometimes with a rounded to irregular apical depression. *Peridium* covered with broad, roughly polygonal dark reddish brown warts; about 140–200 µm thick, formed by pseudo-parenchymatic cells, 12–50 µm diam, thick-walled. The outermost cell layers are reddish and have dark walls, while these become lighter inwards. *Gleba* whitish to pale pinkish, compact or frequently presenting small labyrinth-like cavities, with well-defined sinuous veins, formed by a prosenchymatic structure of interwoven hyphae 8–15 µm diam. Sinuose *paraphyses* not well-defined, 5–7 µm diam. *Asci* clavate to broadly ellipsoid, indehiscent, immersed into the gleba, forming a definite hymenium, hyaline, hardly observable in mature ascomata, 8-spored, 110–130 × 30–50 µm. *Ascospores* ellipsoidal, 29–36 × (16–)18–22 µm, hyaline, smooth, not amyloid or dextrinoid, with an obtuse apex and a large oil droplet (L/l = 1.6–1.7). Smell and taste not recorded.

Habitat & Distribution — So far found only under *Cedrus atlantica*, at Ifrane, Morocco, 1 760 m asl.

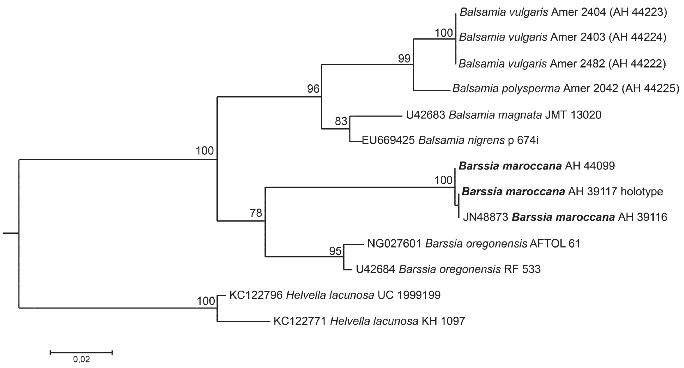
Typus. Morocco, Azrou, province of Ifrane, *Cedrus atlantica* forest, 18 Nov. 2010, *M.A. Sanz*, *J. Álvarez*, *P. Alvarado & J.L. Manjón* (holotype AH 39117; ITS sequence GenBank KM243649, LSU sequence GenBank KM243655, MycoBank MB809666); Ifrane, *Cedrus atlantica* forest, 18 Nov. 2010, *M.Á. Sanz*, *P. Alvarado & J.L. Manjón*, paratype AH 39116; ibid., AH 44221; Ifrane, *Cedrus atlantica* forest with some *Quercus ilex* species, 1760 m asl, *J.L. Manjón*, *J. Álvarez-Jiménez & M.Á. Sanz*, 21 Feb. 2014, paratype AH 44099 (ITS, LSU sequences GenBank KM243648, KM243654).

Additional specimens examined. *Balsamia vulgaris*: Italy, Reggio Emilia, Regnano, *Quercus* and *Pinus* mixed forest, 450 m asl, 11 Dec. 2005, *A. Montecchi*, Amer 2482 = AH 44222 (ITS, LSU sequences GenBank KM243645, KM243651); Reggio Emilia, Rio delle Viole, *Quercus pubescens* forest, 350 m asl, 9 Dec. 2002, *A. Montecchi*, Amer 2404 = AH 44223 (ITS, LSU sequences GenBank KM243646, KM243652); Reggio Emilia, Montalvo, *Quercus pubescens* forest, 350 m asl, 21 Apr. 2003, *A. Montecchi*, Amer 2403 = AH 44224 (ITS, LSU sequences GenBank KM243647, KM243653). *Balsamia polysperma*: Italy, Reggio Emilia, Monte Duro, *Ostrya* and conifers, 650 m asl, 14 Dec. 1999, *A. Montecchi*, Amer 2042 = AH 44225 (ITS, LSU sequences GenBank KM243650, KM243656).

Notes — *Barssia maroccana* is morphologically characterised by its large and broad spores with obtuse apex, growing under *Cedrus atlantica*. The deviant phylogenetic placement of this lineage was first reported by Alvarado et al. (2011). *Barssia maroccana* is very similar to *Balsamia polysperma*, but the latter has smaller ascomata 0.5–2(–3) cm diam, with narrower ellipsoidal spores, 18–25 × 9–16 µm, L/l = 1.6–1.7, and different ecology (Montecchi & Sarasini 2000). The monotypic genus *Barssia* was created by Gilkey (1925) to accommodate the American species *B. oregonensis*. This species was originally found in Oregon and the Pacific Northwest of the USA (Trappe 1979), but later reports cited it also in Poland (Ławrynowicz & Skirgiełło 1984). *Barssia oregonensis* differs from *B. maroccana* because of its ascomata being excavated with a deep apical depression covered by the peridium, and smaller spores about 24–29 × 14.5–17 µm, L/l = 1.6–1.7, and a different ecology (Ławrynowicz & Skirgiełło 1984). The only other species in the genus, *Barssia yezomontana*, with globose spores (Trappe 1979), was combined into *Barssia* from the monotypic genus *Phymatomyces*. Unfortunately, the type specimen of *P. yezomontanus* was lost in World War II (Gilkey 1961) and it is therefore not possible to confirm this taxonomic decision until this Japanese taxon is recollected.

Gilkey (1925) placed the genus *Barssia* in the family *Tuberaceae*, but later Trappe (1979) transferred it to the family *Balsamiaceae*. Kimbrough et al. (1996) performed an ultrastructural study of *Barssia* and concluded it should be classified within the family *Helvellaceae*. Later Percudani et al. (1999) put *Balsamia* and *Barssia* back into the family *Balsamiaceae*, which was nested within *Helvellaceae*. Macro- and microscopical differences between *Balsamia* and *Barssia* are very subtle. Gilkey (1925) highlights the apical depression observed in *B. oregonensis*, and compares it to the analogous structures present in *Genea*, *Pseudobalsamia* (currently considered a synonym of *Balsamia*), *Pachyphloeus* and *Hydnotrya*. The similarities between *Barssia* and *Balsamia* are also commented on by Montecchi & Sarasini (2000). Glebal chambers, smooth spores under the light microscope, and the presence of paraphyses are shared by both genera. The present molecular data confirm that both genera are monophyletic, with the new species from Morocco being better accommodated within *Barssia*.

Colour illustrations. Morocco, Ifrane, forest of *Cedrus atlantica* where the holotype was collected; ascomata; peridium and gleba; detail of the outermost layer of the peridium with pseudoparenchymatic structure; prosenchymatic gleba, asci and ascospores; ascospores (holotype AH 39117). Scale bars = 1 cm (ascomata), 100 µm (cortex), 20 µm (pseudoparenchymatic and prosenchymatic cells), 10 µm (ascus and spores).



Phylogenetic tree of *Helvellaceae* species constructed with a maximum likelihood (ML) analysis of LSU sequences by running RAxML-HPC2 on XSEDE online v. 8.0.24. *Helvella lacunosa* (KC122796 and KC122771) is the outgroup. Bootstrap support values ≥ 75 % are given above branches. The phylogenetic position of *Barssia maroccana* is indicated in **bold**.

Gabriel Moreno, Juan R. Carlavilla, Julio Álvarez & José L. Manjón, Departamento de Ciencias de la Vida (Área de Botánica),
Universidad de Alcalá, E-28805 Alcalá de Henares, Spain;
e-mail: gabriel.moreno@uah.es, jramon787@gmail.com, julio.jimenez@uah.es & josel.manjon@uah.es
Pablo Alvarado, ALVALAB, La Rochela 47, E-39012, Santander, Spain;
e-mail: pablo.alvarado@gmail.com


Acremoniopsis suttonii

Fungal Planet 308 – 24 November 2014

Acremoniopsis Giraldo, Gené & Guarro, *gen. nov.*

Etymology. Referring to the similarity with the genus *Acremonium*.

Mycelium consisting of branched, septate, smooth-walled hyphae. *Conidiophores* erect, simple or poorly branched. *Conidiogenous cells* enteroblastic, monophialidic, discrete, cylindrical to subulate, subhyaline. *Conidia* unicellular, globose or subglobose, hyaline, arranged in slimy heads.

Type species. *Acremoniopsis suttonii*.
MycoBank MB809883.

Acremoniopsis suttonii Giraldo, Gené & Guarro, *sp. nov.*

Etymology. Named in honour of the American mycologist Deanna A. Sutton.

Mycelium consisting of septate, hyaline, smooth- and thin-walled hyphae, 1–1.5 µm wide. *Conidiophores* consisting of single phialides arising orthotropically and directly from vegetative hyphae or ropes of hyphae. *Phialides* cylindrical to subulate, (12–)16–30(–40) µm long, 1.5–2 µm wide at the base, with distinct periclinal thickening at the conidiogenous locus, hyaline, thin-walled and rugose towards the base. *Conidia* unicellular, globose or subglobose, 2–3 × 2 µm, hyaline, smooth- and thick-walled, in slimy heads. Chlamydospores and sexual morph not observed.

Culture characteristics — Colonies on OA at 25 °C attaining 8–9 mm diam after 2 wk, yellowish white (2A2) (Kornerup & Wanscher 1978), flat, membranous; reverse pastel yellow (1A4). On PDA at 25 °C reaching 15–21 mm diam after 2 wk, white (1A1), radially folded, dusty; reverse pastel yellow (2A4); exudate and diffusible pale yellow pigment (2A5). Optimum growth temperature 25 °C, minimum 12 °C, maximum 35 °C.

Typus. Spain, Burgos, natural area of Sierra de la Demanda, isolated from forest soil, Nov. 2010, coll. *J. Gené & M. Hernández*, isol. *A. Giraldo* (holotype CBS H-21936, cultures ex-type CBS 138708 = FMR 11780; ITS sequence GenBank KJ807182, LSU sequence GenBank KJ807179, MycoBank MB809884).

Notes — *Acremonium* is a polyphyletic genus with species spread across different orders of the *Sordariomycetes*, but are mainly placed in the *Hypocreales* (Glenn et al. 1996, Perdomo et al. 2011, Summerbell et al. 2011, Giraldo et al. 2012). *Acremonium alternatum*, the type species of the genus, was recently epitypified with the strain CBS 407.66, which was placed in the family *Bionectriaceae* (Summerbell et al. 2011). In *Hypocreales*, there are still some traditional species of *Acremonium* phylogenetically distant from *A. alternatum* and *Bionectriaceae* that could represent novel genera. Although *Acremoniopsis* shows the typical *Acremonium* morphology, it is phylogenetically closer to nectriaceous species such as *Pleonectria pyrrhochlora* and *P. virens*, rather than bionectriaceous species, so we preferred to accommodate the species described here within a new genus. *Acremoniopsis suttonii* produces a diffusible pale yellow pigment similar to *Acremonium citrinum*, *A. vitellinum*, *A. chrysogenum* and *A. flavum*. The main difference between the first two species and *Acremoniopsis suttonii* is that they produce conidia arranged in chains (Gams 1971, Giraldo et al. 2014). Additionally, *A. chrysogenum* has colonies with a yeast-like appearance and ellipsoidal conidia, and *A. flavum* produces ellipsoidal conidia, abundant chlamydospores and is thermotolerant. *Acremonium guillematii* exhibits yellow colonies, but does not produce diffusible pigment into the agar (Gams 1971). Previous phylogenetic studies have demonstrated that *Acremonium citrinum*, *A. chrysogenum* and *A. flavum* are members of *Bionectriaceae* (Summerbell et al. 2011, Giraldo et al. 2014) while *A. vitellinum* and *A. guillematii* form a weakly supported clade near to the *Clavicipitaceae* (Summerbell et al. 2011). *Acremonium pteridii* produces similar subglobose conidia to those of *A. suttonii*, but shows chondroid hyphae, abundant crystals and partially branched conidiophores (Gams 1971) nested in the *Gliomastix*/*Bionectria* clade (Summerbell et al. 2011).

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Parasarcopodium ceratocary* CBS 110664 (GenBank AY425026; Identities = 772/796 (97 %), Gaps = 1/796 (0 %)), *Pleonectria pyrrhochlora* CBS 125131 (GenBank HM484570; Identities = 774/799 (97 %), Gaps = 3/799 (0 %)), *P. virens* A.R. 4558 (GenBank JF832754; Identities = 770/795 (97 %), Gaps = 3/795 (0 %)) and '*Acremonium persicinum*' CBS 110646 (GenBank HQ232088; Identities = 773/800 (97 %), Gaps = 4/800 (0 %)). *Parasarcopodium ceratocary* (incertae sedis, *Hypocreales*) has verruculose conidiophores with rows or whorls of phialides and cylindrical conidia with amorphous mucoid appendages at both ends (Mel'nik et al. 2004); while *Pleonectria* species (*Nectriaceae*, *Hypocreales*) produce a pycnidial asexual morph (zythiostroma-like) on the natural substratum, with verticillated conidiophores, intercalary phialides and ellipsoidal conidia; and sporodochial conidiophores, densely branched with cylindrical phialides and allantoid conidia in culture (Hirooka et al. 2012).

Colour illustrations. Forest from the natural area of Sierra de la Demanda (Burgos, Spain), where the soil sample was collected. Colony on PDA after 21 d at 25 °C, phialides and globose or subglobose conidia. Scale bars = 10 µm.

Alejandra Giraldo, Josepa Gené & Josep Guarro, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV),
Sant Llorenç 21, 43201 Reus, Tarragona, Spain;
e-mail: dagiraldol@gmail.com; josepa.gene@urv.cat & josep.guarro@urv.cat


Marasmius vladimirii

Fungal Planet 309 – 24 November 2014

Marasmius vladimirii A.K. Dutta & K. Acharya, *sp. nov.*

Etymology. Named after Vladimír Antonín, for the contribution that he has made to further our understanding of the genus *Marasmius*.

Pileus 25–29 mm diam, convex to broadly convex, orange-scarlet towards margin, disc orange-chestnut, smooth, non-striate; flesh creamy white, thin. *Lamellae* adnexed, creamy white, 2 mm wide at the middle, thinner towards margin, lamellulae of two tiers, intervenose, edge concolorous; collarium absent. *Stipe* central, well developed, 2.6–3.8 cm long, 2 mm broad, more or less equal, yellowish apricot from the middle towards lower part, upper portion whitish, hollow, cartilaginous, curved, surface glabrous. *Basidiospores* 7.5–11.5(–12) × 5.5–6.5(–7) µm (X_m = 10.9 ± 1.7 × 6.5 ± 0.6, Q = 1.3–2.1, Q_m = 1.7 ± 0.3, n = 30, s = 1 specimen), ellipsoid, inamyloid, uni-guttulate, guttulae more or less globose. *Basidia* 36–40 × 8.5–9 µm, clavate, hyaline, tetrasterigmatic, sterigmata 3–3.5 µm long. *Basidioles* 36–39 × 11–12 µm, clavate, hyaline. *Cheilocystidia* present, in the form of *Siccus*-type of broom cells; main body 15.5–19(–20) × 6–8 µm, more or less clavate, hyaline, thin- to thick-walled; apical setulae (5–)8–12(–17) µm long, sub-acute, thin- to thick-walled. *Pleurocystidia* absent. *Pileipellis* a hymeniderm composed of *Siccus*-type broom cells; main body (20–)23–24(–39) × 7–7.5(–8) µm, clavate to broadly clavate, regular to irregular in outline, hyaline, thin- to thick-walled, often branched; apical setulae (5–)7.5–8(–9) × 2–2.5 µm, obtuse to sub-acute, thick-walled, deeply coloured. *Pileus trama* hyphae interwoven, 4–5 µm broad, hyaline, thin-walled, dextrinoid. *Lamellar trama* hyphae interwoven, hyaline, thin-walled. *Stipitipellis* composed of 7.5–8(–11) µm broad, hyaline, smooth, non-gelatinous, thin-walled hyphae. *Caulocystidia* absent. *Clamp connections* present in all tissues.

Typus. India, West Bengal, Darjeeling district, towards the way of Pandama to Lebong, upon leaf litter mixed humus, 23 July 2012, *A.K. Dutta* (holotype CUH AMT003; ITS sequence GenBank KF991002, MycoBank MB807384).

Notes — The absence of a collarium and the presence of *Siccus*-type broom cells in the pileipellis, the absence of pleurocystidia, well-developed long central stipe, and adnexed lamellae suggest that *M. vladimirii* belongs to sect. *Sicci*, ser. *Leonini*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the 5.8S (partial)-ITS2-28S (partial) sequence had highest similarity to *M. hypochroides* (GenBank EU935545; Identities = 299/382 (78 %), Gaps = 17/382 (4 %)), *M. araucariae* var. *siccipes* (GenBank FJ431223; Identities = 123/135 (91 %), Gaps = 6/135 (4 %)) and *M. occultatus* (GenBank FJ917622; Identities = 133/150 (89 %), Gaps = 9/150 (6 %)). *Marasmius vladimirii* differs from *M. hypochroides* (characterised by a rugulose pileus, brown to dark brown coloured at the disc with a brownish orange to yellowish brown margin, a stipe apex buff with an yellowish brown to reddish brown base, basidiospores 8–13 × 5–8 µm; Wannathes et al. 2009), in having a pileus coloured orange-scarlet towards margin with an orange-chestnut disc, a stipe yellowish apricot towards base and whitish at the upper portion and smaller basidiospores (7.5–12 × 5.5–7 µm). The absence of caulocystidia also distinguishes the newly described taxon from *M. araucariae* var. *siccipes* (Wannathes et al. 2009). The macroscopically similar *M. occultatus*, known from eastern Honshu, Japan, differs from *M. vladimirii* by having a smaller-sized pileus (12–27 mm), the presence of white mycelioid bristles at the stipe base, basidiospores 14–16 × 3–4 µm, and fertile lamellar edge (Takahashi 2000). *Marasmius occultatiformis*, described from the Republic of Korea, differs from the newly described taxon in having a smaller pileus (12 mm broad) with inflexed margin, smaller basidiospores (7.0–8.5 × 3.5–4.5 µm, av. = 7.8 × 4.0 µm), different sized cheilocystidia (11–19 × 5–8 µm) and pileipellis cells main body (14–25 × 6–10 µm; Antonín et al. 2012). Another similar taxon, *M. abundans*, differs by having a paler coloured, greyish orange, golden-yellow, orange, brownish yellow or ferrugineous pileus, and even larger basidiospores (12–18(–20) × 4–5 µm; Corner 1996).

Colour illustrations. Collection site at Darjeeling hills, India; basidiomes of *Marasmius vladimirii* (bar = 10 mm); basidiomata showing lamellae and lamellae (10 mm); *Siccus*-type cells of pileipellis (10 µm); basidium (10 µm).

Arun K. Dutta & Krishnendu Acharya, Molecular and Applied Mycology and Plant Pathology Laboratory, Department of Botany,
University of Calcutta, 35, Ballygunge Circular Road, Kolkata 700019, West Bengal, India;
e-mail: arun.botany@gmail.com & krish_paper@yahoo.com


Ganoderma austroafricanum

Fungal Planet 310 – 24 November 2014

Ganoderma austroafricanum M.P.A. Coetzee, M.J. Wingf, Marinc., Blanchette, *sp. nov.*

Etymology. Name reflects the geographical origin from which the fungus was collected.

Mature *basidiomata* annual, pileate, sessile, dimidiate, pileus dark to reddish brown when dry, margin rounded, thickened, red brown when dry. *Pore surface* smooth, pores 3–4 per mm, round to angular, radially elongated, 150–390 µm long, 85–245 µm wide, dissepiments 60–200 µm diam. *Hyphal system* dimitic, generative hyphae, usually collapsed, thin-walled, hyaline. *Vegetative hyphae* observed in the tubes. *Tube trama* intricate and agglutinated skeletal hyphae 4–8 µm thick, with extremities tapering to elongate apices of 2–2.5 µm diam, hyaline to pale yellowish in 5 % KOH. *Basidia* not observed. *Basidiospores* brown, subglobose with a truncate base, bitunicate, verruculose, 8–11 × 5.5–7 µm. *Chlamydospores* on 2 % malt extract agar medium (MEA) ellipsoidal with a hyphal extension at the base, apex occasionally papillated, terminal or intercalary, 10.5–19.5 × 6.5–9.5 µm.

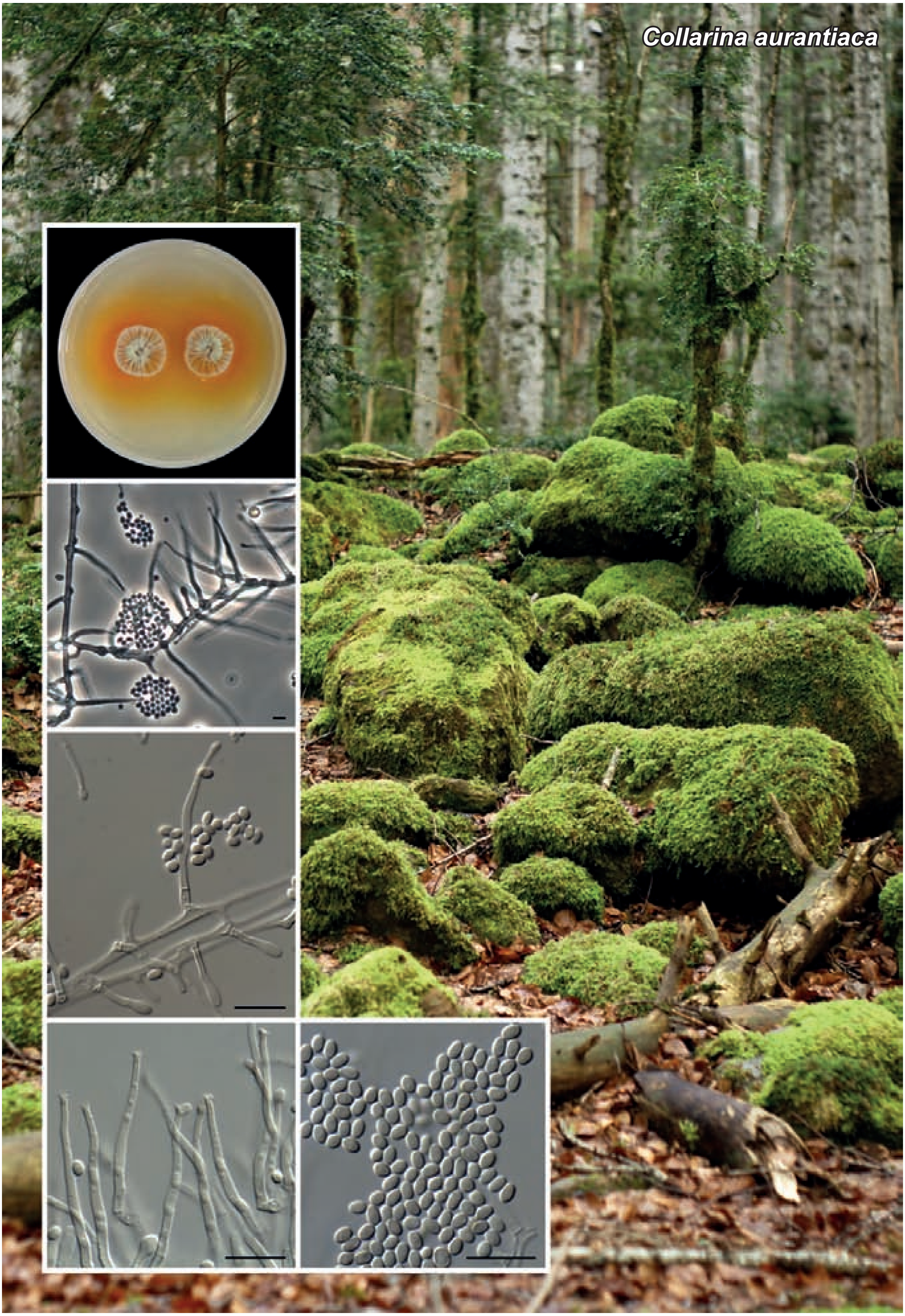
Culture characteristics — Colonies on 2 % MEA fertile, showing the best growth reaching 82 mm at 25 °C in the dark in 8 d, the second best 62 mm at 30 °C, 37 mm at 20 °C, 18 mm at 15 °C, no growth at 35 °C, circular with entire edge, flat, felt-like texture, white at all temperatures, with sporadic tint of yellow at inner 20 mm circle at 30 °C; chlamydospores present.

Typus. South Africa, Gauteng, Pretoria, Brooklyn, Jan. 2014, on *Jacaranda mimosifolia*, *M.J. Wingfield* (holotype PREM 61074, living culture ex-type CBS 138724 = CMW 41454; ITS sequence GenBank KM507324, LSU sequence GenBank KM507325, MycoBank MB810411).

Colour illustrations. *Jacaranda mimosifolia* (Jacaranda tree) growing as street tree in the suburb of Brooklyn, Pretoria, South Africa (background); crown of infected Jacaranda tree showing branch die-back; purple flowers of Jacaranda tree; basidiocarps; basidiospores (10 µm); skeletal hyphae refractive in phase contrast (25 µm); chlamydospores on 2 % MEA (10 µm).

Notes — *Ganoderma austroafricanum* is the causal agent of root and butt rot disease on large numbers of jacaranda trees in the suburb of Brooklyn (Pretoria, South Africa). ITS sequence comparisons using Blastn searches against sequences in GenBank yielded the closest hits with *G. subamboinense* var. *laevisporum* (JQ520205; query cover: 100 %, similarity 98 %). It can be differentiated from the closest related sequences of *G. subamboinense var. laevisporum* based on 13 nucleotide differences in the ITS sequence. Phylogenetic trees generated from ITS sequences placed *G. austroafricanum* within a clade that included sequences from GenBank representing *G. weberianum* and *G. stipitatum* but with low bootstrap support (parsimony bootstrap = 52 %). The latter group formed a sister group to a monophyletic clade (bootstrap support = 92 %) that included sequences from GenBank representing *G. lobatum*, *G. lucidum*, *G. neojaponicum*, *G. oregonense* and *G. resinaceum*.

Martin P.A. Coetzee, Seonju Marincowitz & Michael J. Wingfield, Department of Genetics, Centre of Excellence in Tree Health Biotechnology (CTHB),
Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, 0002, South Africa;
e-mail: martin.coetzee@fabi.up.ac.za, seonju.marincowitz@fabi.up.ac.za & mike.wingfield@fabi.up.ac.za
Robert A. Blanchette, University of Minnesota, 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108;
e-mail: robertb@umn.edu
Charles W. Barnes, Centro de Investigación, Estudios y Desarrollo de Ingeniería (CIEDI), Facultad de Ingenierías y Ciencias Agropecuarias (FICA),
Universidad de Las Américas, Calle José Queri s/n entre Av. Granados y Av. Eloy Alfaro, Quito, Ecuador;
e-mail: cbarnes333b@gmail.com


Collarina aurantiaca

Fungal Planet 311 – 24 November 2014

Collarina Giraldo, Gené & Guarro, *gen. nov.*

Etymology. Referring to the presence of conspicuous collarettes.

Mycelium consisting of branched, septate, smooth-walled hyphae. *Setae* interspersed with conidiophores, erect, unbranched, septate at the base, swollen at the apex, hyaline. *Conidiophores* erect, simple or poorly branched. *Conidiogenous cells* enteroblastic, monophialidic, discrete, cylindrical to acicular, with conspicuous collarettes, subhyaline or pale brown. *Conidia* unicellular, ellipsoidal or subglobose, hyaline to brownish in mass, arranged in slimy heads.

Type species. *Collarina aurantiaca*.
MycoBank MB809407.

Collarina aurantiaca Giraldo, Gené & Guarro, *sp. nov.*

Etymology. Referring to the diffusible orange pigment produced on PDA medium.

Mycelum consisting of septate, hyaline, smooth- and thin-walled hyphae, 1.5–2 µm wide. *Setae* arising directly from vegetative hyphae and interspersed with conidiophores, erect, unbranched, with a basal septum, straight to slightly flexuose, cylindrical and thick-walled towards the base, swollen and thin-walled at the apex, up to 20 µm long, 2 µm wide at the base, 3–4 µm at the apex, hyaline, smooth-walled. *Conidiophores* erect, simple or poorly branched, up to 40 µm long, hyaline or pale brown, smooth-walled. *Phialides* arising directly from vegetative hyphae or ropes of hyphae, cylindrical, slightly tapering at the apex, straight or slightly bent, 10–40 × 1–1.5 µm, with a brownish funnel-shaped collarette, subhyaline to pale brown with age, thick- and smooth-walled. *Conidia* ellipsoidal or subglobose, 2.5–3(–4) × 1–2 µm, hyaline to brownish in mass, smooth- and thin-walled. Chlamydospores and sexual morph not observed.

Culture characteristics — Colonies on OA and PCA at 25 °C attaining 8–14 mm diam in 14 d, brownish grey (6E2) (Kornerup & Wanscher 1978), flat, dusty. On PDA at 25 °C reaching 14–18 mm diam in 14 d, greyish white (1B1), radially folded, felt-like or fasciculate, reverse brownish grey (6D3) with a diffusible orange pigment. Optimum temperature for growth 25 °C, minimum 12 °C, maximum 30 °C.

Typus. Spain, Aragón, Huesca province, Ordesa y Monte Perdido National Park, isolated from sediments of Ara River, 23 Mar. 2011, coll. *A. Giraldo*, *M. Hernández & J. Capilla*, isol. *A. Giraldo* (holotype CBS H-21781, cultures ex-type CBS 138274 = FMR 11784; ITS sequence GenBank KJ807180, LSU sequence GenBank KJ807177, MycoBank MB809408).

Additional specimen examined. Spain, Aragón, Huesca province, Torla to direction Bujaruelos, from forest soil, 19 June 2009, coll. *M. Hernández*, *J. Mena-Portales*, *J. Cano*, isol. *A. Giraldo* (CBS 138273 = FMR 11134; ITS sequence GenBank KJ807181, LSU sequence GenBank KJ807178).

Colour illustrations. Forest from Ordesa y Monte Perdido National Park (Aragón, Spain), where the sample was collected (photo: Javier Capilla). Colony on PDA after 21 d at 25 °C, conidiophores simple with conidia arranged in slimy heads, phialides with brownish funnel-shaped collarettes and setae, ellipsoidal conidia. Scale bars = 10 µm.

Notes — The SSU sequence of *Collarina aurantiaca* revealed that it belongs to the *Clavicipitaceae* s.str. (*Hypocreales*, *Sordariomycetes*), with *Chamaeleomyces viridis*, *C. granulomatis*, *Pochonia bulbillosa*, *P. rubescens* and *Nomuraea rileyi* being the closest species. *Chamaeleomyces* differs from *Collarina* by pale green to greenish grey colonies, and a yeast-like growth, phialides basally swollen with narrow necks and conidia in fragile chains; *Pochonia* has yellowish white colonies, slender acicular phialides commonly arranged in whorls, and some species produce dictyochlamydospores and conidia in chains; *N. rileyi* has pale green slow-growing colonies, cylindrical phialides with short necks and greenish coloured conidia (Zare et al. 2001, Sung et al. 2007, Sigler et al. 2010). Although members of *Clavicipitaceae* s.str. have been reported as important entomopathogens of *Lepidoptera*, *Homoptera* and *Coleoptera*, they are common soil fungi.

Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cordyceps* sp. (GenBank AB027378, Identities = 975/1029 (95 %), Gaps = 12/1029 (1 %)), *Eucasphaeria capensis* CBS 120027 (GenBank EF110619, Identities = 973/1029 (95 %), Gaps = 5/1029 (0 %)) and *Ascopolyporus philodendrus* (GenBank AY886545, Identities = 977/1037 (94 %), Gaps = 14/1037 (1 %)). The closest hits using the ITS sequence had the highest similarity to '*Acremonium psammosporum*' H28 (GenBank GU566287, Identities = 593/593 (100 %), no gaps) and with an unidentified hypocrealean fungus (GenBank KC007264, Identities = 544/550 (99 %), no gaps). *Acremonium psammosporum* was described by Gams (1971) and is characterised by slow-growing colonies with an orange-ochraceous reverse; conidiophores sometimes branched, up to 50 µm long, straight phialides with short collarettes; subglobose conidia, slightly apiculated at base, hyaline, 1.8–3.3 × 1.2–1.6 µm. *Collarina aurantiaca* differs morphologically from *A. psammosporum* by the presence of setae, conidiophores simple, shorter phialides (up to 40 µm), funnel-shaped collarettes and bigger and brownish conidia. In addition, the LSU sequence of the type strain of *A. psammosporum* (CBS 590.63) was 6.9 % different.

Collarina resembles *Monocillium* (asexual morphs of *Niesslia*) with the presence of thickened walls at the base in both phialides and setae. However, *Monocillium* species produce fast-growing colonies, phialides without collarettes and hyaline conidia that can be elongated and septate in several species (Gams 1971, Gams & Turham 1996, Girlanda & Luppi-Mosca 1998, Ramaley 2001).

Alejandra Giraldo, Josepa Gené & Josep Guarro, Mycology Unit, Medical School and IISPV, Universitat Rovira i Virgili (URV),
Sant Llorenç 21, 43201 Reus, Tarragona, Spain;
e-mail: dagiraldol@gmail.com, josepa.gene@urv.cat & josep.guarro@urv.cat.


Comoclathris spartii

Fungal Planet 312 – 24 November 2014

Comoclathris spartii K.M. Thambugala, E. Camporesi & K.D. Hyde, *sp. nov.*

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

Saprobic on *Spartium junceum*. *Ascomata* solitary, scattered or aggregated in small groups, immersed in host tissue, dark brown to black, globose to subglobose up to 200 µm diam without a distinct ostiole. *Ascomatal wall* of 2–4 layers of medium brown cells of *textura angularis* up to 12–20 µm. *Asci* 8-spored, 100–180 × 23–28 µm, cylindro-clavate, stipitate, bitunicate, fissitunicate, apex rounded, with a small apical chamber. *Pseudoparaphyses* hyaline, cellular, filamentous, septate, anastomosing, 2.5–4 µm diam, extending above the asci. *Ascospores* uni- to biseriate in asci, muriform, yellow to pale brown, broadly fusiform, with obtuse ends, constricted at the primary septum, surrounded by a mucilaginous sheath, 25–34 × 9–14.5 µm.

Culture characteristics — Colonies on PDA surface flat, spreading, reaching 26 mm diam after 1 wk at 25 °C, white to smoke-grey, with moderate aerial mycelium and undulate, smooth to feathery margins, reverse umber.

Typus. ITALY, Castellaccio di Corniolino - Santa Sofia (province of Forlì-Cesena (FC)) on *Spartium junceum* (*Fabaceae*), 13 Oct. 2012, *E. Camporesi* (holotype MFLU 14-0579, culture ex-type MFLUCC 13-0214; ITS sequence GenBank KM577159, LSU sequence GenBank KM577160, SSU sequence GenBank KM577161, MycoBank MB810274).

Notes — The genus *Comoclathris* (based on *Comoclathris lanata*) is characterised by ascomata with circular lid-like openings and applanate reddish brown to dark reddish brown, muriform ascospores, with single longitudinal septa (Zhang et al. 2012, Ariyawansa et al. 2014). Some authors (Zhang et al. 2012, Woudenberg et al. 2013, Ariyawansa et al. 2014) suggested the correct phylogenetic placement of the genus in *Pleosporaceae* rather than *Diademaceae* based on both morphology and molecular phylogeny. *Comoclathris spartii* is phylogenetically closely allied to *C. compressa* (CBS 156.53 and CBS 157.53) and presently, it seems best to place this species in *Comoclathris*.

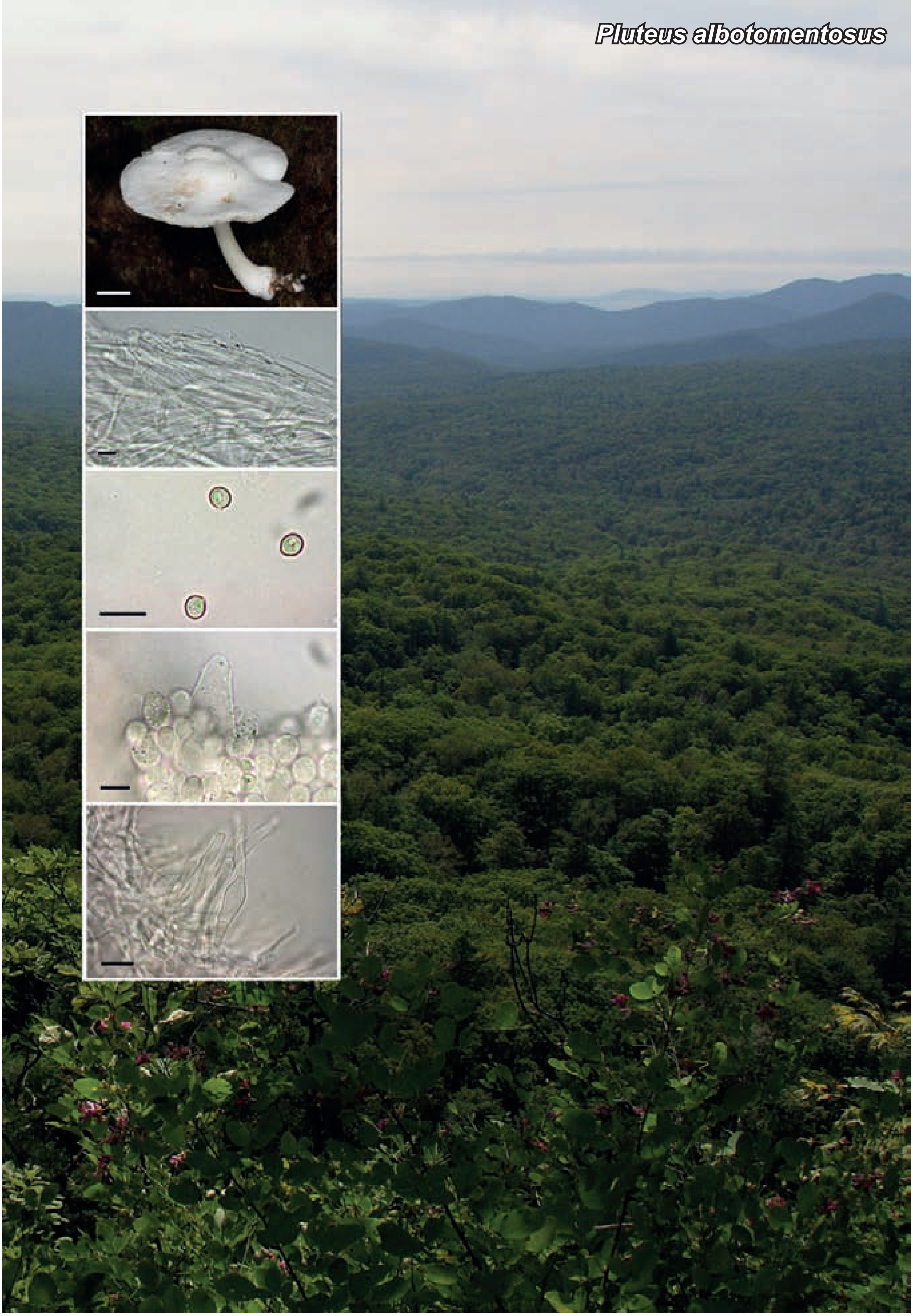
ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequence are Fungal endophyte sp. (GenBank EU977293; Identities = 511/517 (99 %), no gaps), Fungal sp. (GenBank JN578619; Identities = 523/536 (98 %), 4/536 (0 %)) and *Dendryphion penicillatum* (GenBank JN578618; Identities = 459/469 (98 %), no gaps).

LSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Pleospora ambigua* (GenBank KC584630; Identities = 858/872 (98 %), no gaps), *Comoclathris compressa* (GenBank KC584372 ; Identities = 856/872 (98 %), no gaps) and *Pleospora incompta* (GenBank GU238087; Identities = 835/846 (99 %), no gaps).

SSU. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the SSU sequence are *Comoclathris compressa* (GenBank AY787937; Identities = 870/886 (98 %), no gaps), *Comoclathris compressa* (GenBank KC584631; Identities = 870/886 (98 %), no gaps) and *Pleospora typhicola* (GenBank JF740105; Identities = 864/888 (97 %), Gaps = 1/888 (0 %)).

Colour illustrations. Castellaccio di Corniolino - Santa Sofia, Italy; ascomata, ascus and ascospores. Scale bars = 50 µm.

Kasun M. Thambugala, Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Xiaohe District, Guiyang City,
Guizhou Province 550006, People’s Republic of China; Institute of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100,
Thailand; School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand;
e-mail: madhusankathambugala@yahoo.com
Kevin D. Hyde, Institute of Excellence in Fungal Research, Mae Fah Luang University, Chiang Rai 57100, Thailand;
School of Science, Mae Fah Luang University, Chiang Rai 57100, Thailand;
e-mail: kdhyde3@gmail.com
Erio Camporesi, A.M.B. Gruppo Micologico Forlivese ‘Antonio Cicognani’, Via Roma 18, Forlì, Italy;
A.M.B. Circolo Micologico ‘Giovanni Carini’, C.P. 314, Brescia, Italy;
e-mail: eriocamporesi@libero.it


Pluteus albotomentosus

Fungal Planet 313 – 24 November 2014

Pluteus albotomentosus E.F. Malysheva & Malysheva, *sp. nov.*

Etymology. *Albotomentosus* refers to the colour and character of the pileus surface.

Pileus 50–60 mm diam, hemispherical becoming applanate with low, broad umbo, pure white when fresh, yellowish white or cream (4A2–A3) in herbarium; fine-tomentose over the entire surface, slightly flocculose towards margin. *Lamellae* free, crowded, broadly ventricose, white becoming pink with concolorous even edges. *Stipe* 60 × 8–10 mm, broadening downwards, with vague basal bulb up to 12–15 mm wide; solid, longitudinally fibrillose, white to slightly yellowish white, with white basal tomentum. Context white. Smell weak, sourish. *Basidiospores* 6.0–6.6(–6.8) × 5.3–6.0(–6.2) µm, Q = 1.00–1.21(–1.28), Q* = 1.11 (n = 30), subglobose to broadly ellipsoid, some oviform, smooth, thin- to slightly thick-walled, hyaline, contents with guttules. *Basidia* 23–32 × 6–8 µm, 4-spored, broadly clavate. *Pleurocystidia* abundant, 27–70 × 11–26 µm, utriform to broadly lageniform with very short and wide neck, some broadly clavate, hyaline, thin-walled. *Lamellae* edge sterile. *Cheilocystidia* numerous, forming dense layer, 23–65 × 5–11 µm, variable in shape, predominantly cylindrical, narrowly lageniform or narrowly clavate, thin-walled, hyaline. *Pileipellis* a cutis, made up of undifferentiated cylindrical hyphae up to 6–10 µm wide, thin- or slightly thick-walled, colourless. *Stipitipellis* a cutis of 5–12 µm wide hyaline hyphae, at lower part of stipe with scarce hyphae-like, cylindrical or narrowly clavate caulocystidia, 10–30 × 4–7 µm. *Clamp connections* absent in all tissues.

Habitat & Distribution — Solitary on mossy decayed log of deciduous tree. Found once in the south of Primorye Territory.

Typus. Russia, Primorye Territory, ‘Land of the Leopard’ National Park, watershed of Ananjevka and Gryaznaya Rivers, mixed forest (*Quercus mongolica*, *Carpinus cordata*, *Ulmus japonica*, *Abies nephrolepis*), on mossy log of deciduous tree, 1 Sept. 2011, *A. Kovalenko* (holotype LE 289394; ITS sequence GenBank KM658284, MycoBank MB810391).

Colour illustrations. Russia, Primorye Territory, ‘Land of the Leopard’ National Park, area of the East Manchurian mountains, Manchurian mixed forests, where the holotype was collected; basidiocarp, pileipellis, basidiospores, pleurocystidia, cheilocystidia (all from holotype). Scale bars = 1 cm (basidiocarp), 10 µm (microscopic structures).

Notes — The macroscopic description is based on fresh basidiocarps from the original collection and the photos taken at the site. Colour terms are according to Kornerup & Wanscher (1978). Microscopic observations and photos were made from dried material mounted in 5 % KOH using an AxioImagerA1 light microscope.

Pluteus albotomentosus is quite different from the other white-coloured *Pluteus* species because of a combination of distinctive morphological characters, a scilicet distinctly tomentose pure white pileus, thin-walled utriform pleurocystidia, cylindrical cheilocystidia and a cutis-like pileipellis. The pileipellis structure and non-metuloid cystidia place *P. albotomentosus* in sect. *Hispidoderma*. Based on this it can be compared to *P. ephebeus*, which is easily distinguished by its dark basidiocarp colour, larger spore size (5.5–8.5 × 4.5–6.0(–7.0) µm according to Vellinga 1990) and differently shaped cystidia. The molecular data (ITS sequence) indicate that it is closely related to *P. ephebeus* but the percentage of similarity between sequences of the two species is only 95–96 % or less.

Ekaterina F. Malysheva & Vera F. Malysheva, Komarov Botanical Institute of the Russian Academy of Sciences,
Prof. Popov St. 2, RUS-197376, Saint Petersburg, Russia;
e-mail: e_malysheva@binran.ru & v_malysheva@binran.ru


Pluteus extremiorientalis

Fungal Planet 314 – 24 November 2014

Pluteus extremiorientalis E.F. Malysheva & Malysheva, *sp. nov.*

Etymology. Named after the geographical area where it was collected (Russian Far East).

Pileus 10–35 mm diam, firstly hemispherical, then convex becoming applanate, commonly with obtuse low umbo; surface tomentose to squamulose – densely punctate-granulose at centre and fibrillose-squamulose towards margin, often with white context exhibited between rare fibrils or squamules; centre strongly venose-rugose; dark coloured, cocoa brown, leather brown (6E6), often with reddish tint – chestnut brown (6F7–F8) or henna (7E8), with darker disc (7F7–F8) and lighter margin because of scarcity of squamules; margin even or rimose, slightly striate or not, often incurved. *Lamellae* free, moderately crowded, ventricose, white becoming pink; edges even or slightly fimbriate, fuscous (brownish), more rarely concolorous. *Stipe* 20–55 × 1.5–5 mm, cylindrical or slightly broadening downwards (up to 7 mm), but without basal bulb, longitudinally fibrillose, whitish at upper part, covered with dark brown fibrils or squamules at lower part; basal tomentum white. Context white. Smell indistinct. *Basidiospores* 5.6–7 × 4.6–5.7 µm, Q = (1.02–)1.04–1.39(–1.48), Q* = 1.24 (n = 40), subglobose to broadly ellipsoid, some oviform, smooth, slightly thick-walled, hyaline, contents with one large or numerous small guttules. *Basidia* 20–30 × 6–9 µm, 4-spored, clavate. *Pleurocystidia* scattered, 35–70 × 10–17(–25) µm, broadly lageniform to utriform, some broadly fusiform to oviform, with pedices and obtuse apices, thin-walled, hyaline. Lamellae edge sterile. *Cheilocystidia* numerous, 40–90 × 10–33 µm, varying in shape, predominantly lageniform with inflated body and narrow long neck (up to 30 µm long and 6 µm wide), a few narrow utriform to clavate-cylindrical, thin-walled, with brown intracellular pigment (including holotype), but in some specimens hyaline. *Pileipellis* a cystoderm, made up of spheropedunculate, pyriform, broadly clavate cells in combination with lageniform or narrowly fusiform elements with acute apices, 20–75(–90) × 12–30(–35) µm, thin- or slightly thick-walled, with dark brown intracellular pigment in vacuoles. *Stipitipellis* a cutis of hyaline thin- or slightly thick-walled cylindrical hyphae, 5–12 µm wide, in stipe base with brown content and scattered clavate or cylindrical caulocystidia, 35–70(–100) × 8–15 µm, often with yellow-brown intracellular pigment. *Clamp connections* absent in pileipellis, but occasional in stipe context.

Habitat & Distribution — Scattered to gregarious on decaying deciduous wood or soil, in floodplain broadleaf forests. Known from two localities in the Russian Far East.

Typus. Russia, Primorye Territory, Ussuriysky Nature Reserve, vicinities of Peishula field station, floodplain of Koryavaya River, broadleaved forest (with *Ulmus*, *Populus*, *Acer*), on soil, 12 Aug. 2011, *N. Psurtseva* (holotype LE 262872; ITS sequence GenBank KM658280, MycoBank MB810390).

Additional specimens examined. Russia, Primorye Territory, Ussuriysky Nature Reserve, vicinities of Peishula field station, floodplain of Koryavaya and Suvorovka Rivers, broadleaved forest (with *Ulmus*, *Populus*, *Acer*), on wood of *Ulmus*, 12 Aug. 2011, *A. Kovalenko*, LE 262871, ITS sequence GenBank KM658279; ibid., on soil, 12 Aug. 2011, *E. Malysheva*, LE 303463, ITS sequence GenBank KM658282; ibid., *Ulmus japonica* forest, on soil, 13 Aug. 2011, *E. Malysheva*, LE 262865, ITS sequence GenBank KM658281; Primorye Territory, Kedrovaya Pad Nature Reserve, valley of Kedrovaya River, floodplain broadleaved forest (*Quercus mongolica*, *Carpinus cordata*, *Tilia amurensis*, *Juglans mandshurica*), on decaying deciduous wood, 5 Sept. 2011, *A. Kovalenko*, LE 303464, ITS sequence GenBank KM658283.

Notes — Macroscopic descriptions are based on fresh basidiocarps from the original collections and photos taken at the site. Colour terms are according to Kornerup & Wanscher (1978). Microscopic observations and photos were made from dried material mounted in 5 % KOH using an AxioImagerA1 light microscope.

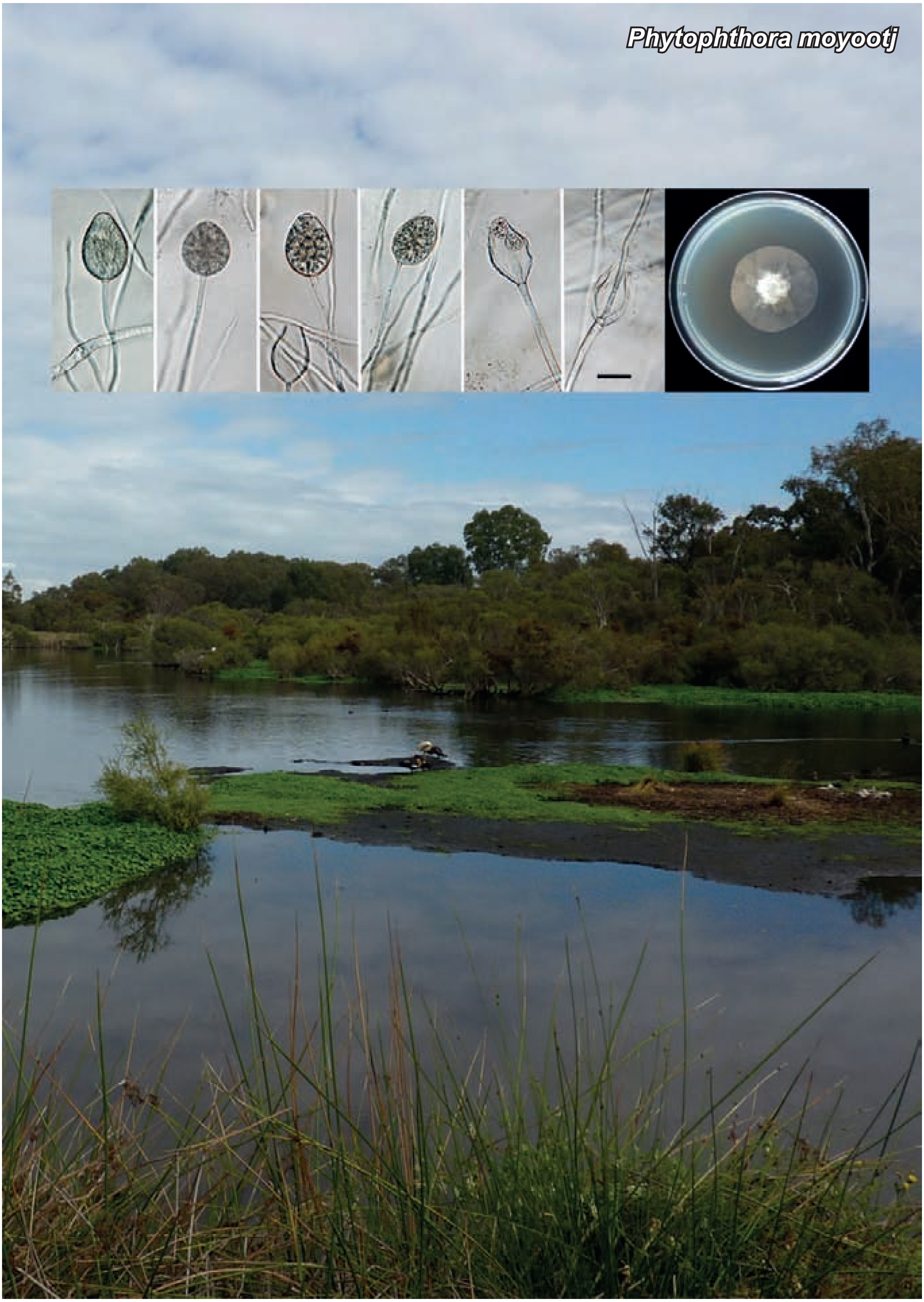
Pluteus extremiorientalis is characterised by small to medium-sized, brownish coloured and tomentose-squamulose pileus, fuscous edges of lamellae and dark fibrils on lower part of stipe. Microscopically, the pileipellis consists of two types of cystidioid elements (broadly clavate to sphaeropedunculate and fusiform); cheilocystidia abundant, variable in pigmentation in different collections, but most contain brown intracellular pigment; pleurocystidia not rare, predominantly lageniform or utriform.

Based on its pileipellis structure *P. extremiorientalis* is placed to sect. *Celluloderma* and subsect. *Mixtini*. The ITS sequences from the five studied collections are 99–100 % identical, but morphological characters differ slightly between collections – this mainly concerns the differences in colour of basidiocarps, density of squamules or fibrils on pileus surface, pigmentation of cheilocystidia and substrate preferences.

Pluteus extremiorientalis mostly resembles *P. podospileus* and *P. seticeps* var. *cystidiosus* in pileus colouration, dark brown fibrils at stipe base, shape of pleurocystidia and pileipellis structure (Minnis & Sundberg 2010). It can be distinguished from both by the strong tomentose-squamulose surface of the pileus, brownish coloured lamellae edges, cheilocystidia shape and smaller elements in the pileipellis. The molecular data (generated ITS sequences) confirmed the morphological differences between all species discussed and supported the recognition of *P. extremiorientalis* as a separate taxon.

Colour illustrations. Russia, Primorye Territory, Ussuriysky Nature Reserve, southern spurs of the Sikhote-Alin mountains, liana coniferous-broadleaved forest; basidiocarps, pileipellis elements, basidiospores, pleurocystidia, sterile edge of lamella (with pigmented cheilocystidia), stipitipellis (all from holotype). Scale bars = 1 cm (basidiocarps), 10 µm (microscopic structures).

Ekaterina F. Malysheva & Vera F. Malysheva, Komarov Botanical Institute of the Russian Academy of Sciences,
Prof. Popov St. 2, RUS-197376, Saint Petersburg, Russia;
e-mail: e_malysheva@binran.ru & v_malysheva@binran.ru


Phytophthora moyootj

Fungal Planet 315 – 24 November 2014

Phytophthora moyootj T.I. Burgess, *sp. nov.*

Etymology. Named for the swamp or wetlands from which isolates were recovered (moyootj = swamp country in the local Aboriginal Nyoongar language).

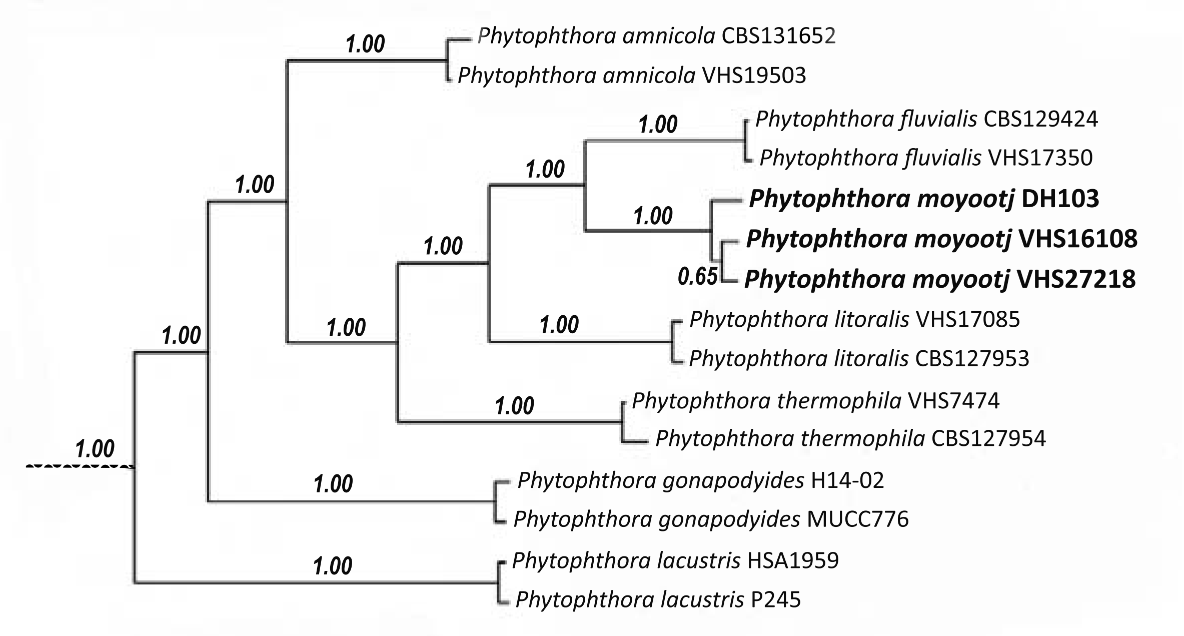
Sporangia produced abundantly in non-sterile soil extract; non-caducous, non-papillate with long unbranched sporangiophores, most commonly ovoid (63 %), with broad ovoid (11.5 %), limoniform (9 %), elongated ovoid (8.5 %), globose (5 %) and mouse shapes (3 %) also found; 39.6 ± 10.8 × 26.5 ± 4.2 µm (overall range 18–73.3 × 18.3–38.4 µm), length/breadth ratio 1.5 ± 0.4. *Sporangial proliferation* in chains of internally proliferating sporangia, both nested and extended. *Hyphal swellings* absent although rarely sporangia failed to produce septa and these then continued to grow from the apex to produce 'sporangia shaped' swellings. *Chlamydospores* not observed. *Gametangia* not produced in single culture or when paired with A1 and A2 tester strains of *P. cinnamomi*. Radial growth rates on V8 agar at optimum temperature (25–30 °C) and near the maximum temperature (32.5 °C), 5.5 ± 0.5 mm/d and 0.8 ± 0.1 mm/d, respectively.

Culture characteristics — Colonies have a stellate pattern on carrot agar and V8 agar and a fluffy irregular pattern on potato dextrose agar.

Typus. AUSTRALIA, Western Australia, Walpole, mud from vehicle, 2012, collected by Department of Parks and Wildlife (holotype MURU 469, cultures ex-type CBS 138759 = VHS27218; ITS sequence GenBank KJ372256, ß-tubulin sequence GenBank KJ372303, HSP90 sequence GenBank KJ396730, *cox*I sequence GenBank KJ396702, NADH sequence GenBank KJ396681, LSU sequence GenBank KP004501, MycoBank MB809152).

Additional specimens examined. AUSTRALIA, Western Australia, Fitzgerald River National Park, baited from soil in native heathland, 2006, collected by Department of Parks and Wildlife, VHS16108; Jarrahdale, isolated from water from restored pit at mine site, 2012, *D. Hüberli*, DH103.

Notes — Phylogenetically, *P. moyootj* resides in a strongly supported terminal clade and shares a common ancestor with *P. fluvialis*, *P. litoralis* and *P. thermophila* (Jung et al. 2011, Crous et al. 2011, 2012a). In a multigene phylogeny of the ITS, HSP90, BT, NADH and *cox*I gene regions, *P. moyootj* differs from *P. fluvialis* by 87 bp (1.8 %), *P. litoralis* by 107 bp (2.3 %) and *P. thermophila* by 118 bp (2.6 %). These four species have all been isolated from waterways and wetlands in the south-west of Western Australia. *Phytophthora moyootj* has a life strategy similar to *P. litoralis* and *P. fluvialis*, being sterile in culture and having abundant and continuous asexual multiplication chains of nested and extended internally proliferating sporangia. *Phytophthora moyootj* can be separated from these species because it lacks external proliferation of sporangia and hyphal swellings and it has lower optimum and maximum temperatures for growth.



Bayesian inference tree based on concatenated ITS, BT, HSP90, *cox*I and NADH sequence alignment generated in MrBayes using the GTR substitution model. The posterior probability is shown at the nodes. The species described here is printed in **bold** face. The tree was rooted to *P. humicola* (not shown). The alignment and tree are available in TreeBASE (Submission ID 15985).

Colour illustrations. Typical niche for recovery of *P. moyootj*; mature sporangia, ovoid, broad ovoid, ovoid just before release of zoospores, nested proliferation, empty sporangia with trapped encysted zoospores, internal nested and extended proliferation. Scale bar = 25 µm. Stellate colony on V8 agar (T.I. Burgess).

Treena I. Burgess, Centre for Phytophthora Science and Management, Murdoch University, 90 South Street, Murdoch, WA 6150, Australia;
e-mail: tburgess@murdoch.edu.au
Michael J.C. Stukely, Science Division, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia;
e-mail: mike.stukely@DPaW.wa.gov.au


Phoma tamaricicola

Fungal Planet 316 – 24 November 2014

Phoma tamaricicola Wanasinghe, Camporesi, E.B.G. Jones & K.D. Hyde, *sp. nov.*

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

Saprobic on dead herbaceous branches. *Sexual state*: *Ascomata* 120–150 µm high, 170–210 µm diam ($\bar{x}$ = 132 × 196 µm, n = 10) slightly erumpent, solitary, scattered, hardly removed from the host substrate, dark brown to black, coriaceous. *Peridium* 10–20 µm wide at the base, 20–25 µm wide in sides, thick, comprising 6–8 layers, outer layer heavily pigmented, thick-walled, comprising blackish to dark brown cells of *textura angularis*, inner layer composed of hyaline thin-walled cells of *textura angularis*. *Hamathecium* comprising numerous, 2.3 µm (n = 30) wide, filamentous, branched, septate, pseudoparaphyses. *Asci* (70–110) × (10–20) µm ($\bar{x}$ = 14.5 × 95 µm, n = 40), 8-spored, bitunicate, fissitunicate, cylindrical to cylindric-clavate, pedicellate, thick-walled at the apex, with a minute ocular chamber. *Ascospores* (15–20) × (7–10) µm ($\bar{x}$ = 18 × 9 µm, n = 50), overlapping 1–2-seriate, muriform, mostly ellipsoidal, 4–6 transversely septate, with 3–4 vertical septa, constricted at the septa, initially hyaline, becoming yellowish brown at maturity, conical and narrowly rounded at the ends, without a mucilaginous sheath. *Asexual state*: *Conidiomata* superficial or immersed in the agar, dark brown to black, clothed with white hyphal projections, 0.5–1.5 mm diam, simple, or complex with several merging cavities. Conidiomatal wall composed of a 30–45 µm thick outer layer and a 35–60 µm thick inner layer of *textura angularis* cells. *Conidiogenous cells* (4–7 × 3–4 µm) discrete, assembled into protruding masses of cells, or integrated in very compact conidiophores. *Conidia* (4–7 × 2.5–3.5 µm) narrowly ellipsoidal or short-cylindrical, straight or slightly curved, rounded at both ends, 1-celled, with 1–2 small, polar guttules, and with thin and smooth walls that are hyaline at secession, becoming light brown.

Culture characteristics — Colonies on PDA reaching 30–35 mm diam in 21 d, with abundant, fluffy grey aerial mycelium on surface, reverse smoke-grey.

Known distribution — On dead branches of *Tamarix gallica* (*Tamaricaceae*), Italy.

Typus. Italy, Forlì-Cesena Province, Ravaldino in Monte, dead and hanging branches of *Tamarix gallica*, 15 Jan. 2014, *E. Camporesi* (holotype MFLU 14-0333, ex-type living culture = MFLUCC 14-0602, ITS sequence GenBank KM408753, LSU sequence GenBank KM408754, SSU sequence GenBank KM408755, MycoBank MB810072).

Colour illustrations. Ravaldino in Monte, Italy. Ascomata on host substrate, section of ascoma, asci, ascospores, colonies on PDA; section of conidiomata, conidiomatal wall and conidia. Scale bars = 20 µm.

Notes — Species belonging to the genus *Phoma* are important plant pathogens (de Gruyter et al. 2009, Aveskamp et al. 2010, Wijayawardene et al. 2014) and characterised by 'hyaline, unicellular conidia that may become septate due to secondary septation, phialidic, ampulliform to doliiform conidiogenous cells and (sub)globose, glabrous to pilose or setose, pseudoparenchymatous or scleroplectenchymatous pycnidia' (de Gruyter et al. 2010).

Phoma was shown to be highly polyphyletic, and molecular based studies have shown that species are scattered throughout the *Pleosporales* (de Gruyter et al. 2009, 2010, 2013, Aveskamp et al. 2010), with *Phoma herbarum* clustering in *Didymellaceae* as the type species of *Phoma* (de Gruyter et al. 2013).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence had highest similarity to *Ascochyta pisi* (GenBank DQ678070; Identities = 888/890 (99 %), no gaps), *Peyronellaea prosopidis* (GenBank KF777232; Identities = 887/890 (99 %), no gaps) and *Coniothyrium prosopidis* (GenBank KF777205; Identities = 887/890 (99 %), no gaps).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the ITS sequences are *Microsphaeropsis proteae* (GenBank JN712497; Identities = 517/523 (99 %), Gaps = 1/523 (0 %)), *Phoma macrostoma* (GenBank HM036611; Identities = 514/519 (99 %), no gaps) and *Phoma herbarum* (GenBank FN868459; Identities = 518/525 (99 %), Gaps = 3/525 (0 %)).

Dhanushka N. Wanasinghe & Kevin D. Hyde, World Agro forestry Centre East and Central Asia Office, 132 Lanhei Road, Kunming 650201, China;
Key Laboratory for Plant Biodiversity and Biogeography of East Asia (KLPB), Kunming Institute of Botany, Chinese Academy of Science, Kunming 650201, Yunnan China;
Institute of Excellence in Fungal Research and School of Science, Mae Fah Luang University, Chiang Rai, 57100, Thailand;
e-mail: dnadeeshan@gmail.com & kdhyde3@gmail.com
Erio Camporesi, A.M.B. Gruppo Micologico Forlivese 'Antonio Cicognani', Via Roma 18, Forlì, Italy; A.M.B. Circolo Micologico 'Giovanni Carini', C.P. 314, Brescia, Italy; Società per gli Studi Naturalisticidella Romagna, C.P. 144, Bagnacavallo (RA), Italy;
e-mail: eriocamporesi@libero.it
E.B. Gareth Jones, Department of Botany and Microbiology, College of Science, King Saudi University, Riyadh, Saudi Arabia;
e-mail: torperadgj@gmail.com


Stagonospora chrysopyla

Fungal Planet 317 – 24 November 2014

Stagonospora chrysopyla Romberg & Rooney-Latham, *sp. nov.*

Etymology. Named after the location where this fungus was collected, Golden Gate Park Conservancy, San Francisco, California, USA, *chryso* = gold, *pyla* = gate.

Leaf spots spreading longitudinally along the leaf, angular, reddish brown, up to 5 cm in length, edges indistinct. *Conidiomata* immersed, globose to subglobose, up to 250 µm diam, dark brown, scattered, subepidermal; wall of 3–6 layers of brown *textura intricata*, ostiole indistinct, only present on abaxial surface, 30–50 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline, smooth, lining inner cavity, ampulliform to subglobose, 10–20 × 5–12 µm. *Conidia* solitary, hyaline, smooth, cylindrical, straight, apex obtuse to subobtuse, base truncate, (3–)5–6(–7)-septate, (48–)50–65(–69) × (5–)7–8(–10) µm.

Culture characteristics — Colonies flat, circular, with even margins, 50 mm diam after 2 wk at 20 °C in dark on PDA. Aerial mycelium sparse, cream-coloured at first, becoming pale olivaceous-grey to olivaceous-grey, reverse olivaceous-grey (Rayner 1970).

Typus. USA, California, Marin County, Golden Gate Park Conservancy, on leaves of *Scirpus microcarpus* (*Cyperaceae*), 15 Jan. 2014, *A. Shor* (holotype BPI892895, culture ex-type CBS 137792; ITS sequence GenBank KM033942, TUB sequence GenBank KM033943, MycoBank MB809083).

Notes — Of the more than 500 names in *Stagonospora*, fewer than 20 are represented in the NCBI GenBank. Shown in the table is a comparison of conidial measurements and number of septa for the species of *Stagonospora* currently described from *Scirpus*, as well as larger-spored *Stagonospora* spp. described from hosts in the *Cyperaceae* that are not represented in GenBank (Tehon 1933, Cunnell 1957, Castellani & Germano 1977). The conidia of *Stagonospora chrysopyla* are larger than those of other species of *Stagonospora* on *Scirpus* and it is also the first *Stagonospora* described from *Scirpus microcarpus*. Of the larger-spored *Stagonospora* on *Cyperaceae*, *S. chrysopyla* most resembles *S. dolosa*, but differs in having smaller and thinner conidia that are 5–6-septate rather than mainly 5-septate. The conidial size of *S. chrysopyla* also overlaps with that of *S. foliicola*; however, the examined herbarium specimens of *S. foliicola* show a great deal of variation and the circumscription of this species may need to be re-examined. The ITS region of *S. chrysopyla* has 90 % identity to *S. foliicola* (GenBank KF251256).

ITS. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of the ITS sequence had highest similarity to *S. paludosa* (GenBank KF251257; Identities = 493/518 (95 %)) and *S. pseudocaricis* (GenBank KF251260; Identities = 494/517 (96 %)). Both of these species differ from *S. chrysopyla* in conidial size and reported host (Crous et al. 2013, Quaedvlieg et al. 2013).

TUB. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits of the TUB sequences are *S. paludosa* (GenBank KF252740, Identities = 392/416 (94 %)) and *S. pseudocaricis* (GenBank KF252741, Identities = 395/420 (94 %)).

Table Comparison of conidial measurements and number of septa for selected species of *Stagonospora*.

Species	Conidia (µm)[1]	No. of septa	Specimen(s) examined	Reported host(s)
Stagonospora aquatica	25–30 × 5–6	3	–	*Scirpus*
S. aquatica var. *sexseptata*	32–35 × 5–6	6	–	*Scirpus*
S. chrysopyla	**50–65 × 7–8**	**5–6**	**BPI 892895**	***Scirpus***
S. cylindrica	48–78 × 8–11.5	3(–4)	–	*Phragmites*
S. dolosa	60–70 × 10	5	BPI 374901	*Phragmites*
S. elegans	52–84 × 8.5–14	(3–)4–6	–	*Phragmites*
S. foliicola	35–90 × 5.5–9.5	6–12	BPI 374911 / BPI 374909	Various
S. gigaspora	58–84 × 10–14	6–9	BPI 374955	*Carex*
S. maritima	16–20 × 4–6.5	2	–	Various
S. scirpi	20–28 × 5–6.5	(3–)4–5	–	*Scirpus*
S. scirpicola	12–18 × 2.5–3	3	BPI375122	*Scirpus*
S. scirpini	20 × 3–4	1–4	BPI375126	*Scirpus*

[1] Conidial measurements as presented in species descriptions in Tehon (1933), Cunnell (1957), Castellani & Germano (1977) and/or determined upon examination of herbarium specimens.

Colour illustrations. Leaves of *Scirpus microcarpus* growing at the Golden Gate Park Conservancy (photo: A. Shor); leaf surface with ostiole, pycnidial surface (bar = 100 µm), pycnidium (bar = 100 µm), conidiogenous cells and conidia (bars = 10 µm).

Megan K. Romberg, USDA APHIS PPQ NIS, 10300 Baltimore Ave, Beltsville, MD 20705;
e-mail: Megan.K.Romberg@aphis.usda.gov
Suzanne Rooney-Latham, California Department of Food and Agriculture, 3294 Meadowview Road, Sacramento, CA 95832;
e-mail: slatham@cdfa.ca.gov


Penicillium coccotrypicola

Fungal Planet 318 – 24 November 2014

Penicillium coccotrypicola Holdom, Y.P. Tan & R.G. Shivas, *sp. nov.*

Etymology. Derived from the generic name of the palm seed borer weevil (*Coccotrypes*) that formed the galleries from which the fungus was isolated.

Mycelium ramified in galleries of palm seed borer (*Coccotrypes carpophagus*) scolytine weevils that infest seeds of *Archontophoenix cunninghamiana*. *Synnemata* protrude from the fibrous seed husk, blue-grey, clavate, often furcated and slightly flattened, up to 1 cm high, solitary or clustered in small coralloid groups. *Conidiophores* in vivo borne on surface of synnemata; stipes 30–120 µm, verruculose or finely roughened to partly smooth, subhyaline to pale olivaceous; penicilli biverticillate or terverticillate, rarely monoverticillate; 2–5 metulae, one metula often larger than others, (9–)10.5–13.5(–16.5) × (2.5–)3.5 × 4.5(–5) µm, smooth or finely roughened, subhyaline to pale grey-olivaceous. *Conidiogenous cells* phialides, in verticils of 2–6, acerose, smooth, 9–15 × 2–3.5 µm, with a distinct neck, hyaline to subhyaline. *Conidia* globose to subglobose (2.5–)3 × 3.5(–4) µm, smooth, pale grey-olivaceous. Synnemata produced in vitro on Czapek yeast extract agar (CYA) after 14 d in the dark at 25 °C, with similar conidiophores borne from hyphae with stipes up to 200 µm; metulae (8.5–)9–11.5(–14.5) × 2.5–3.5(–4) µm and phialides (7–)8–10(–12) × 2–2.5(–3) µm.

Culture characteristics — (after 7 d in the dark at 25 °C). On CYA colonies 40–43 mm diam, velutinous, weakly sulcate, glaucous grey to greenish grey; tinged sienna at centre and white margins, apricot droplets exuded at centre and pale brown soluble pigment released into agar; cinnamon in reverse; no growth at 5 or 37 °C. Conidial mass becoming cinnamon on older cultures on most media; increasing Cu and Zn had no effect; rare (< 1 %) germination but no growth at 30 °C. On oatmeal agar (OA) and potato dextrose agar (PDA) colonies 40–42 mm diam, with irregular concentric rings of greenish grey sporulation, synnemata form in rings. On 25 % glycerol nitrate agar colonies 12–14 mm diam with no sporulation. On creatine sucrose agar colonies 27–31 mm diam with acid production. On Czapek agar (CzA) colonies 24–30 mm diam. On malt extract agar (Pitt 1979) colonies 29–30 mm, sporulation sparse, soluble pigment not released, and colour of culture not changing to cinnamon with age. On yeast extract sucrose agar colonies 43–47 mm diam, no sporulation, primrose around a darker centre. On CYA + 5 % NaCl colonies 26–28 mm diam. On nitrite-sucrose agar colonies 27–30 mm diam. No growth on CzA + proprionic acid. On CzA + sorbic and benzoic acids colonies 5–11 mm diam.

Typus. Australia, Queensland, Bli Bli, Maroochy Wetlands, on seeds of *Archontophoenix cunninghamiana* and in galleries infested by *Coccotrypes carpophagus*, 6 July 2013, *D. Holdom & J. Hewett* (holotype BRIP 59608; ITS sequence GenBank KM605436, LSU sequence GenBank KM605437, beta-tubulin sequence GenBank KM605438, MycoBank MB810327).

Colour illustrations. *Archontophoenix cunninghamiana* at Mapleton Falls National Park Queensland; seeds of *A. cunninghamia* with synnemata of *Penicillium coccotrypicola*; 7-d-old cultures on CYA (left) and OA (right); synnemata on OA; conidia and conidiophores on CYA after 14 d. Scale bars (from top to bottom) = 1 cm, 1 cm, 1 cm, 1 mm, 10 µm.

Notes — *Penicillium* s.str. has recently been redefined as a monophyletic genus by multilocus (RPB1, RPB2, Tsr1 and Cct8) phylogenetic analysis (Houbraken & Samson 2011). The formation of synnemata by species of *Penicillium* is uncommon (Pitt 1979, Seifert et al. 2004). *Penicillium coccotrypicola* is morphologically distinct from other species by having furcated synnemata. *Penicillium coccotrypicola* produced ramified mycelium in the galleries of palm seed borer weevils (*Coccotrypes carpophagus*: *Coleoptera*, *Curculionidae*, *Scolytinae*) in seeds of *Archontophoenix cunninghamiana* (*Arecaceae*). The palm seed borer weevils in the galleries were not colonised by *P. coccotrypicola*, which provides evidence that these ambrosia insects were farming the fungus. Possible mutualistic associations between *Penicillium* species and various scolytine weevil genera (*Crypturgus*, *Dendroctonus*, *Hypothenemus*, *Ips*, *Pityogenes* and *Tomicus*) have been noted before (Peterson et al. 2003, Giordano et al. 2013).

ITS. Based on a megablast search of the NCBI GenBank nucleotide database, the closest hits using the ITS sequence are *Penicillium mononematosum* (ex-type strain CBS 172.87; GenBank JX997082; Identities = 507/512 (99 %), Gaps = 0 (0 %)), *P. gladioli* (ex-type strain NRRL 939; GenBank DQ339568; Identities = 658/665 (99 %), Gaps = 1/665 (0 %)), *P. confertum* (ex-type strain CBS 171.87; GenBank JX997081; Identities = 506/512 (99 %), Gaps 0/512 (0 %)) and *P. flavigenum* (ex-type strain CBS 419.89; GenBank JX997105; Identities = 506/512 (99 %), Gaps = 0/512 (0 %)).

BT. Based on a megablast search of the NCBI GenBank nucleotide database, the closest hits using the BT sequence are *Penicillium expansum* (ex-type strain CBS 325.48; GenBank JQ965099; Identities = 585/634 (92 %), Gaps = 8/634 (1 %)) and *P. sclerotigenum* (ex-type strain CBS 101033; GenBank AY674393; Identities = 429/467 (92 %), Gaps = 6/467 (1 %)).

David G. Holdom, Yu Pei Tan, Justin S. Bartlett & Roger G. Shivas, Biosecurity Queensland, Ecosciences Precinct,
Department of Agriculture, Fisheries and Forestry, Dutton Park 4102, Queensland, Australia
e-mail: david.holdom@daff.qld.gov.au, yupei.tan@daff.qld.gov.au, justin.bartlett@daff.qld.gov.au & roger.shivas@daff.qld.gov.au


Sistotrema epiphyllum

Fungal Planet 319 – 24 November 2014

Sistotrema epiphyllum Stalpers, Stielow & B. de Vries, *sp. nov.*

Etymology. Growing on leaves: *epi* = on, *phyllon* = leaf.

Basidiome resupinate, effused, arachnoid to pellicular and separable, 70–100 µm thick. *Hymenium* even, smooth, becoming more or less continuous, white to slightly greyish. *Margin* not differentiated, hyphal strands absent. *Subiculum* very loose. *Subicular hyphae* hyaline to slightly yellowish brownish, thin-walled, 3.5–7(–8) µm wide, contents hyaline to granular, individual cells sometimes swollen. *Subhymenial hyphae* hyaline, thin-walled, 3.5–4.5(–5) µm wide. All septa with prominent clamps. *Cystidia* absent. *Basidia* in small clusters, originating from a sprouting clamp, typically urniform, 18–25 × 4.5–5.5 µm, with 4–6(–7) sterigmata. Sterigmata 3–4 µm long. *Spores* hyaline, thin-walled, ellipsoid, sometimes slightly pip-shaped, flattened at the apicular side, (5.4–)5.7–6.5(–7) × 3.3–4(–4.3) µm, not amyloid, not dextrinoid, not cyanophilous. *Apiculus* short but distinct.

Habitat & Distribution — On the underside of brown, fallen leaves of *Fagus sylvatica*, which were heaped up in a depression in the terrain. The affected leaves were not directly on the surface of the leaf stack, but lower down.

Typus. Netherlands, Duivekate, park forest, 20 Apr. 2013, *J.A. Stalpers* (holotype CBS H-21517; leg. *B. de Vries*, paratype BdV 7510; ITS sequence GenBank KM401576, MycoBank MB809154).

Colour illustrations. Leaves of *Fagus sylvatica* in beech park; basidia, spores, clamps, basidiome on leaf. Scale bars = 5 µm.

Notes — *Sistotrema epiphyllum* is characterised by the combination of even and pellicular hymenium and the ellipsoid-flattened spores in the range of 5.5–7 × 3.3–4.3 µm, while also the substrate is uncommon for *Sistotrema* spp., which are usually found on wood, or on old *Ganoderma* basidiomes. The impression here is that the species is actually soil-bound and fruits on more solid material, a situation also found in *Tomentella*. Molecular data have proven *Sistotrema* to be a heterogenous genus, a situation which has only been partly resolved yet. Based on the available sequences, the closest relative of *S. epiphyllum* is *S. hypogaeum* (Warcup & Talbot 1962), repeatedly isolated from soil in Adelaide, Australia. It differs in the cylindrical to subnavicular spores, (5–)7–9 × 2–2.5 µm.

Remarkably, the closest relatives to the *S. epiphyllum* clade belong to the genera *Minimedusa* and *Burgoa*, athelioid species with cylindrical, 4-spored basidia and characterised by the production of bulbils or sclerotioid bodies in culture. Such bodies (yellowish irregular sclerotium-like mass) are also reported for *S. hypogaeum* (Warcup & Talbot 1962). Unfortunately, cultures of the present species could not yet be obtained.

Weresub & LeClair (1971) mentioned a connection of *Burgoa* with the *Sistotrema brinkmannii* complex, based on the occurrence of swollen cells strongly resembling those of *Sistotrema brinkmannii. Minimedusa* was considered related, but not congeneric. The type species of *Sistotrema* is *S. confluens*.

ITS. Based on a megablast search against the INSDC (GenBank) nucleotide database, the closest hits using the generated ITS sequence are several environmental (clone) sequences only (e.g. DQ309120; Identities = 581/593 (98 %), Gaps = 8/593 (1 %) and KF617443; Identities = 562/591 (95 %), Gaps = 8/591 (1 %)); the closest voucher-derived sequence is of *Sistotrema coronilla* AFTOL-ID 618 (DQ397337; Identities = 513/550 (93 %), Gaps = 13/550 (2 %)). Amplification of the large subunit D1/D2 (28S nrDNA) failed.

Joost A. Stalpers & Benjamin Stielow, Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands;
e-mail: j.stalpers@cbs.knaw.nl & b.stielow@cbs.knaw.nl
Bernard de Vries, Roerdomplaan 222, 7905 EL Hoogeveen, The Netherlands; e-mail: elbern@planet.nl

REFERENCES

Aa HA van der, Vanev S. 2002. A revision of the species described in Phyllosticta. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands.

Alvarado P, Moreno G, Manjón JL, et al. 2011. First molecular data on Delastria rosea, Fischerula macrospora and Hydnocystis piligera. Boletín de la Sociedad Micológica de Madrid 35: 31–37.

Antonín V, Ryoo R, Shin HD. 2012. Marasmioid and gymnopoid fungi of the Republic of Korea. 4. Marasmius sect. Sicci. Mycological Progress 11: 615–638.

Ariyawansa HA, Phookamsak R, Tibpromma S, et al. 2014. A molecular and morphological reassessment of Diademaceae. The Scientific World Journal: doi.org/10.1155/2014/675348.

Arzanlou M, Groenewald JZ, Gams W, et al. 2007. Phylogenetic and morphotaxonomic revision of Ramichloridium and allied genera. Studies in Mycology 58: 57–93.

Aveskamp MM, Gruyter J de, Woudenberg JHC, et al. 2010. Highlights of the Didymellaceae: A polyphasic approach to characterize Phoma and related pleosporalean genera. Studies in Mycology 65: 1–60.

Bensch K, Braun U, Groenewald JZ, et al. 2012. The genus Cladosporium. Studies in Mycology 72: 1–401.

Braun U, Crous PW, Schubert K, et al. 2010. Some reallocations of Stenella species to Zasmidium. Schlechtendalia 20: 99–104.

Braun U, Hill CF. 2008. New species and new records of foliicolous hyphomycetes from New Zealand. Australasian Mycologist 27: 45–56.

Castellani E, Germano G. 1977. Le Stagonosporae graminicole. Annali della Facoltà di Scienze Agrarie della Università degli Studi di Torino 10: 1–135.

Chomnunti P, Bhat DJ, Gareth Jones EB, et al. 2012. Trichomeriaceae, a new sooty mould family of Chaetothyriales. Fungal Diversity 56: 63–76.

Corner EJH. 1996. The agaric genera Marasmius, Chaetocalathus, Crinipellis, Heimiomyces, Resupinatus, Xerula and Xerulina in Malesia. Nova Hedwigia Beihefte 111: 1–175.

Crous PW, Braun U, Groenewald JZ. 2007a. Mycosphaerella is polyphyletic. Studies in Mycology 58: 1–32.

Crous PW, Braun U, Schubert K, et al. 2007b. Delimiting Cladosporium from morphologically similar genera. Studies in Mycology 58: 33–56.

Crous PW, Groenewald JZ, Shivas RG, et al. 2011. Fungal Planet description sheets: 69–91. Persoonia 26: 108–156.

Crous PW, Schoch CL, Hyde KD, et al. 2009a. Phylogenetic lineages in the Capnodiales. Studies in Mycology 64: 17–47.

Crous PW, Schubert K, Braun U, et al. 2007c. Opportunistic, human-pathogenic species in the Herpotrichiellaceae are phenotypically similar to saprobic or phytopathogenic species in the Venturiaceae. Studies in Mycology 58: 185–217.

Crous PW, Shivas RG, Quaedvlieg W, et al. 2014. Fungal Planet description sheets: 214–280. Persoonia 32: 184–306.

Crous PW, Summerell BA, Carnegie AJ, et al. 2009b. Unravelling Mycosphaerella: do you believe in genera? Persoonia 23: 99–118.

Crous PW, Summerell BA, Shivas RG, et al. 2012a. Fungal Planet description sheets: 107–127. Persoonia 28: 138–182.

Crous PW, Verkley GJM, Christensen M, et al. 2012b. How important are conidial appendages? Persoonia 28: 126–137.

Crous PW, Wingfield MJ, Guarro J, et al. 2013. Fungal Planet description sheets: 154–213. Persoonia 31: 188–296.

Crous PW, Wingfield MJ, Koch SH. 1990. New and interesting records of South African fungi. X. New records of Eucalyptus leaf fungi. South African Journal of Botany 56: 583–586.

Cunnell GJ. 1957. Stagonospora spp. on Phragmites communis Trin. Transactions of the British Mycological Society 40: 443–445.

Dai DQ, Jayarama Bhat D, Liu JK, et al. 2012. Bambusicola, a new genus from bamboo with asexual and sexual morphs. Cryptogamie, Mycologie 33: 363–379.

Doidge EM. 1942. Revised descriptions of South African species of Phyllachora and related genera. Bothalia 4: 421–463.

Ellis MB. 1971. Dematiaceous Hyphomycetes. CMI, Kew, England.

Ellis MB. 1976. More Dematiaceous Hyphomycetes. CMI, Kew, England.

Gams W. 1971. Cephalosporium-artige Schimmelpilze (Hyphomycetes). Stuttgart, Gustav Fischer Verlag.

Gams W, Turham G. 1996. An extreme modification of Monocillium: Monocillium curvisetosum n. sp. Mycotaxon 59: 343–348.

Gilkey HM. 1925. Five new hypogaeous fungi. Mycologia 17: 250–255.

Gilkey HM. 1961. New species and revisions in the order Tuberales. Mycologia 53: 215–220.

Giordano L, Garbelotto M, Nicolotti G, et al. 2013. Characterization of fungal communities associated with the bark beetle Ips typographus varies depending on detection method, location, and beetle population levels. Mycological Progress 12: 127–140.

Giraldo A, Gené J, Cano J, et al. 2012. Two new species of Acremonium from Spanish soils. Mycologia 104: 1456–1465.

Giraldo A, Gené J, Cano J, et al. 2014. Acremonium with catenate elongate conidia: phylogeny of Acremonium fusidioides and related species. Mycologia 106: 328–338.

Girlanda M, Luppi-Mosca AM. 1998. Monocillium ligusticum, a new species from mycorrhizal roots in Mediterranean north Italy. Mycotaxon 67: 265–274.

Glenn A, Bacon CW, Price R, et al. 1996. Molecular phylogeny of Acremonium and its taxonomic implications. Mycologia 88: 369–383.

Gomes RR, Glienke C, Videira SIR, et al. 2013. Diaporthe: a genus of endophytic, saprobic and plant pathogenic fungi. Persoonia 31: 1–41.

Gruyter J de, Aveskamp MM, Woudenberg JHC, et al. 2009. Molecular phylogeny of Phoma and allied anamorph genera: Towards a re-classification of the Phoma complex. Mycological Research 113: 508–519.

Gruyter J de, Woudenberg JHC, Aveskamp MM, et al. 2010. Systematic reappraisal of species in Phoma section Paraphoma, Pyrenochaeta and Pleurophoma. Mycologia 102: 1066–1081.

Gruyter J de, Woudenberg JHC, Aveskamp MM, et al. 2013. Redisposition of Phoma-like anamorphs in Pleosporales. Studies in Mycology 75: 1–36.

Hashimoto A, Sato G, Matsuda T, et al. 2014. Molecular taxonomy of Dinemasporium and its allied genera. Mycoscience (in press) doi.org/10.1016/j.myc.2014.04.001.

Hirooka Y, Rossman AY, Samuels GJ, et al. 2012. A monograph of Allantonectria, Nectria, and Pleonectria (Nectriaceae, Hypocreales, Ascomycota) and their pycnidial, sporodochial, and synnematous anamorphs. Studies in Mycology 71: 1–210.

Houbraken J, Samson RA. 2011. Phylogeny of Penicillium and the segregation of Trichocomaceae into three families. Studies in Mycology 70: 1–51.

Hughes SJ, Kendrick WB. 1968. New Zealand fungi 12. Menispora, Codinaea, Menisporopsis. New Zealand Journal of Botany 6: 323–375.

Hyde KD, Jones EBG, Lui J-K, et al. 2013. Families of Dothideomycetes. Fungal Diversity 63: 1–313.

Johnston P, Seifert KA, Stone J, et al. 2014. Recommendations on generic names competing for use in Leotiomycetes (Ascomycota). IMA Fungus 5: 91–120.

Jung T, Stukely MJC, Hardy GEStJ, et al. 2011. Multiple new Phytophthora species from ITS Clade 6 associated with natural ecosystems in Australia: evolutionary and ecological implications. Persoonia 26: 13–39.

Kimbrough JW, Li LTL, Wu CG. 1996. Ultrastructural evidence for the placement of the truffle Barssia in the Helvellaceae (Pezizales). Mycologia 88: 38–46.

Kornerup A, Wanscher JH. 1978. Methuen handbook of colour. 3rd ed. London, Eyre Methuen.

Kuthubutheen AJ, Nawawi A. l991. A key to Dictyochaeta and Codinaea species. Mycological Research 95: 1224–1229.

Ławrynowicz M, Skirgiełło A. 1984. Barssia, a new genus in Europe. Acta Mycologia 20: 277–280.

Liu J-K, Phooksamsak R, Dai D-Q, et al. 2014. Roussoellaceae, a new pleosporalean family to accommodate the genera Neoroussoella gen. nov., Roussoella and Roussoellopsis. Phytotaxa 181: 1–33.

Lombard L, Leeuwen GCM van, Guarnaccia V, et al. 2014. Diaporthe species associated with Vaccinium, with specific reference to Europe. Phytopathologia Mediterranea 53: 85–97.

Mel'nik V, Lee S, Groenewald JZE, et al. 2004. New hyphomycetes from Restionaceae in fynbos: Parasarcopodium ceratocaryi gen. et sp. nov., and Rhexodenticula elegiae sp. nov. Mycological Progress 3: 19–28.

Minnis AM, Sundberg WJ. 2010. Pluteus section Celluloderma in the U.S.A. North American Fungi 5: 1–107.

Montecchi A, Sarasini M. 2000. Funghi ipogei d'Europa. Associazione Micologica Bresadola. Fondazione Centro Studi Micologici. Trento.

Nag Raj TR. 1993. Coelomycetous anamorphs with appendage-bearing conidia. Mycologue Publications, Waterloo, Ontario.

Papendorf MC. 1967. Two new genera of soil fungi from South Africa. Transactions of the British Mycological Society 50: 69–75.

Park RF, Keane PJ, Wingfield MJ, et al. 2000. Fungal diseases of eucalypt foliage. In: Keane PJ, Kile GA, Podger FD, et al. (eds), Diseases and pathogens of eucalypts: 153–239. CSIRO publishing, Australia.

Pascoe IG. 1990. Observations on ascus structure of Plectosphaera eucalypti (Phyllachoraceae). Mycological Research 94: 675–684.

Percudani R, Trevisi A, Zambonelli A, et al. 1999. Molecular phylogeny of truffles (Pezizales: Terfeziaceae, Tuberaceae) derived from nuclear rDNA sequence analysis. Molecular Phylogenetics and Evolution 13: 169–180.

Perdomo H, Sutton DA, García D, et al. 2011. Spectrum of clinically relevant Acremonium species in the United States. Journal of Clinical Microbiology 49: 243–256.

Peterson SW, Pérez J, Vega FE, et al. 2003. Penicillium brocae, a new species associated with the coffee berry borer in Chipas, Mexico. Mycologia 95: 141–147.

Phillips AJL, Alves A, Abdollahzadeh J, et al. 2013. The Botryosphaeriaceae: genera and species known from culture. Studies in Mycology 76: 51–167.

Pitt JI. 1979. The genus Penicillium and its teleomorphic states Eupenicillium and Talaromyces. Academic Press, London.

Quaedvlieg W, Verkley GJM, Shin H-D, et al. 2013. Sizing up Septoria. Studies in Mycology 75: 307–390.

Ramaley AW. 2001. Hyaloseta nolinae, its anamorph Monocillium nolinae and Niesslia agavacearum, new members of the Niessliaceae, Hypocreales, from leaves of Agavaceae. Mycotaxon 79: 267–274.

Rayner RW. 1970. A mycological colour chart. Commonwealth Mycological Institute, Kew, Surrey, UK.

Reblová M, Winka K. 2000. Phylogeny of Chaetosphaeria and its anamorphs based on morphological and molecular data. Mycologia 92: 939–954.

Ruscoe QW. 1970. Arxiella lunata sp. nov. Transactions of the British Mycological Society 55: 506–509.

Seifert KA, Hoekstra ES, Frisvad JC, et al. 2004. Penicillium cecidicola, a new species on cynipid insect galls on Quercus pacifica in the western United States. Studies in Mycology 50: 517–523.

Siboe GM, Kirk PM, Cannon PF. 1999. New dematiaceous hyphomycetes from Kenyan rare plants. Mycotaxon 73: 283–302.

Sigler L, Gibas CFC, Kokotovic B, et al. 2010. Disseminated mycosis in veiled Chameleons (Chamaeleo calyptratus) caused by Chamaeleomyces granulomatis, a new fungus related to Paecilomyces viridis. Journal of Clinical Microbiology 48: 3182–3192.

Summerbell RC, Gueidan C, Schroers HJ, et al. 2011. Acremonium phylogenetic overview and revision of Gliomastix, Trichothecium and Sarocladium. Studies in Mycology 68: 139–162.

Sung GH, Hywel-Jones NL, Sung JM, et al. 2007. Phylogenetic classification of Cordyceps and the clavicipitaceous fungi. Studies in Mycology 57: 5–63.

Sutton BC. 1980. The Coelomycetes: Fungi imperfecti with pycnidia, acervuli and stromata. Commonwealth Mycological Institute, Kew, Surrey, England.

Takahashi H. 2000. Three new species of Marasmius section Sicci from eastern Honshu, Japan. Mycoscience 41: 313–321.

Tehon LR. 1933. Notes on the parasitic fungi of Illinois. Mycologia 4: 237–257.

Trappe JM. 1979. The orders, families, and genera of hypogenous Ascomycotina (truffles and their relatives). Mycotaxon 9: 297–340.

Uecker FA. 1988. A world list of Phomopsis names with notes on nomenclature, morphology, and biology. Mycologia Memoirs 13: 1–231.

Vellinga EC. 1990. Pluteus. In: Bas C, Kuyper ThW, Noordeloos ME, et al. (eds), Flora Agaricina Neerlandica, vol. 2: 31–55. Balkema, Rotterdam.

Verkley GJM, Crous PW, Groenewald JZ, et al. 2004. Mycosphaerella punctiformis revisited: morphology, phylogeny, and epitypification of the type species of the genus Mycosphaerella (Dothideales, Ascomycota). Mycological Research 108: 1271–1282.

Verkley GJM, Quaedvlieg W, Shin HD, et al. 2013. A new approach to species delimitation in Septoria. Studies in Mycology 75: 213–305.

Wannathes N, Desjardin DE, Hyde KD, et al. 2009. A monograph of Marasmius (Basidiomycota) from Northern Thailand based on morphological and molecular (ITS sequences) data. Fungal Diversity 37: 209–306.

Warcup JH, Talbot PHB. 1962. Ecology and identity of mycelia isolated from soil. Transactions of the British Mycological Society 45: 495–518.

Weresub LK, LeClair PM. 1971. On Papulaspora and bulbilliferous basidiomycetes Burgoa and Minimedusa. Canadian Journal of Botany 49: 2203–2213.

Whitton SR, McKenzie EHC, Hyde KD. 2000. Dictyochaeta and Dictyochaetopsis species from the Pandanaceae. Fungal Diversity 4: 133–158.

Wijayawardene NN, Crous PW, Kirk PM, et al. 2014. Naming and outline of Dothideomycetes – 2014. Fungal Diversity (in press).

Wikee S, Lombard L, Nakashima C, et al. 2013. A phylogenetic re-evaluation of Phyllosticta (Botryosphaeriales). Studies in Mycology 76: 1–29.

Woudenberg JHC, Groenewald JZ, Binder M, et al. 2013. Alternaria redefined. Studies in Mycology 75: 171–212.

Zare R, Gams W, Evans HC. 2001. A revision of Verticillium section Prostrata. V. The genus Pochonia, with notes on Rotiferophthora. Nova Hedwigia 73: 51–86.

Zhang Y, Crous PW, Schoch CL, et al. 2012. Pleosporales. Fungal Diversity 53: 1–221.

Zhang Y, Schoch CL, Fournier J, et al. 2009. Multi-locus phylogeny of Pleosporales: a taxonomic, ecological and evolutionary re-evaluation. Studies in Mycology 64: 85–102.