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RESEARCH ARTICLE

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Key words

ITS DNA barcodes
LSU
novel fungal species
systematics

Abstract Novel species of microfungi described in the present study include the following from Australia: *Catenulostroma corymbiae* from *Corymbia, Devriesia stirlingiae* from *Stirlingia*, *Penidiella carpentariae* from *Carpentaria, Phaeococcomyces eucalypti* from *Eucalyptus*, *Phialophora livistonae* from *Livistona*, *Phyllosticta aristolochiicola* from *Aristolochia, Clitopilus austroprunulus* on sclerophyll forest litter of *Eucalyptus regnans* and *Toxicocladosporium posoqueriae* from *Posoqueria.* Several species are also described from South Africa, namely: *Ceramothyrium podocarpi* from *Podocarpus*, *Cercospora chrysanthemoides* from *Chrysanthemoides*, *Devriesia shakazului* from *Aloe*, *Penidiella drakensbergensis* from *Protea*, *Strelitziana cliviae* from *Clivia* and *Zasmidium syzygii* from *Syzygium*. Other species include *Bipolaris microstegii* from *Microstegium* and *Synchaetomella acerina* from *Acer* (USA), *Brunneiapiospora austropalmicola* from *Rhopalostylis* (New Zealand), *Calonectria pentaseptata* from *Eucalyptus* and *Macadamia* (Vietnam), *Ceramothyrium melastoma* from *Melastoma* (Indonesia), *Collembolispora aristata* from stream foam (Czech Republic), *Devriesia imbrexigena* from glazed decorative tiles (Portugal), *Microcyclospora rhoicola* from *Rhus* (Canada), *Seiridium phylicae* from *Phylica* (Tristan de Cunha, Inaccessible Island), *Passalora lobeliae-fistulosis* from *Lobelia* (Brazil) and *Zymoseptoria verkleyi* from *Poa* (The Netherlands). *Valsalnicola* represents a new ascomycete genus from *Alnus* (Austria) and *Parapenidiella* a new hyphomycete genus from *Eucalyptus* (Australia). Morphological and culture characteristics along with ITS DNA barcodes are also provided.

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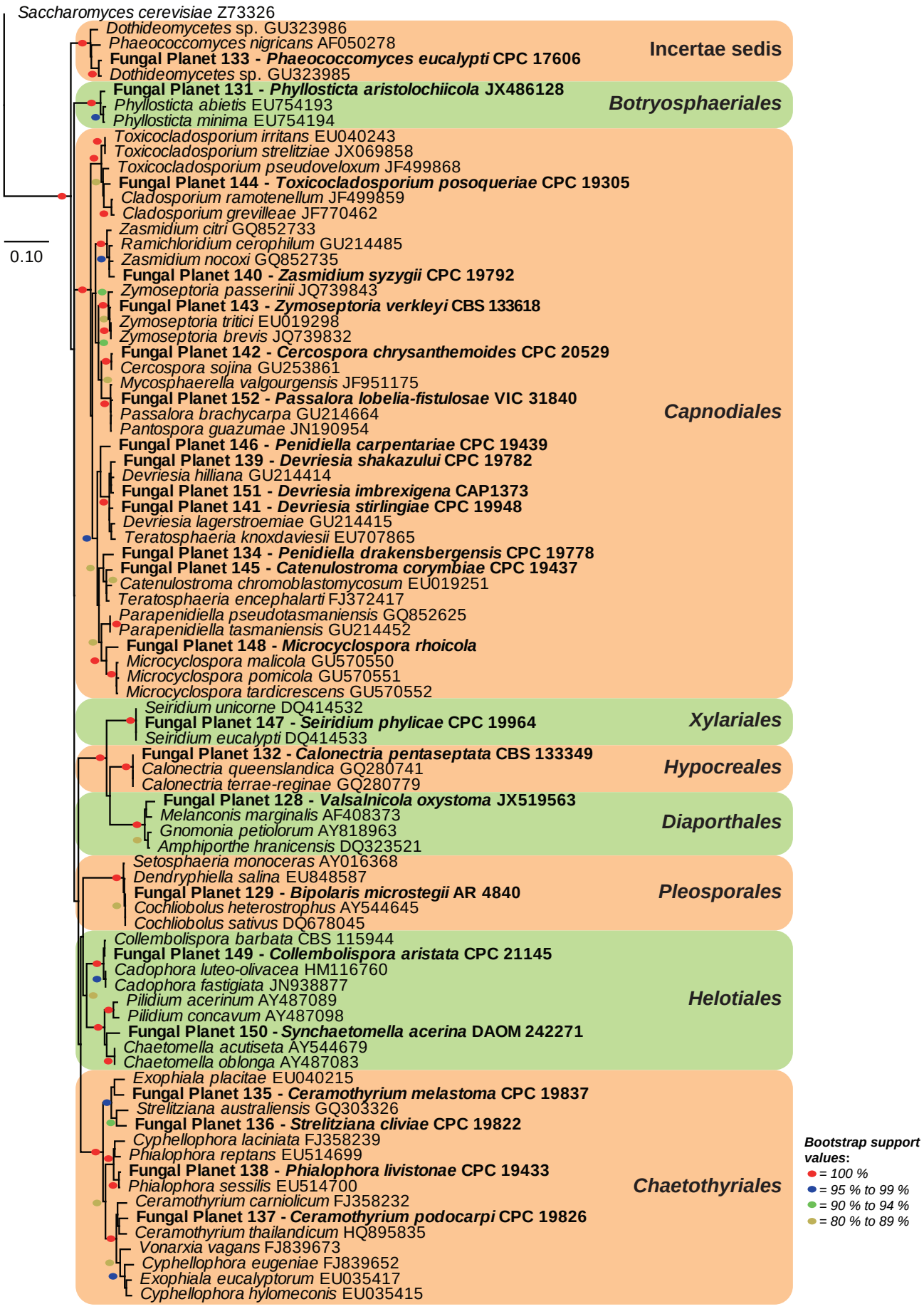

Neighbour-joining tree obtained using a distance analysis with a general time reversible (GTR) substitution model on the partial 28S nrRNA gene alignment (817 nucleotides including alignment gaps) as implemented in PAUP v. 4.0b10 (Swofford 2003). Novel species are indicated in a **bold** font and the orders are indicated on the right-hand side of the figure. The scale bar indicates the number of substitutions per site and the bootstrap support values (based on 1 000 replicates) are shown by colour-coded dots for values > 79 % (see legend on figure). The tree was rooted to a sequence of *Saccharomyces cerevisiae* (GenBank Z73326.)


Valsalnicola oxystoma
a
b
c
d
e

Fungal Planet 128 – 20 December 2012

Valsalnicola D.M. Walker & Rossman, *gen. nov.*

Etymology. Named for its valsa-like appearance and occurrence on species of *Alnus*.

Causing linear cankers and lesions. *Ectostromata* well-developed, brown to black, thick disc from which perithecial necks emerge. *Ascomata* perithecial, immersed beneath ectostroma, aggregated in groups of 13–23, converging into 5–20 necks. *Asci* fusiform, with indistinct apical ring. *Ascospores* allantoid with rounded ends, 1-septate, hyaline.

Type species. *Valsalnicola oxystoma*.
MycoBank MB801277.

Valsalnicola oxystoma (Rehm) D.M. Walker & Rossman, *comb. nov*.

Basionym. *Valsa oxystoma* Rehm, Ber. Naturhist. Vereins Augsburg 26: 70. 1881.

≡ *Cryptodiaporthe oxystoma* (Rehm) Z. Urb., Preslia 29: 395. 1957.

Twig lesions in surface view (511–)591–890(–893) µm diam (mean = 654, S.D. 122, n = 13). *Ectostroma* well-developed, brown to black, thick disc from which perithecial necks emerge. *Ascomatal cavity* (690–)765–909(–950) µm high × (1610–)1710–2346(–3947) µm diam (mean = 816 × 2198, S.D. 109, 703, n1 = 5, n2 = 9). *Ascomata* perithecial, immersed beneath ectostroma, causing host tissue to swell and rupture, perithecia converging into 5–20 necks, emerging at surface through ectostromatic disc, perithecia grouped 13–23. Ascomata glossy black, subglobose to globose (240–)266–298(–320) µm high × (253–)260–335(–337) µm diam (mean = 282 × 294, S.D. 25, 36, n1 = 7, n2 = 13); necks central, straight to curved, length (426–)428–550(–563) µm (mean = 476, S.D. 54, n = 9). *Asci* fusiform, (38–)39–48(–49) × (8–)9–12(–13) µm (mean = 44 × 11, S.D. 4, 1.2, n1 = 17, n2 = 18), apex broadly rounded, with indistinct apical ring, stipe acute, rounded, or tapering to a point, ascospores arranged irregularly multiseriate. *Ascospores* allantoid with rounded ends, mostly curved, rarely straight, (9–)10–11(–12) × 2–3 µm (mean = 11 × 2, S.D. 0.9, 0.5, n = 30), 1-septate, median, slightly constricted or not at septum, each cell with several small guttules, hyaline. *Cultures* slow-growing, 3–6 mm in 10 d on potato-dextrose agar, mycelium low, pale brown to greyish brown, reverse dark brown.

In culture on synthetic nutrient-poor agar — Dimorphic, forming a synanamorph. *Conidiomata* pycnidial, exuding masses of brown conidia. *Conidiophores* reduced to conidiogenous cells, or one supporting cell, proliferating percurrently. *Conidia* cylindrical, brown, finely verruculose, apex obtuse, base truncate, 3–5-euseptate, 15–23 × 4–5 µm. *Conidia* of synanamorph intermingled in same conidioma, but conidiogenous cells proliferating percurrently or sympodially; conidia hyaline to subhyaline, narrowly obclavate, apex subobtuse, base truncate, straight to curved, 25–80 × 2.5–3 µm, up to 11-septate. Synanamorph also developing in aerial mycelium (on PNA); conidiophores subcylindrical, straight to curved, 0–2-septate, hyaline to subhyaline, 8–15 × 2–3 µm, proliferating sympodially at apex. *Conidiophores* solitary or fasciculate or on a reduced stroma.

Colour illustrations. Italy, Trentino, Val Sadole, showing trees of *Alnus viridis* with green alder decline (Giorgio Maresi). a. Rehm: Ascomyceten 280, scale bar = 500 µm. b–d. BPI 884137, scale bars of perithecia = 100 µm, scale bar of ascus = 10 µm. e. Rehm: Ascomyceten 280, scale bar = 10 µm.

Typus. Austria, Tyrol, Längenfeld, on dead branch of *Alnus viridis*, c. 3 500 ft., Aug. 1874, coll. *Rehm*. This type specimen was issued as Rehm, Ascomyceten no. 280. Of the two specimens at BPI, the more plentiful one is in the bound set of Rehm, Ascomyceten, and is herein designated as Lectotype BPI 884138. Isolectotypes examined BPI 738235 and NY, MycoBank MB801277.

Additional specimens examined. Belgium, Brussels, Soignes, on branch of *Alnus glutinosa*, Oct. 1899, *P. Nypels*, comm. *H. Rehm*, Vestergren, Micromycetes rariores selecti 409 as *Valsa oxystoma* (BPI 574854). – Canada, British Columbia, Yoho National Park, Chancellor Mountain Camp, on *Alnus* sp., 11 Aug. 1962, *R.F. Cain*, TRTC 40116 (NY); Ontario, Kenora District, Tustin Township, Gordon Lake, Rd., on *Alnus* sp., 26 Sept. 1959, coll. *D. Bowen*, det. *J. Reid* as *Valsa oxystoma* (BPI 574855). – Italy, Trento, Monte Bondone Trento, E11°03'51" N46°02'20", on *Alnus viridis*, Apr. 2011, *G. Maresi*, isol. *A. Rossman* AR 4833 = CBS 133337, ITS sequence JX519559, and LSU sequence JX519563 (BPI 884137); Trento, val Sadole (E11.60, N46.15), 2009, *G. Maresi & C.M.O. Longa* (BPI 884136). – Sweden, Umea, on dead branch of *Alnus* '*borealis*', Sept. 1910, Vlengel, det. *F. Bubak* (BPI 574856). – USA, Alaska, near Fairbanks, Moose Creek, Environmental Monitoring Plot 316 MC UM11 MRC, N64.72, W147.23, elev. 150 m, on *Alnus incana* var. *tenuifolia*, May 2010, *G.C. Adams*, culture AR 5137 = CBS 133329, ITS sequence JX519561 (BPI 884135).

Habitat — *Alnus viridis* ssp. *viridis*, causing a twig colonization and canker disease involved in green alder decline (Pisetta et al. 2012); also known from *Alnus glutinosa, A. incana, A. incana* var. *tenuifolia, A. rubra, A. viridis* ssp. *fruticosa* and *A. viridis* ssp. *maximowiczii.*

Distribution — Asia: Japan (Kobayashi 2007); Europe: Austria, Belgium, Italy, Sweden, also United Kingdom (Cannon et al. 1985); North America: Canada (Ontario); USA: Alaska.

Notes — *Valsalnicola* is based on a species that was described in the genus *Valsa*. Although it resembles *Valsa* in having allantoid ascospores, the ascospores of *Valsalnicola* are 1-septate while the majority of species of *Valsa* and closely related *Leucostoma* and *Valsella* have aseptate ascospores. However, one species of *Valsa, V. melanodiscus,* also has 1-septate ascospores, occurs on *Alnus* spp., and produces linear cankers on the host. A distinguishing feature of *Valsalnicola* is the lack of a black line surrounding stromata in the ascomatal cavity, which is characteristic of *Valsa melanodiscus.* In addition, the growth rate of cultures of *Valsalnicola oxystoma* is considerably slower than species of *Valsa*. Molecular sequence data place this new genus within the *Gnomoniaceae-Melanconidaceae* complex. Allantoid, 1-septate ascospores have not previously been reported in the *Gnomoniaceae* or *Melanconidiaceae*. ITS sequences of specimens from Alaska and Italy are identical. The basionym has been cited as Rehm: Ascomyceten 270 (1875) in 'Index Fungorum' reflecting an error in Saccardo (1882) but the correct number is Rehm: Ascomyceten 280, which does not include a description.

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Bipolaris microstegii

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Bipolaris microstegii Minnis, Rossman, Kleczewski & S.L. Flory, *sp. nov*.

Etymology. Named after the host, *Microstegium vimineum* (*Poaceae*), from which the species was isolated originally.

Leaf spots on *Microstegium*, up to 2 × 0.5 cm, ellipsoid to irregular, brown with a darker, near black border. *Conidiophores* macronematous, mononematous, erect, more or less straight to slightly flexuous, simple or with a single dichotomous branch, cylindrical, geniculate at apex, pale to medium brown, often darker towards apices, smooth walled, septate, up to at least 750 µm long × 5–8 µm diam. *Conidiogenous cells* integrated, terminal or intercalary, with sympodial proliferation, monotretic or polytretic with darkened, circular scars. *Conidia* solitary, curved, cylindrical to obclavate, apex obtuse, base obtuse with inconspicuous hilum, pale brown, becoming medium to dark brown, end cells usually paler, walls smooth or faintly granulose, 5–10 distoseptate, with septa becoming accentuated at maturity, 40–97.5(–105) × 12.5–15(–17.5) µm, Q = 3.2–7.8 (L^m = 69.6 µm, W^m = 13.5 µm, Q^m = 5.2). *Germination* via a germ tube at each end cell of conidium.

Culture characteristics — Colonies 10–44(–70) mm diam on potato-dextrose agar (Difco) after 7 d at 24 °C with a 12 h light/dark diurnal cycle; surface near dull green (30D4, 30E3), dark green (28F3, 30F3), to greenish grey (28F2), velutinous to tomentose with sparse, white, aerial hyphae and dark conidiophores; margin uneven and lobed, whitish; reverse near greenish grey (30F2), dark green (30F5), to almost black.

Typus. USA, West Virginia, near Arnoldsburg, Crummies Creek Tree Farm, on living leaves of *Microstegium vimineum*, Aug. 2009, coll. *R. Richardson*, *Bipolaris* 4 isolated by *N.M. Kleczewski*, holotype BPI 883727 (dried culture on PDA); culture ex-type CBS 132550; ITS sequence GenBank JX089579, *gpd* sequence GenBank JX089575, LSU sequence GenBank JX100808, MycoBank MB801569.

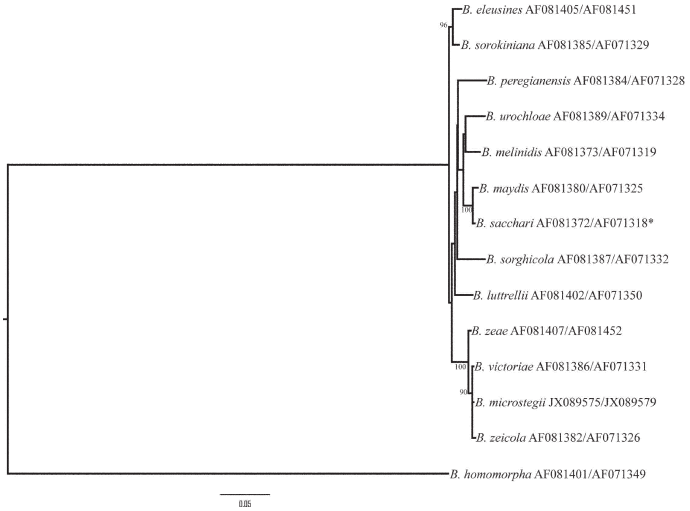
Additional specimens examined. USA, West Virginia, near Arnoldsburg, cove near Crummies Creek Tree Farm, on living leaves of *Microstegium vimineum*, Aug. 2009, coll. *R. Richardson*, *Bipolaris* 2 isolated by *N.M. Kleczewski*, BPI 883728 (dried culture on PDA); culture CBS 132549; ITS sequence GenBank JX089577 and *gpd* sequence GenBank JX089573; savannah near Crummies Creek Tree Farm, on living leaves of *Microstegium vimineum*, Aug. 2009, coll. *R. Richardson*, *Bipolaris* 3 isolated by *N.M. Kleczewski*, BPI 883729 (dried culture on PDA); culture CBS 132548; ITS sequence GenBank JX089578 and *gpd* sequence GenBank JX089574.

Phylogenetic analysis — The *gpd* and ITS sequences for all three isolates, *Bipolaris* 2–4 (Flory et al. 2011), were identical. A concatenated alignment of both loci was made using sequence data from the ex-type and Group 1 species (Berbee et al. 1999). A maximum likelihood search was then performed using the RAxML BlackBox (http://phylobench.vital-it.ch/raxml-bb/) with gamma, partitioned model, and per gene branch length optimization; 100 bootstrap replicates were included.

Notes — The microscopic description is based on PDA cultures and colony colour is based on Kornerup & Wanscher (1978). Many species of *Bipolaris* are important pathogens of grasses. This new species was isolated from *Microstegium vimineum*, an invasive plant in the USA. The fungus causes disease on *Microstegium*, but it also infects a wider range of hosts (Kleczewski & Flory 2010, Flory et al. 2011, Kleczewski et al. 2012). Comparison of ITS and *gpd* sequence data to sequences in GenBank and subsequent phylogenetic analyses based on Group 1 species (Berbee et al. 1999), referred to herein as *Bipolaris* (sensu Manamgoda et al. 2012), suggest that the present species is distinct and closely related to *B. victoriae* and *B. zeicola*. These species of *Bipolaris* consist of a highly pathogenic species complex that shows large differences in virulence and host ranges in spite of few genetic differences in the sequenced loci. Using Sivanesan (1987), *B. microstegii* is morphologically similar to *B. miyakei* and *B. zeicola*. A probable original culture of *B. miyakei* (CBS 197.29) is not closely related to *B. microstegii* based on ITS (JX089580) and *gpd* (JX089576) sequences. *Bipolaris microstegii* differs from *B. zeicola* by its longer and sometimes branched conidiophores.

Microstegium vimineum is native to Asia. Several isolates of *Bipolaris* are known from *Microstegium* in Asia (Shimizu et al. 1998), but the origin of *B. microstegii* is unknown. Species of *Bipolaris* in Group 1 (Berbee et al. 1999) are highly pathogenic on a wide range of native and non-native hosts and these include major pathogens of corn and oats.

The best scoring tree from the maximum likelihood analysis. Bootstrap values ≥ 70 % are indicated. GenBank numbers of included sequences for each species are given as *gpd*/ITS. An asterisk denotes that *gpd* and ITS sequences were from different isolates.



Colour illustrations. Landscape invaded by *Microstegium vimineum*; leaf spots on *M. vimineum*; surface view of culture on PDA; conidiophore; conidia. Scale bars = 30 µm.

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Brunneiapiospora austropalmicola

Fungal Planet 130 – 20 December 2012

Brunneiapiospora austropalmicola A.E. Bell & Mahoney, *sp. nov*.

Etymology. *austropalmicola,* meaning *Southern palm* referring to the Nikau palm (*Rhopalostylis sapida*) upon which the fungus was found.

Ascomata perithecial, in small clusters developing on blackened stroma bursting through the plant tissue. Individual ascomata black, c. 1 mm diam, densely covered with brown, septate hairs mixed with host tissue, each with small papillate ostiole. Outer peridium black, brittle and structure less, inner peridium composed of areolate tissue. Copious centrum contents embedded in sticky material. *Paraphyses* hyaline, free-ended, longer than asci with densely granular contents c. 3–4 µm wide. *Asci* cylindrical, c. 250 × 7 µm, (tapering stipe constituting approx. a quarter of the length), ascus with prominent apical J+ ring, each ascus containing 8 uniseriate to overlapping ascospores. *Ascospores* 2-celled, septate in the lower part, upper cell pale brown, fusiform and symmetrical in one view, but flattened on one side sometimes strongly so, rather variable in size ranging from 19–30 × 3–5 µm (n = 50), lower hyaline cell 3–4 µm long.

Typus. New Zealand, on dead water-soaked fibrous *Rhopalostylis sapida*, Rimutaka Forest Park, 9 Nov. 2011, *Bell & Mahoney* Herb. no. 1172 (holotype PDD 102614), MycoBank MB800261.

Notes — During a recent foray into Rimutaka Forest Park near Wellington a new species of *Brunneiapiospora* was found on dead portions of *Rhopalostylis sapida* (Nikau palm). For a full description of the former placement of fungi with apiosporous ascospores the reader is referred to the paper by Hyde et al. (1998). In it the genus *Brunneiapiospora* was established to accommodate apiosporous species with cylindrical asci and whose ascospores consist of a larger brown cell and a smaller basal hyaline cell. It differs from the apiosporous genus *Anthostomella* which have broadly cylindrical asci and ascospores usually provided with a prominent longitudinal germ slit in the darker ascospore cell. Hyde et al. (1998) provide a key to the six known species of *Brunneiapiospora* all of which are pan-tropical in origin found on decaying material of palms in Ecuador, tropical Australia, Sierra Leone, Tanzania and Indonesia. They placed the genus (together with other genera), in a new family the *Apiosporaceae.* Kang et al. (1999) redefine the family *Clypeosphaeriaceae*, and indicate that the genus *Brunneiapiospora* might be placed therein, although their earlier molecular studies on the *Amphisphaeriales* (Kang et al. 1998) did not include any *Brunneiapiospora* samples. Our species ***B. austropalmicola*** differs in the ascospore dimensions from those previously described. They are approximately the length of *B*. *deightoniella* but much narrower (3–5 µm wide vs 7.5–10 µm for *B*. *deightoniella*). It is also the first described species of the genus from the cooler climates typical of the temperate rain forests of New Zealand.

The substrate upon which this species was found was quite unlike the woody substrate, which we normally collect on forays. It was quite friable and light in both colour and weight. At first we considered it could be from a tree fern trunk but this was proved not to be the case when we consulted those with a good knowledge of fern anatomy. Since all other species of *Brunneiapiospora* have been found on palms, we set about making several slides of the substrate together with portions of freshly collected *Rhopalostylis sapida*. By examination of these and conferring with the article by Tomlinson (2006), we are confident that the abraded material upon which *B*. *austropalmicola* was growing is a stem portion of the palm *Rhopalostylis sapida.* This palm is common in the Rimutaka Forest Park.

Colour illustrations. Forest of *Rhopalostylis sapida* in Nikau Reserve, Paraparaumu, New Zealand (www.wikimedia.org). Photo plate: A–A¹. Paraphyses, asci and ascospores; B. ascus and ascospores; C, D. ascospores; E. areolate peridial fragment; F. ascus apical ring complex in Melzer's reagent. All except F in Shear's mounting fluid. A–A¹ phase microscopy, others brightfield. Scale bars: A–A¹, B, E = 25 µm, C, D = 10 µm, F = 5 µm. Water colour: A. Perithecia on substrate; B. excised perithecium showing vestiture; C. aerolate inner perithecial tissue; D. paraphyses and asci; E. mature ascospores; F. scus apical rings showing J+ reaction in Melzer's reagent.

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Phyllosticta aristolochiicola

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Phyllosticta aristolochiicola R.G. Shivas, Y.P. Tan & Grice, *sp. nov.*

Etymology. Name derived from the host plant genus, *Aristolochia* (*Aristolochiaceae*).

Leaf spots amphigenous, circular, up to 1 cm diam, grey to pale brown, solitary, surrounded by a slightly raised black border about 1 mm wide; centres of lesions often tear or fall out producing symptoms of shot-hole. *Conidiomata* pycnidial, mostly epiphyllous, black, solitary, unilocular, globose, 40–70 µm diam, erumpent; wall composed of layers of *textura angularis*, outer layer dark reddish brown. *Conidiophores* reduced to conidiogenous cells or with a supporting branched cell. *Conidiogenous cells* terminal, hyaline, smooth, subcylindrical to ampulliform, 10–20 × 2–4 µm. *Conidia* globose, subglobose, broadly ellipsoidal or obovoid, with a truncate base and rounded apex, hyaline, 7–16 × 6.5–11 µm, aseptate; wall uniformly 0.5–1 µm thick, enclosed in a mucilaginous sheath, with a minute basal frill and an apical hyaline tapered appendage 3–7 µm long. *Teleomorph* not observed.

Culture characteristics — (after 1 wk in the dark and a further 2 wk under 12 h ultraviolet light / 12 h dark cycle, at 23 °C): Colonies on potato-dextrose agar 4 cm diam, flat with no aerial mycelium, olivaceous black (Rayner 1970) with a white-grey, 2 mm entire margin, narrowly zonate towards the margin.

Typus. Australia, Queensland, Kuranda, Kennedy Highway, on leaves of *Aristolochia acuminata*, 1 Apr. 2010, *K.R.E. Grice & P. Wright* (holotype BRIP 53316a; includes ex-type culture), ITS sequence GenBank JX486129, LSU sequence GenBank JX486128; Queensland, Emmagen Creek, Cape Tribulation National Park, 1 Aug. 1993, *R.G. Shivas*, paratype BRIP 21785, MycoBank MB801322.

Notes — Species of *Phyllosticta* have *Guignardia* sexual morphs, and are common endophytes or pathogens, occurring on a wide range of plant hosts (Glienke et al. 2011). Two species of *Phyllosticta*, *P. aristolochiae* on *A. clematitis* and *P. aristolochiae* (replacement name *P. tassiana*) on *A. sempervirens*, have been described from *Aristolochia*. Neither species was considered a *Phyllosticta* in a more recent revision of the genus (van der Aa & Vanev 2002). Furthermore, the latter name and its replacement name (*P. tassiana*) were both homonyms and thus both are illegitimate (van der Aa & Vanev 2002). *Phyllosticta aristolochiicola* was first collected in north Queensland in 1993 in association with leaf spot and shot-hole of *Aristolochia* (Shivas & Alcorn 1996). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hit using the ITS sequence is *Phyllosticta cordylinophili* (GenBank AB454357; Identities = 591/612 (97 %), Gaps = 5/612 (1 %)), followed by *Phyllostica ardisiicola* (GenBank AB454274; Identities = 584/614 (95 %), Gaps = 10/614 (2 %)), and *Guignardia vaccinii* (GenBank JQ936158; Identities = 583/614 (95 %), Gaps = 6/614 (1 %)). Using the LSU sequence, the closest hits are to *Phyllosticta abietis* (GenBank EU754193; Identities = 1311/1328 (99 %), Gaps 0/1328 (0 %)), followed by *Phyllosticta bidwellii* (GenBank DQ678085; Identities = 1299/1313 (99 %), Gaps = 0/1313 (0 %)), and *Phyllosticta minima* (GenBank EU754194; Identities = 1291/1303 (99 %), Gaps = 0/1303 (0 %)).

Colour illustrations. *Aristolochia acuminata* with leaf spots associated with *P. aristolochiicola* at Kuranda, northern Queensland; leaf spot with pycnidia; 3 wk old culture on potato-dextrose agar; conidiophores and conidia; conidia with appendages apparent. Scale bars (from top left to bottom right) = 1 mm, 1 cm, 10 µm, 10 µm.

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Calonectria pentaseptata

Fungal Planet 132 – 20 December 2012

Calonectria pentaseptata L. Lombard, M.J. Wingf., P.Q. Thu & Crous, *sp. nov*.

Etymology. Name refers to the 5-septate macroconidia produced by this fungus.

Sexual morph unknown. *Conidiophores* consisting of a stipe bearing a suit of penicillate fertile branches, a stipe extension, and terminal vesicle; stipe septate, hyaline, smooth 47–133 × 6–10 µm; stipe extension septate, straight to flexuous, 168–350 µm long, 3–6 µm wide at the apical septum, terminating in a narrowly clavate vesicle, 2–6 µm diam. *Conidiogenous apparatus* 70–99 µm long, 23–90 µm wide; primary branches 0–1-septate, 19–31 × 4–7 µm; secondary branches aseptate, 16–34 × 4–7 µm; tertiary branches aseptate, 14–22 × 4–6 µm, each terminal branch producing 1–3 phialides; phialides cylindrical to allantoid, obpyriform when carried singly, hyaline, aseptate, 15–24 × 4–6 µm; apex with minute periclinal thickening and inconspicuous collarette. *Macroconidia* cylindrical, rounded at both ends, straight, (75–)87–109(–115) × (5–)6–8(–10) µm (av. = 98 × 7 µm), 5(–8)-septate, lacking a visible abscission scar, held in parallel cylindrical clusters by colourless slime. *Megaconidia* and *microconidia* not seen.

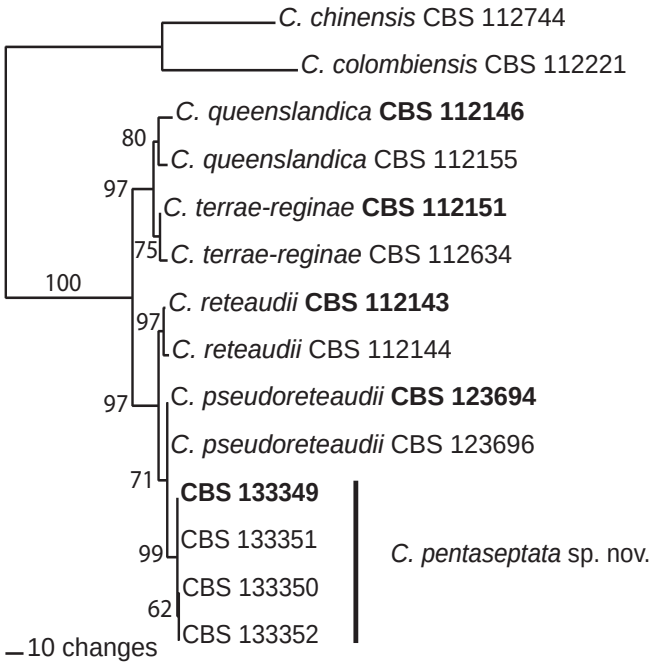
Culture characteristics — (in the dark, 24 °C after 1 wk): Colonies fast growing, with optimum growth at 24 °C on MEA; surface sienna to dark brick, reverse sepia-brown; abundant aerial mycelium and sporulation; chlamydospores extensive throughout the medium, forming microsclerotia.

Typus. Vietnam, Bavi, Hanoi, *Eucalyptus* hybrid, Sept. 2011, P.Q. Thu, holotype CBS H-21062, culture ex-type CBS 133349, β-tubulin (TUB) sequence GenBank JX855942, Histone H3 (HIS3) sequence GenBank JX855946, ITS sequence GenBank JX855950, LSU sequence GenBank JX855954 and translations elongation factor 1-alpha (TEF1-α) sequence GenBank JX855958, MycoBank MB801468.

Other specimens examined. Vietnam, Bavi, Hanoi, *Macadamia* sp., Sept. 2011, P.Q. Thu, CBS 133351, TUB sequence GenBank JX855944, HIS3 sequence GenBank JX855948, ITS sequence GenBank JX855952, LSU sequence GenBank JX855956 and TEF1-α sequence GenBank JX855960; ibid., *E. urophylla*, Sept. 2011, P.Q. Thu, CBS 133350, TUB sequence GenBank JX855943, HIS3 sequence GenBank JX855947, ITS sequence GenBank JX855951 and TEF1-α sequence GenBank JX855959; ibid., *Eucalyptus* hybrid, Sept. 2011, P.Q. Thu, CBS 133352, TUB sequence GenBank JX855945, HIS3 sequence GenBank JX855949, ITS sequence GenBank JX855953 and TEF1-α sequence GenBank JX855961.

Notes — *Calonectria pentaseptata* resides in the *C. reteaudii* species complex (Kang et al. 2001, Lombard et al. 2010a, b, c) based on morphological characteristics supported by phylogenetic inference. The macroconidia of *C. pentaseptata* (av. = 98 × 7 µm) are smaller than those of *C. pseudoreteaudii* (av. = 104 × 8 µm), and larger than those of *C. queenslandica* (av. = 69 × 6 µm), *C. reteaudii* (av. = 84 × 6.5 µm) and *C. terrae-reginae* (av. = 76 × 6 µm) (Lombard et al. 2010c). As with *C. queenslandica* and *C. terrae-reginae*, *C. pentaseptata* failed to produce microconidiophores and microconidia, distinguishing this fungus from *C. pseudoreteaudii* and *C. reteaudii*, which readily form these structures in culture (Lombard et al. 2010a, b, c).

One of two equally most parsimonious trees (TI = 380, CI = 0.942, RI = 0.921, RC = 0.868) obtained from a heuristic search with 1 000 random taxon additions of the combined sequences of TUB, HIS3 and TEF1-α sequence alignments of the *C. reteaudii* complex using PAUP v. 4.0b10. The bootstrap support values from 1 000 replicates are shown at the nodes. The tree was rooted to *C. chinensis* (CBS 112744) and *C. colombiensis* (CBS 112221). The ex-type strains are printed in **bold**.



Colour illustrations. *Eucalyptus* plantation in Vietnam; conidiophore; clavate vesicles; conidiogenous apparatus; conidia. Scale bars = 10 µm.

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Phaeococcomyces eucalypti

Fungal Planet 133 – 20 December 2012

Phaeococcomyces eucalypti Crous & R.G. Shivas, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Eucalyptus*.

Colonies lacking mycelium but consisting of a globular mass of chlamydospore-like cells; cells aseptate, brown (hyaline when young), 4–8 µm diam, verruculose, covered in mucus, globose, thick-walled, remaining attached to one another through younger end cells at colony margin, which detach during slide preparation; ellipsoid to globose, hyaline, thick-walled, covered in mucus, finely verruculose, 3–5 × 2.5–5 µm. Colonies dense, with cells remaining attached on malt extract agar (MEA), potato-dextrose agar (PDA) and synthetic nutrient-poor agar (SNA), but on oatmeal agar (OA) colonies form profuse amounts of mucous and appear looser with cells forming smaller clusters, and many conidia separate from one another; conidia also darker brown, and have a thicker wall and are more verruculose than on other media.

Culture characteristics — (in the dark, 25 °C after 3 wk): Colonies erumpent, spreading, surface folded, lacking aerial mycelium, and margins with lobate, irregular margins, reaching 25 mm diam. On MEA, PDA and OA, iron-grey, slimy.

Typus. Australia, Queensland, Anderson Park Botanic Garden, Townsville, S19°17'28.5" E146°47'13.5", on leaf litter of *Eucalyptus* sp., together with ascomata of *Thyriopsis sphaerospora,* 5 Aug. 2009, *P.W. Crous*, holotype CBS H-21091, cultures ex-type CPC 17606 = CBS 132526, ITS sequence GenBank KC005769, LSU sequence GenBank KC005791, MycoBank MB801769.

Notes — *Phaeococcomyces eucalypti* was isolated while trying to culture *Thyriopsis sphaerospora*, a foliar leaf pathogen of eucalypts that is known from South Africa, South America (Brazil, Chile) (Park et al. 2000) and Australia. Ascospores of *T. sphaerospora* germinate (on MEA and PDA), but die soon afterwards, which is probably due to its biotrophic growth habit. Colonies of *Phaeococcomyces eucalypti* started growing from an ascoma with a portion of host tissue that was plated onto malt extract agar. The logical inference that *P. eucalypti* represents the yeast phase of *T. sphaerospora*, is highly unlikely, as *T. sphaerospora* appears to be an obligate pathogen, with ascomata occurring on green, healthy leaf tissue. *Phaeococcomyces eucalypti* clusters among unidentified species of *Dothideomycetes* (rock fungi), and is allied to *P. nigricans*, although it has smaller conidia (de Hoog 1977).

Based on a megablast search of NCBIs GenBank nucleotide database, only more distant hits were obtained using the ITS sequence, e.g. with *Umbilicaria rigida* (GenBank AF096212; Identities = 457/533 (86 %), Gaps = 35/533 (7 %)), *Endoconidioma populi* (GenBank AY604526; Identities = 454/537 (85 %), Gaps = 33/537 (6 %)) and *Phaeococcomyces nigricans* (GenBank AY843154; Identities = 432/509 (85 %), Gaps = 18/509 (4 %)). Closest hits using the LSU sequence had highest similarity to '*Dothideomycetes* sp. TRN 452' (GenBank GU323985; Identities = 805/812 (99 %), Gaps = 0/812 (0 %)), '*Dothideomycetes* sp. TRN 456' (GenBank GU323986; Identities = 788/812 (97 %), Gaps = 0/812 (0 %)) and *Phaeococcomyces nigricans* (GenBank AF050278; Identities = 830/860 (97 %), Gaps = 2/860 (0 %)).

Colour illustrations. Giant *Eucalyptus* tree in Anderson Park Botanic Garden, Townsville; colonies on PDA; colony sporulating in culture, forming brown melanised cells, and small, ellipsoid, hyaline conidia. Scale bars = 10 µm.

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Penidiella drakensbergensis

Fungal Planet 134 – 20 December 2012

Penidiella drakensbergensis Crous, *sp. nov.*

Etymology. Named after the Drakensberg Mountains, where this fungus was collected.

Colonies on synthetic nutrient-poor agar. Mycelium consisting of smooth, pale brown, septate, branched, 3–4 µm diam hyphae. *Conidiophores* solitary, erect, subcylindrical, pale brown, smooth, straight or geniculate-sinuous, unbranched to branched, 3–5-septate, up to 70 µm tall, 4–6 µm wide at base. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, medium brown, proliferating sympodially, 8–15 × 4–5 µm; scars flattened, unthickened, aggregated, somewhat darkened, not refractive, 2–3 µm diam. *Primary ramoconidia* subcylindrical, brown, smooth, 0–1-septate, 10–15 × 4–5 µm. *Secondary ramoconidia* ellipsoid to obclavate or obovoid, with 1–3 apical hila, 9–13 × 3–4 µm. *Intermediate and terminal conidia* subcylindrical to ellipsoidal, brown, smooth, in branched chains, with up to six conidia, (6–)7–8(–10) × 2.5–3(–3.5) µm, aseptate; hila flattened, truncate, unthickened, somewhat darkened, 0.5–1 µm diam.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on malt extract agar, potato-dextrose agar and oatmeal agar spreading, erumpent, with smooth, lobate margin, and sparse aerial mycelium. Surface and reverse olivaceous-grey; reaching 7 mm diam.

Typus. South Africa, KwaZulu-Natal, Drakensberg Mountains, Giant's Castle, close to Bushman's Pass, on leaves of *Protea* sp. (*Proteaceae*), 18 July 2011, *P.W. Crous*, holotype CBS H-21076, cultures ex-type CPC 19778 = CBS 133575, ITS sequence GenBank KC005770, LSU sequence GenBank KC005792, MycoBank MB801770.

Notes — A blast search of NCBIs GenBank nucleotide database using the LSU sequence placed this species in *Teratosphaeriaceae* with closest hits being *Penidiella aggregata* (GenBank JF499862; Identities = 849/858 (99 %), Gaps = 0/858(0 %)),*Readeriellabrunneotingens*(GenBankEU019286; Identities = 839/860 (98 %), Gaps = 2/860 (0 %)) and *Teratosphaeria profusa* (GenBank FJ493220; Identities = 838/860 (97 %), Gaps = 2/860 (0 %)). Closest hits using the ITS sequence had highest similarity to *Penidiella aggregata* (GenBank JF499862; Identities = 502/551 (91 %), Gaps = 18/551 (3 %)), *Catenulostroma hermanusense* (GenBank JF499833; Identities = 496/560 (89 %), Gaps = 24/560 (4 %)) and *Teratosphaeria jonkershoekensis* (GenBank EU707864; Identities = 486/547 (89 %), Gaps = 20/547 (4 %)). Although phylogenetically allied to *P. aggregata* (conidia (5–)6–8 × (2–)2.5(–3) µm), *P. drakensbergensis* has larger intermediate and terminal conidia (Crous & Groenewald 2011).

Colour illustrations. *Protea* sp. growing at Giant's Castle, Drakensberg Mountains; colony sporulating on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Ceramothyrium melastoma

Fungal Planet 135 – 20 December 2012

Ceramothyrium melastoma Crous & M.J. Wingf., *sp. nov*.

Etymology. Named reflects the host genus, *Melastoma*.

Description of colonies sporulating on synthetic nutrient-poor agar (SNA). *Mycelium* consisting of pale brown, septate, branched, finely verruculose, 2–3 µm diam hyphae. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral on hyphae, phialidic with small collarette (flaring or not), 2 µm wide, 1–1.5 µm high. *Conidia* pale brown to subhyaline, subcylindrical to obclavate, apex subobtuse, base tapering, truncate, 1–12-septate, but commonly forming lateral branches as in *Stanhughesia* morphs of *Ceratothyrium* (especially on potato-dextrose agar (PDA) and malt extract agar (MEA), but less so on SNA), conidial body (25–)40–60(–90) × (2.5–)3 µm, lateral branches 7–25 × 2.5–3 µm. *Triposporium* morph on PDA and MEA: *central conidial body* 15–30 µm long, 3–4 µm wide at clavate apex, giving rise to two apical, lateral branches that angle upwards, of unequal length, lateral arms 15–35 × 2.5–3 µm; constricted at septa where lateral arms join the conidial body.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on MEA, PDA and oatmeal agar erumpent, spreading, with smooth, even margin and sparse aerial mycelium. Surface pale olivaceous-grey, reverse olivaceous-grey, reaching 5 mm diam.

Typus. Indonesia, North Sumatra, Lake Toba, on leaves of *Melastoma* sp. (*Melastomataceae*), 20 Aug. 2011, *M.J. Wingfield*, holotype CBS H-21077, culture ex-type CPC 19837 = CBS 133576, ITS sequence GenBank KC005771, LSU sequence GenBank KC005793, MycoBank MB801771.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phaeococcomyces catenatus* (GenBank AF050277; Identities = 847/875 (97 %), Gaps = 0/875 (0 %)), *Exophiala placitae* (GenBank EU040215; Identities = 841/871 (97 %), Gaps = 0/871 (0 %)), and *Sarcinomyces petricola* (GenBank FJ358249; Identities = 835/865 (97 %), Gaps = 0/865 (0 %)). Closest hits using the ITS sequence had highest similarity to *Trichomerium deniqulatum* (GenBank JX313654; Identities = 559/664 (84 %), Gaps = 38/664 (6 %)), *Phaeococcomyces chersonesos* (GenBank AJ507323; Identities = 534/641 (83 %), Gaps = 43/641 (7 %)), and *Trichomerium gleosporum* (GenBank JX313656; Identities = 417/480 (87 %), Gaps = 18/480 (4 %)). *Ceramothyrium melastoma* clusters in a basal lineage to the *Chaetothyriales*, and renders *Ceramothyrium* paraphyletic. For a discussion on *Ceramothyrium*, see Fungal Planet 137.

Colour illustrations. Flower and leaves of *Melastoma* sp.; colonies growing on synthetic nutrient-poor agar; conidiogenous cells giving rise to conidia, which become star-shaped with age. Scale bars = 10 µm.

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Strelitziana cliviae

Fungal Planet 136 – 20 December 2012

Strelitziana cliviae Crous, *sp. nov*.

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

Description of colonies sporulating on synthetic nutrient-poor agar. *Mycelium* consisting of pale brown, septate, branched, smooth, 3–4 µm diam hyphae, frequently constricted at septa, forming sterile, brown, globose, sclerotium-like bodies, 20–40 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral or terminal on hyphae, phialidic with small collarette (flaring or not), solitary or aggregated (–3), 2–3 µm high, 2 µm wide. *Conidia* pale brown, smooth, obclavate, apex subobtuse, base obconically truncate, 3–7-septate, (35–)42–55(–70) × (3–)3.5(–4) µm, apex and base frequently with mucoid caps, and conidia forming lateral branches in older cultures (onset of microcyclic conidiation).

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar, malt extract agar and oatmeal agar erumpent, spreading, with lobate margins and moderate aerial mycelium; surface folded, pale olivaceous-grey; reverse iron-grey, reaching 15 mm diam.

Typus. South Africa, Mpumalanga, Nelspruit, Lowveld Botanical Garden, on leaves of *Clivia miniata* (*Amaryllidaceae*), 16 July 2011, *P.W. Crous*, holotype CBS H-21078, culture ex-type CPC 19822 = CBS 133577, ITS sequence GenBank KC005772, LSU sequence GenBank KC005794, MycoBank MB801772.

Notes — Four species are presently known from the genus *Strelitziana* (Table 1), which is characterised by having polyphialides, rhexolytic conidiation, pigmented structures, and unthickened conidial scars (Arzanlou & Crous 2006). Although *S. africana* lacks mucoid conidial appendages, these have since been observed in *S. eucalypti*, *S. australiensis*, and now also in *S. cliviae* (Cheewangkoon et al. 2009). Conidia of *S. eucalypti* (40–130 × 3–4 µm; Crous et al. 2010b) are larger than those of *S. cliviae*, while those of *S. australiensis* are again narrower (30–73 × 2.8–3.2 µm; Cheewangkoon et al. 2009). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Strelitziana australiensis* (GenBank GQ303326; Identities = 870/903 (96 %), Gaps = 0/903 (0 %)), *Capronia peltigerae* (GenBank HQ613813; Identities = 870/904 (96 %), Gaps = 2/904 (0 %)), and *Glyphium elatum* (GenBank AF346420; Identities = 870/905 (96 %), Gaps = 2/905 (0 %)). Closest hits using the ITS sequence had highest similarity to *Strelitziana albiziae* (GenBank HQ599584; Identities = 546/646 (85 %), Gaps = 33/646 (5 %)), *Strelitziana africana* (GenBank DQ885895; Identities = 550/653 (84 %), Gaps = 42/653 (6 %)) and *Strelitziana eucalypti* (GenBank HQ599596; Identities = 548/653 (84 %), Gaps = 45/653 (7 %)).

Table 1 Comparison of hosts, distribution and micromorphology of currently described *Strelitziana* species.

Species	Host	Origin	Morphology		Reference
			Conidial dimensions (µm)	Conidial septation	
S. africana	*Strelitzia*	South Africa	(18–)50–70(–95) × 3(–3.5)	3–5(–10)	Arzanlou & Crous 2006
S. australiensis	*Eucalyptus*	Australia	(30–)50–60(–73) × 2.8–3.2	4–8	Cheewangkoon et al. 2009
S. cliviae	*Clivia*	South Africa	(35–)42–55(–70) × (3–)3.5(–4)	3–7	Present study
S. eucalypti	*Rumex*	Iran	(40–)60–80(–130) × (3–)3.5(–4)	6–10	Crous et al. (2010b)
S. mali	*Malus*	China	(12–)35–60(–100) × 7(–35)	(2–)5–10	Zhang et al. (2009)

Colour illustrations. *Clivia miniata* growing in the Lowveld Botanical Garden; colony on synthetic nutrient-poor agar; microsclerotia or sterile fruiting bodies; conidiogenous cells giving rise to conidia that can undergo microcyclic conidiation. Scale bar = 10 µm.

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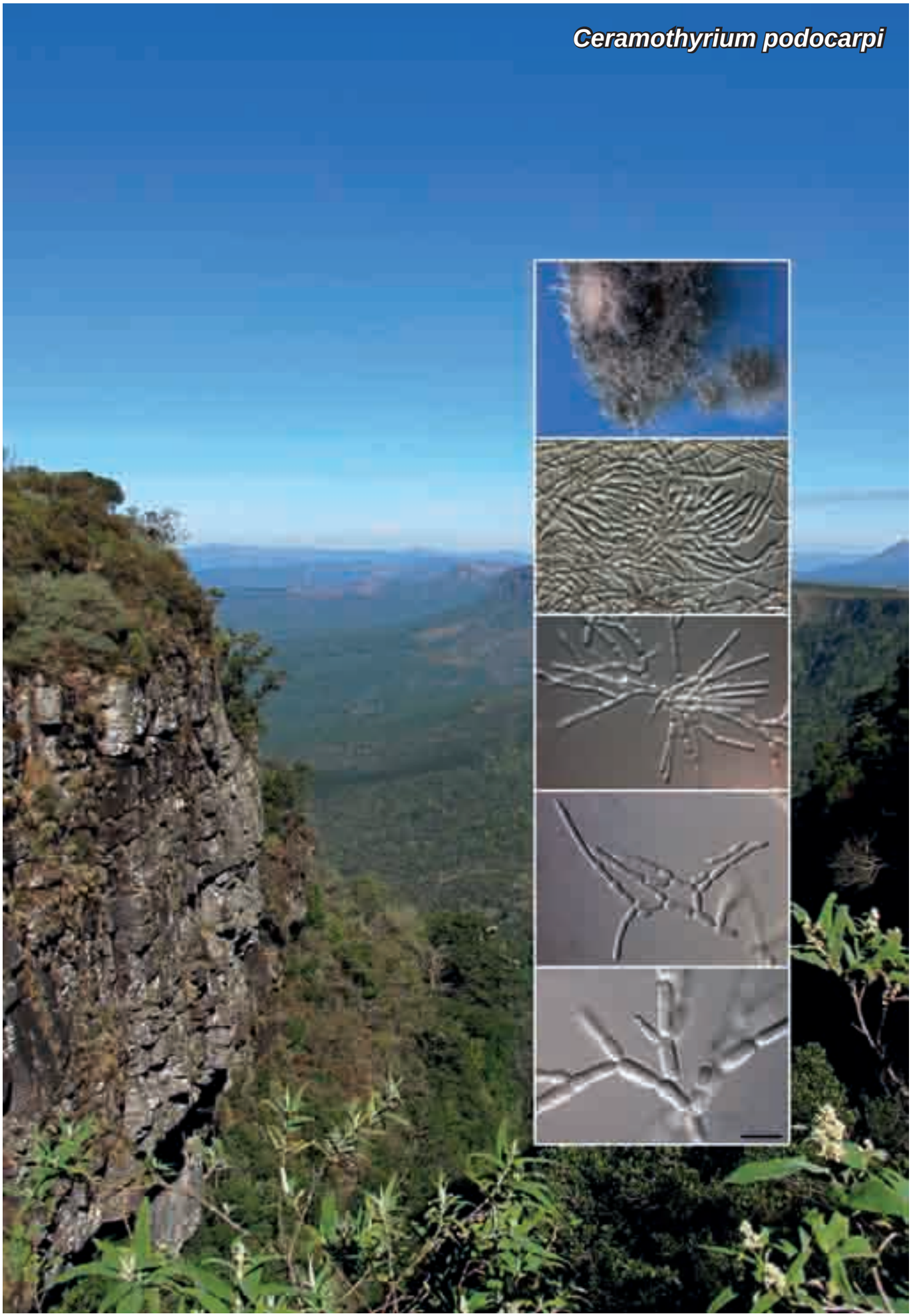
Ceramothyrium podocarpi

Fungal Planet 137 – 20 December 2012

Ceramothyrium podocarpi Crous, *sp. nov*.

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

Description of colonies sporulating on synthetic nutrient-poor agar. *Mycelium* consisting of pale brown, septate, branched, smooth, 3–4 µm diam hyphae, frequently constricted at septa. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral on hyphae, 20–30 × 3–5 µm, phialidic with small collarette, solitary, 1 µm high, 1–2 µm wide, rather inconspicuous. *Conidia* highly variable regarding morphology, hyaline to subhyaline, smooth, obclavate, but quickly constricting at septa, and developing lateral branches, which again branch further, forming a star-shaped conidium with numerous branches; conidial cells 4–6 µm wide, arms 25–90 µm long, 1–9-septate, apices obtuse, base truncate, with hilum 1.5–2 µm diam, at times with marginal frill.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar, malt extract agar and oatmeal agar erumpent, spreading, with uneven, feathery margins and sparse aerial mycelium. Surface folded, pale olivaceous-grey; reverse olivaceous-grey, reaching 10 mm diam.

Typus. South Africa, Mpumalanga, Drakensberg escarpment, God's Window, on leaves of *Podocarpus falcatus* (*Podocarpaceae*), 14 July 2011, *P.W. Crous*, holotype CBS H-21079, culture ex-type CPC 19826 = CBS 133578, ITS sequence GenBank KC005773, LSU sequence GenBank KC005795, MycoBank MB801773.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Ceramothyrium thailandicum* (GenBank HQ895835; Identities = 817/843 (97 %), Gaps = 2/843 (0 %)), *Ceramothyrium carniolicum* (GenBank FJ358232; Identities = 811/845 (96 %), Gaps = 3/845 (0 %)) and *Cyphellophora hylomeconis* (GenBank EU035415; Identities = 809/844 (96 %), Gaps = 2/844 (0 %)). Closest hits using the ITS sequence had highest similarity to *Cyphellophora hylomeconis* (GenBank EU035415; Identities = 510/593 (86 %), Gaps = 39/593 (7 %)), *Exophiala eucalyptorum* (GenBank EU035417; Identities = 500/587 (85 %), Gaps = 25/587 (4 %)), and *Cyphellophora eugeniae* (GenBank FJ839617; Identities = 514/606 (85 %), Gaps = 36/606 (6 %)).

The genus *Ceramothyrium* has *Stanhughesia* asexual morphs (Constantinescu et al. 1989) and represents a genus of epiphyllous ascomycetes in the *Chaetothyriales* for which DNA data has been lacking until the recent study of Chomnunti et al. (2012). Although only the asexual morph of *Ceramothyrium podocarpi* was observed in the present study, we choose to name it in the older sexual genus, *Ceramothyrium* (1955; with 34 taxa), accepting *Stanhughesia* (1989; with only four taxa, three having existing names in *Ceramothyrium*) as later synonym.

Colour illustrations. View from God's Window, Mpumalanga; colony growing on synthetic nutrient-poor agar; conidiophores giving rise to star-shaped conidia. Scale bars = 10 µm.

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Phialophora livistonae

Fungal Planet 138 – 20 December 2012

Phialophora livistonae Crous & Summerell, *sp. nov.*

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

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of spreading, septate, branched hyphae, smooth, pale brown, 2–3 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* intercalary and integrated on hyphae, pale brown, subcylindrical to narrowly ellipsoid, at times erect on hyphae, ampulliform to doliiform, monophialidic, 4–10 × 3–4 µm; collarette flaring, 1–2 × 1–1.5 µm. *Conidia* solitary, hyaline to pale brown, smooth, clavate to fusoid-ellipsoid, apex obtuse, tapering to a truncate base, 0.5–1 µm diam, (4–)7–8(–10) × (2–)3(–3.5) µm; at times becoming 1-septate with age. *Chlamydospores* intercalary, pale brown to brown, smooth, globose to narrowly ellipsoid, 0–1-septate, 8–10 × 3–5 µm.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar, malt extract agar and oatmeal agar erumpent, spreading, with even, smooth margin and sparse aerial mycelium; surface olivaceous-grey to iron-grey; reverse iron-grey; reaching 8 mm diam.

Typus. Australia, Northern Territory, Litchfield National Park, S13°01.226' E130°56.349', on leaves of *Livistona humilis* (*Arecaceae*), 25 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-21080, cultures ex-type CPC 19433 = CBS 133589, ITS sequence GenBank KC005774, LSU sequence GenBank KC005796, MycoBank MB801774.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Phialophora sessilis* (GenBank FJ147173; Identities = 728/733 (99 %), Gaps = 1/733 (0 %)), *Cyphellophora eucalypti* (GenBank GQ303305; Identities = 859/882 (97 %), Gaps = 4/882 (0 %)) and *Cyphellophora fusarioides* (GenBank JQ766486; Identities = 745/766 (97 %), Gaps = 4/766 (1 %)). Closest hits using the ITS sequence had highest similarity to *Phialophora sessilis* (GenBank AB190381; Identities = 570/630 (90 %), Gaps = 27/630 (4 %)), *Cyphellophora eucalypti* (GenBank GQ303274; Identities = 536/622 (86 %), Gaps = 33/622 (5 %)) and *Phialophora olivacea* (GenBank AB190379; Identities = 544/633(86 %),Gaps = 41/633(6 %)). Although phylogenetically allied to *P. sessilis* (conidia 3 × 1.8 µm; de Hoog et al. 1999), conidia of *P. livistonae* are larger and easily distinguishable.

Colour illustrations. *Livistona humilis* growing in Litchfield National Park, Northern Territory; colony on synthetic nutrient-poor agar; hyphae, conidiogenous cells and conidia. Scale bars = 10 µm.

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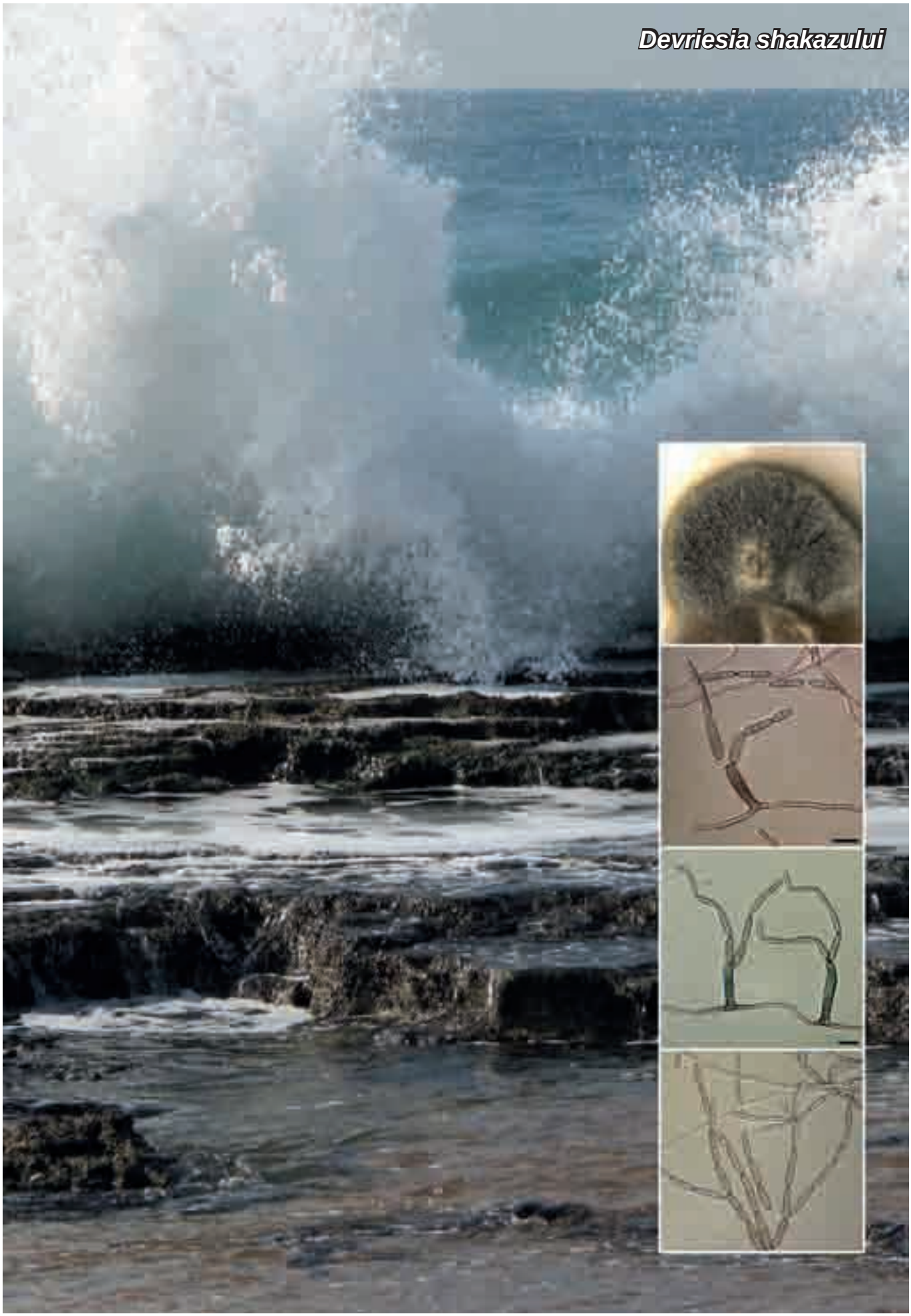
Devriesia shakazului

Fungal Planet 139 – 20 December 2012

Devriesia shakazului Crous, *sp. nov.*

Etymology. Named after Shaka kaSenzangakhona (also known as Shaka Zulu), a former king of the Zulu Nation, who used to send his handmaidens to collect dried salt off the rocks (Salt Rock) at low tide.

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of smooth, pale brown, septate, branched, 1.5–2 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth, straight or flexuous, branched or not, reduced to conidiogenous cells or up to 2-septate, 5–25 × 3–4 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 5–15 × 2.5–4 µm; scars flattened, thickened, somewhat darkened, 0.5–1.5 µm diam. *Ramoconidia* 0(–1)-septate, guttulate, subcylindrical, smooth, pale brown, 10–15 × 2–3 µm; hila somewhat thickened and darkened, 1–1.5 µm diam, giving rise to conidia in long branched or unbranched chains (–15). *Intercalary conidia* subcylindrical to somewhat fusoid-ellipsoidal, pale brown, smooth, guttulate, 1-septate, 10–15 × 2–2.5 µm. *Terminal conidia* subcylindrical to fusoid-ellipsoidal, apex obtuse, pale brown, smooth, guttulate, (6–)8–9(–11) × 2(–2.5) µm, (0–)1-septate; hila flattened, truncate, somewhat thickened and darkened, 0.5–1 µm diam. *Chlamydospores* not observed.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies on potato-dextrose agar (PDA), malt extract agar (MEA) and oatmeal agar (OA) erumpent, spreading, with smooth, even margin and moderate aerial mycelium. Surface grey-olivaceous (OA and PDA) to hazel (MEA), reverse iron-grey, reaching 16 mm diam.

Typus. South Africa, KwaZulu-Natal, Durban, Salt Rock, on leaves of *Aloe* sp. (*Xanthorrhoeaceae*), 24 July 2011, *P.W. Crous*, holotype CBS H-21081, cultures ex-type CPC 19784, CPC 19782 = CBS 133579, ITS sequence GenBank KC005775–KC005776, LSU sequence GenBank KC005797, MycoBank MB801775.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Devriesia queenslandica* (GenBank JF951168; Identities = 880/887 (99 %), Gaps = 0/887 (0 %)), *Devriesia hilliana* (GenBank GU214414; Identities = 875/885 (99 %), Gaps = 0/885 (0 %)) and *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 867/879 (99 %), Gaps = 0/879 (0 %)). Closest hits using the ITS sequence had highest similarity to *Devriesia queenslandica* (GenBank JF951148; Identities = 554/575 (96 %), Gaps = 8/575 (1 %)), *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 526/577 (91 %), Gaps = 24/577 (4 %)) and *Devriesia hilliana* (GenBank GU214633; Identities = 530/587 (90 %), Gaps = 27/587 (5 %)). Although phylogenetically closely related to *D. queenslandica* (conidiophores 5–45 × 3–4 µm, ramoconidia 10–20 × 2–3 µm, terminal conidia (5–)7–9(–11) × 2–2.5 µm; Crous et al. 2011), structures of *D. shakazului* are slightly shorter.

Colour illustrations. Salt Rock, KwaZulu-Natal; colony sporulating on oatmeal agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Zasmidium syzygii

Fungal Planet 140 – 20 December 2012

Zasmidium syzygii Crous, *sp. nov.*

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

Occurring as secondary invader on leaf spots of *Pseudocercospora punctata*, sporulating sparsely between prominent, dense fascicles (sporodochia) of *P. punctata*. Description based on colonies on synthetic nutrient-poor agar (SNA). *Mycelium* consisting of septate, branched, verruculose, brown, 2–3 µm diam hyphae. *Conidiophores* solitary on superficial mycelium, erect, unbranched, straight to somewhat flexuous, subcylindrical, brown, finely verruculose, 1–5-septate, 30–70 × 2–3 µm. *Conidiogenous cells* integrated, terminal, subcylindrical, finely verruculose, brown, 10–20 × 2–3 µm, with apical taper towards rounded or flattened apex, with one to several conidiogenous loci; scars thickened, darkened, somewhat refractive, 0.5 µm diam. *Conidia* brown, verruculose, narrowly obclavate or subcylindrical, apex obtusely rounded, base long obconically truncate, hilum thickened, darkened, somewhat refractive, 1 µm diam, 1–2(–5)-septate, (10–)22–25(–50) × (2–)3(–3.5) µm; conidia occurring in branched chains.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies spreading, flat with even, lobate margin and moderate aerial mycelium. On malt extract agar olivaceous-grey (surface), iron-grey (reverse). On oatmeal agar iron-grey in centre, surrounded by broad orange outer zone. On potato-dextrose agar olivaceous-grey and iron-grey in reverse. On SNA sienna, reaching 25 mm diam.

Typus. South Africa, Mpumalanga, Nelspruit, Lowveld Botanical Garden, on leaves of *Syzygium cordatum* (*Myrtaceae*), 16 July 2011, *P.W. Crous*, *M.K. Crous, M. Crous & K.L. Crous*, holotype CBS H-21082, cultures ex-type CPC 19792 = CBS 133580, ITS sequence GenBank KC005777, LSU sequence GenBank KC005798, MycoBank MB801776.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Zasmidium angulare* (GenBank JQ622096; Identities = 785/798 (98 %), Gaps = 1/798 (0 %)), *Mycosphaerella aleuritidis* (GenBank EU167594; Identities = 825/839 (98 %), Gaps = 0/839 (0 %)) and *Ramichloridium cerophilum* (GenBank GU214485; Identities = 873/888 (98 %), Gaps = 0/888 (0 %)). Closest hits using the ITS sequence had highest similarity to '*Ramichloridium* sp. CATASR1' (GenBank JQ768795; Identities = 531/535 (99 %), Gaps = 1/535 (0 %)), *Zasmidium nocoxi* (GenBank GQ852842; Identities = 518/544 (95 %), Gaps = 9/544 (2 %)) and *Mycosphaerella aleuritidis* (GenBank EU167594; Identities = 515/543 (95 %), Gaps = 8/543 (1 %)). Morphologically *Z. syzygii* is distinguishable from other species of *Zasmidium* occurring on *Syzygium* based on its smaller conidia (Crous 1999).

Colour illustrations. Lowveld Botanical Garden, Nelspruit; verruculose hyphae giving rise to conidiophores and conidia in chains. Scale bars = 10 µm.

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Devriesia stirlingiae

Fungal Planet 141 – 20 December 2012

Devriesia stirlingiae Crous, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Stirlingia*.

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth, straight or flexuous, branched or not, reduced to conidiogenous cells or 1–8-septate, 10–50 × 4–5 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 8–15 × 3–4 µm; scars flattened, thickened, somewhat darkened, 1–2 µm diam. *Ramoconidia* 1–3-septate, granular to guttulate, subcylindrical, smooth, pale brown, 15–30 × 4–5 µm, frequently with lateral branch at apex, up to 10 µm long, hila somewhat thickened and darkened, 1.5–2(–3) µm diam. *Conidia* subcylindrical to fusoid-ellipsoidal, apex obtuse, pale brown, smooth, guttulate, (7–)12–16(–20) × (3–)4(–5) µm, 0–3-septate; hila flattened, truncate, somewhat thickened and darkened, 1–2 µm diam. *Chlamydospores* thick-walled, brown, globose, in intercalary chains, up to 10 µm diam.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent with even, smooth margins and sparse aerial mycelium. On potato-dextrose agar, malt extract agar and oatmeal agar surface olivaceous-grey, reverse iron-grey, reaching 7 mm diam.

Typus. Western Australia, Perth, Wandoo National Park, on leaves of *Stirlingia latifolia* (*Proteaceae*), 13 July 2011, *W. Gams*, holotype CBS H-21083, cultures ex-type CPC 19948 = CBS 133581, ITS sequence GenBank KC005778, LSU sequence GenBank KC005799, MycoBank MB801777.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Devriesia hilliana* (GenBank GU214414; Identities = 843/856 (98 %), Gaps = 2/856 (0 %)), *Devriesia xanthorrhoeae* (GenBank HQ599606; Identities = 841/856 (98 %), Gaps = 2/856 (0 %)), and *Teratosphaeria knoxdaviesii* (GenBank EU707865; Identities = 839/853 (98 %), Gaps = 0/853 (0 %)). Closest hits using the ITS sequence had highest similarity to *Devriesia fraseriae* (GenBank HQ599602; Identities = 491/501 (98 %), Gaps = 2/501 (0 %)), *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 478/508 (94 %), Gaps = 13/508 (3 %)), and *Teratosphaeria knoxdaviesii* (GenBank EU707866; Identities = 473/507 (93 %), Gaps = 11/507 (2 %)). Although phylogenetically closely related to *D. fraseriae* (intercalary and terminal conidia (6–)8–10(–11) × 3(–4) µm; Crous et al. 2010a), *D. stirlingiae* is easily distinguishable by having larger conidia.

Colour illustrations. Flowers of *Stirlingia latifolia*; colony sporulating on potato-dextrose agar; conidiophores, conidiogenous cells and conidia. Scale bar = 10 µm.

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Cercospora chrysanthemoides

Fungal Planet 142 – 20 December 2012

Cercospora chrysanthemoides Crous & W.J. Swart, *sp. nov.*

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

Description based on host material, incubated in moist chambers. *Leaf spots* amphigenous, subcircular, 2–10 mm diam, with concentric darker circles, margin dark brown, raised. Sporulation amphigenous, but more prominently hypophyllous. *Mycelium* internal, consisting of branched, septate, smooth, pale brown, 2–3 µm diam hyphae. *Stromata* substomatal, globose, consisting of brown, pseudoparenchymatal cells, becoming erumpent, up to 60 µm diam, giving rise to conidiophores. *Conidiophores* fasciculate, containing numerous conidiophores in dense clusters, subcylindrical, straight, rarely once-geniculate, brown, finely verruculose, 1–3-septate, 30–70 × 6–7 µm. *Conidiogenous cells* terminal, integrated, 25–55 × 5–7 µm, brown, finely verruculose, subcylindrical; loci terminal, single, rarely with lateral locus, scars flattened, darkened, thickened, 3–4 µm diam. *Conidia* solitary, hyaline, obclavate to subcylindrical, straight to slightly curved, apex subobtuse, widest at or below basal septum, (38–)42–55 (–70) × (4–)5(–6) µm, 3–5-septate; hila thickened, darkened and refractive, 3–4 µm diam.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies spreading, with moderate aerial mycelium and even, lobate margin. On potato-dextrose agar surface dirty white, surrounded by broad red-purple zone of diffuse pigment in agar, dark red in reverse. On oatmeal agar centre dirty white, outer region olivaceous-grey. On malt extract agar surface dirty white with patches of olivaceous-grey, reverse iron-grey, reaching 30 mm diam.

Typus. South Africa, Free State Province, Bloemfontein, Free State National Botanical Garden, on leaves of *Chrysanthemoides monilifera* (*Asteraceae*), 7 May 2012, *P.W. Crous & W.J. Swart*, holotype CBS H-21084, cultures ex-type CPC 20605, CPC 20529 = CBS 133582, ITS sequences GenBank KC005779–KC005780, ACT sequences GenBank KC005764–KC005765, TEF sequences GenBank KC005813–KC005814, CAL sequences GenBank KC005767–KC005768, LSU sequences GenBank KC005800–KC005801, MycoBank MB801778.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cercospora* cf. *apii* (GenBank JN941176; Identities = 900/902 (99 %), Gaps = 1/902 (0 %)), *Cercospora acaciaemangii* (GenBank JN941175; Identities = 900/902 (99 %), Gaps = 1/902 (0 %)) and *Cercospora* sp. (GenBank JN941174; Identities = 900/902 (99 %), Gaps = 1/902 (0 %)). Closest hits using the ITS sequence had highest similarity to *Cercospora zebrina* (GenBank JX390615; Identities = 529/530 (99 %), Gaps = 0/530 (0 %)), *Cercospora piaropi* (GenBank HQ902254; Identities = 529/530 (99 %), Gaps = 0/530 (0 %)) and *Cercospora capsici* (GenBank GU214654; Identities = 529/530 (99 %), Gaps = 0/530 (0 %)). Closest hits using the ACT sequence had highest similarity to *Cercospora althaeina* (GenBank JX143036; Identities = 192/194 (99 %), Gaps = 0/194 (0 %)), *Cercospora zebrina* (GenBank JX143260; Identities = 211/214 (99 %), Gaps = 0/214 (0 %)) and *Cercospora armoraciae* (GenBank JX143058; Identities = 190/194 (98 %), Gaps = 0/194 (0 %)). Closest hits using the TEF sequence had highest similarity to *Cercospora delaireae* (GenBank JX143346; Identities = 288/292 (99 %), Gaps = 0/292 (0 %)), *Cercospora ricinella* (GenBank JX143406; Identities = 287/291 (99 %), Gaps = 0/291 (0 %)) and *Cercospora* cf. *zinniae* CPC 15075 (GenBank JX143519; Identities = 287/292 (98 %), Gaps = 0/292 (0 %)). Closest hits using the CAL sequence had highest similarity to *Cercospora* cf. *chenopodii* (GenBank JX142839; Identities = 388/398 (97 %), Gaps = 0/398 (0 %)), *Cercospora ricinella* (GenBank JX142913; Identities = 287/297 (97 %), Gaps = 0/297 (0 %)) and *Cercospora* cf. *coreopsidis* (GenBank JX142851; Identities = 285/296 (96 %), Gaps = 0/296 (0 %)) (see Groenewald et al. (In press) for morphological details pertaining to the species cited above).

Colour illustrations. *Chrysanthemoides monilifera* in the Free State National Botanical Garden; leaf spots; lesion; conidiophores and conidia. Scale bars = 10 µm.

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Zymoseptoria verkleyi

Fungal Planet 143 – 20 December 2012

Zymoseptoria verkleyi Crous, Videira & Quaedvlieg, *sp. nov.*

Etymology. Named after Gerard J.M. Verkley, for the contribution that he has made to further our understanding of the genus *Septoria*.

On sterile barley leaves on water agar: *Conidiomata* pycnidial, substomatal, immersed to erumpent, globose, dark brown, up to 200 µm diam, with central ostiole, 10–15 µm diam; wall of 3–4 layers of brown *textura angularis*. *Conidiophores* reduced to conidiogenous cells, or with one supporting cell, lining the inner cavity. *Conidiogenous cells* hyaline, smooth (in older cultures on malt extract agar becoming brownish, verruculose), tightly aggregated, subcylindrical to ampulliform, straight to curved, 7–15 × 3–4.5 µm, with inconspicuous, percurrent proliferations at apex, but also proliferating sympodially. Conidia of all three types present. *Type I conidia* (pycnidial conidia) solitary, hyaline, smooth, granular, acicular to narrowly obclavate, tapering towards subacutely rounded apex, with truncate or obconically truncate base, straight to flexuous, 1–6(–12)-septate, (30–)40–65(–80) × (2–)2.5(–3) µm; hila not thickened nor darkened, 1–2 µm. On synthetic nutrient-poor agar, yeast-like growth and microcyclic conidiation (*Type III conidia*) present, as well as aerial hyphae and older conidia disarticulating into phragmoconidia (*Type II conidia*).

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent, with even to feathery margins and sparse aerial mycelium. On potato-dextrose agar and malt extract agar surface pale olivaceous-grey to olivaceous-grey; reverse iron-grey, colonies reaching 12 mm diam.

Typus. Netherlands, Utrecht, Houten, on leaves of *Poa annua* (*Poaceae*), 2012, *S. Videira*, holotype CBS H-21085, cultures ex-type S657 = CBS 133618, ITS sequence GenBank KC005781 and LSU sequence GenBank KC005802, MycoBank MB801779.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Zymoseptoria brevis* (GenBank JQ739832; Identities = 862/865 (99 %), Gaps = 2/865 (0 %)), *Zymoseptoria tritici* (GenBank GU214436; Identities = 862/865 (99 %), Gaps = 2/865 (0 %)) and *Zymoseptoria passerinii* (GenBank JQ739843; Identities = 855/863 (99 %), Gaps = 0/863 (0 %)). Closest hits using the ITS sequence had highest similarity to *Zymoseptoria passerinii* (GenBank AF181699; Identities = 494/508 (97 %), Gaps = 5/508 (1 %)), *Zymoseptoria tritici* (GenBank FN428877; Identities = 473/479 (99 %), Gaps = 3/479 (1 %)) and *Zymoseptoria halophila* (GenBank JF700876; Identities = 461/475 (97 %), Gaps = 5/475 (1 %)). Although phylogenetically closely related to *Z. passerinii* (conidia 1–3-septate, 21–52 × 1.5–2.2 µm; Quaedvlieg et al. 2011, Stukenbrock et al. 2012), conidia of *Z. verkleyi* are much larger.

Table 1 Comparison of hosts, distribution and micromorphology of currently described *Zymoseptoria* species.

Species	Host	Origin	Morphology		Reference
			Conidial dimensions (µm)	Conidial septation	
Z. ardabiliae	*Lolium*	Iran	(15–)20–25(–30) × 2(–3)	(0–)1	Stukenbrock et al. (2012)
Z. brevis	*Phalaris*	Iran	(12–)13–16(–17) × 2(–2.5)	0–1	Quaedvlieg et al. (2011)
Z. halophila	*Hordeum*	Iran	(30–)33–38(–50) × 2(–3)	1(–3)	Quaedvlieg et al. (2011)
Z. passerinii	*Hordeum*	Italy	21–52 × 1.5–2.2	1–3	Quaedvlieg et al. (2011)
Z. pseudotritici	*Dactylis*	Iran	(7–)10–12(–22) × 2.5(–3)	0(–1)	Stukenbrock et al. (2012)
Z. tritici	*Triticum*	France	28–85 × 1.5–2	(0–)3	Quaedvlieg et al. (2011)
Z. verkleyi	*Poa*	Netherlands	(30–)40–65(–80) × (2–)2.5(–3)	1–6(–12)	Present study

Colour illustrations. *Poa annua* growing next to the roadside in Houten; colony sporulating on synthetic-nutrient poor agar; conidiogenous cells and conidia with microcyclic conidiation and phragmoconidia. Scale bars = 10 µm.

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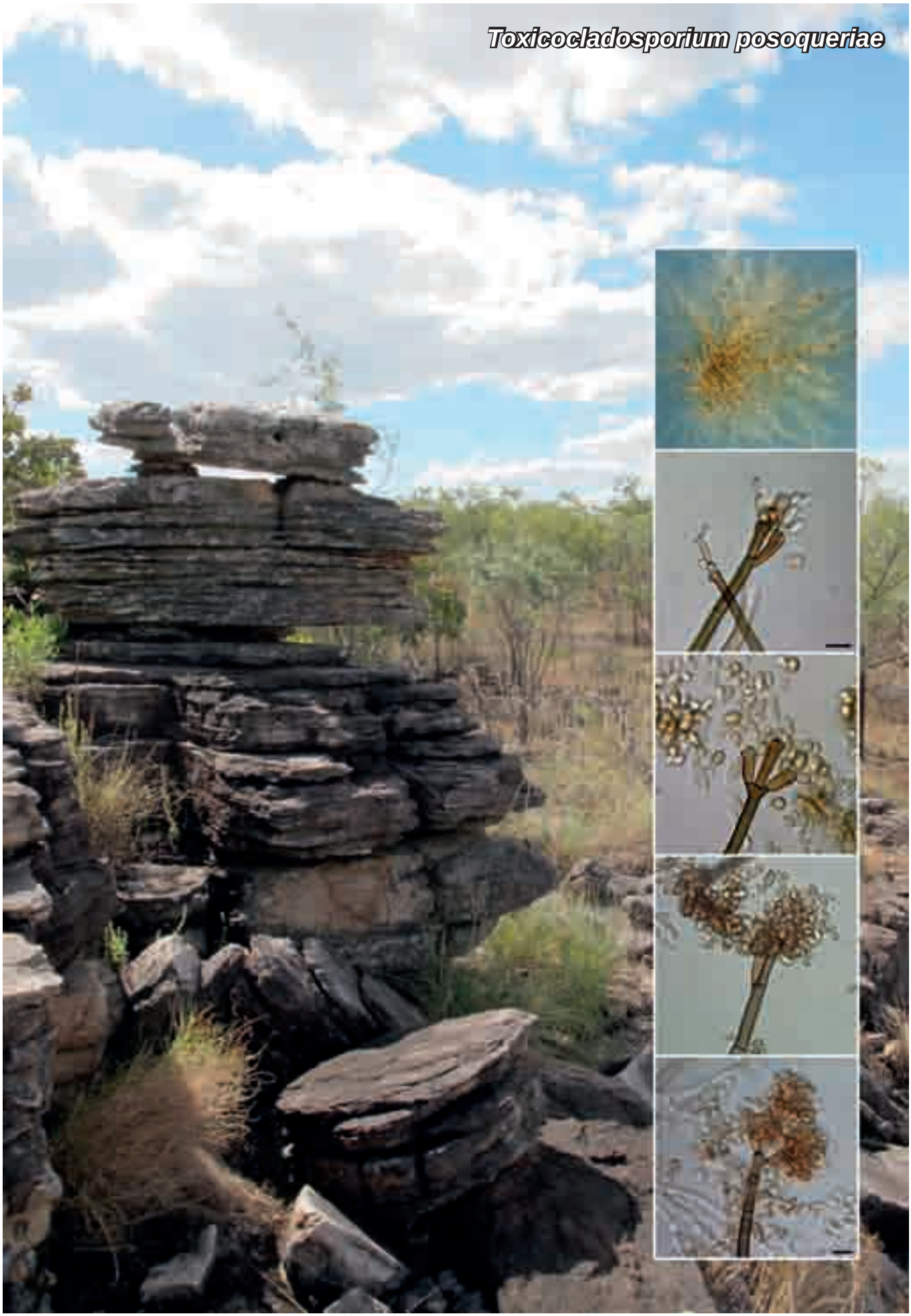
Toxicocladosporium posoqueriae

Fungal Planet 144 – 20 December 2012

Toxicocladosporium posoqueriae Crous & R.G. Shivas, *sp. nov.*

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

Description based on colonies sporulating on synthetic nutrient poor agar. *Mycelium* internal, pale brown, smooth, 2–3 µm diam (in culture brown, thick-walled, constricted at septa, smooth, 3–7 µm diam); giving rise to conidiophores that arise from stomata (hypophyllous, on brown leaf spots with concentric brown rings, associated with a *Colletotrichum* sp., the presumed primary pathogen), erect, solitary, straight, subcylindrical, main axis unbranched on host (frequently branched in culture), 50–200 × 4–7 µm; apex branched with lateral branches, 15–50 × 3–5 µm, 1–3-septate, becoming clavate towards apex, thick-walled, smooth to finely verruculose. *Conidiogenous cells* integrated, terminal and lateral, in whorls of 3–4, clavate or broadly cylindrical to doliiform, 10–20 × 4–7 µm, aseptate, medium to dark brown, concolorous with conidiophores, polyblastic with numerous loci at conidiogenous tip; loci truncate, circular, thickened, slightly darkened and refractive, 0.5–1(–1.5) µm. *Ramoconidia* dark brown, clavate to subcylindrical, finely verruculose, thick-walled, aseptate, 5–15 × 4–5 µm, with numerous apical loci, resembling those on conidiogenous cells. *Conidia* in branched, short chains, subglobose, ellipsoid to fusoid, (4–)6–7 × (3–)4 µm, pale brown, smooth, thin-walled; hila with circular, thickened, darkened and refractive loci, 1–1.5 µm diam.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margins. On malt extract agar surface folded, grey-olivaceous, reverse olivaceous-grey. On oatmeal agar surface grey-olivaceous in centre, sienna in outer region. On potato-dextrose agar grey-olivaceous in centre, olivaceous-grey in outer region, iron-grey in reverse, reaching 30 mm diam.

Typus. Australia, Northern Territory, Darwin, on leaves of *Posoqueria latifolia* (*Rubiaceae*), 12 Apr. 2011, *R.G. Shivas,* holotype CBS H-21086, cultures ex-type CPC 19305 = CBS 133583, ITS sequence GenBank KC005782, LSU sequence GenBank KC005803, MycoBank MB801780.

Notes — The genus *Toxicocladosporium*, based on *T. irritans*, presently accommodates eight species (Crous et al. 2007, 2009d, Crous & Groenewald 2011). *Toxicocladosporium posoqueriae* differs from other members of the genus in that it has whorls of conidiogenous cells, resembling *Parapericoniella asterinae*, the type species of the genus *Parapericoniella* (Bensch et al. 2012). However, *P. asterinae* is mycophylic, growing on *Asterina contigua*, thus it differs ecologically from *T. posoqueriae*, which appears to be plant pathogenic, colonising lesions of a *Colletotrichum* sp. Nevertheless, if these genera are eventually found to be synonymous, *Parapericoniella* (2005) would represent an older name than *Toxicocladosporium* (2007). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Toxicocladosporium pseudoveloxum* (GenBank JF499868; Identities = 924/938 (99 %), Gaps = 0/938 (0 %)), *Toxicocladosporium strelitziae* (GenBank JX069858; Identities = 922/938 (98 %), Gaps = 0/938 (0 %)) and *Toxicocladosporium irritans* (GenBank EU040243; Identities = 922/938 (98 %), Gaps = 0/938 (0 %)). Closest hits using the ITS sequence had highest similarity to *Toxicocladosporium strelitziae* (GenBank JX069874; Identities = 532/562 (95 %), Gaps = 10/562 (2 %)), *Toxicocladosporium pseudoveloxum* (GenBank JF499847; Identities = 660/698 (95 %), Gaps = 11/698 (2 %)) and *Toxicocladosporium rubrigenum* (GenBank FJ790285; Identities = 638/675 (95 %), Gaps = 7/675 (1 %)).

Colour illustrations. Rocky outcrop in Northern Territories, Darwin; colony on synthetic nutrient-poor agar; conidiophores with whorls of conidiogenous cells and conidia. Scale bars = 10 µm.

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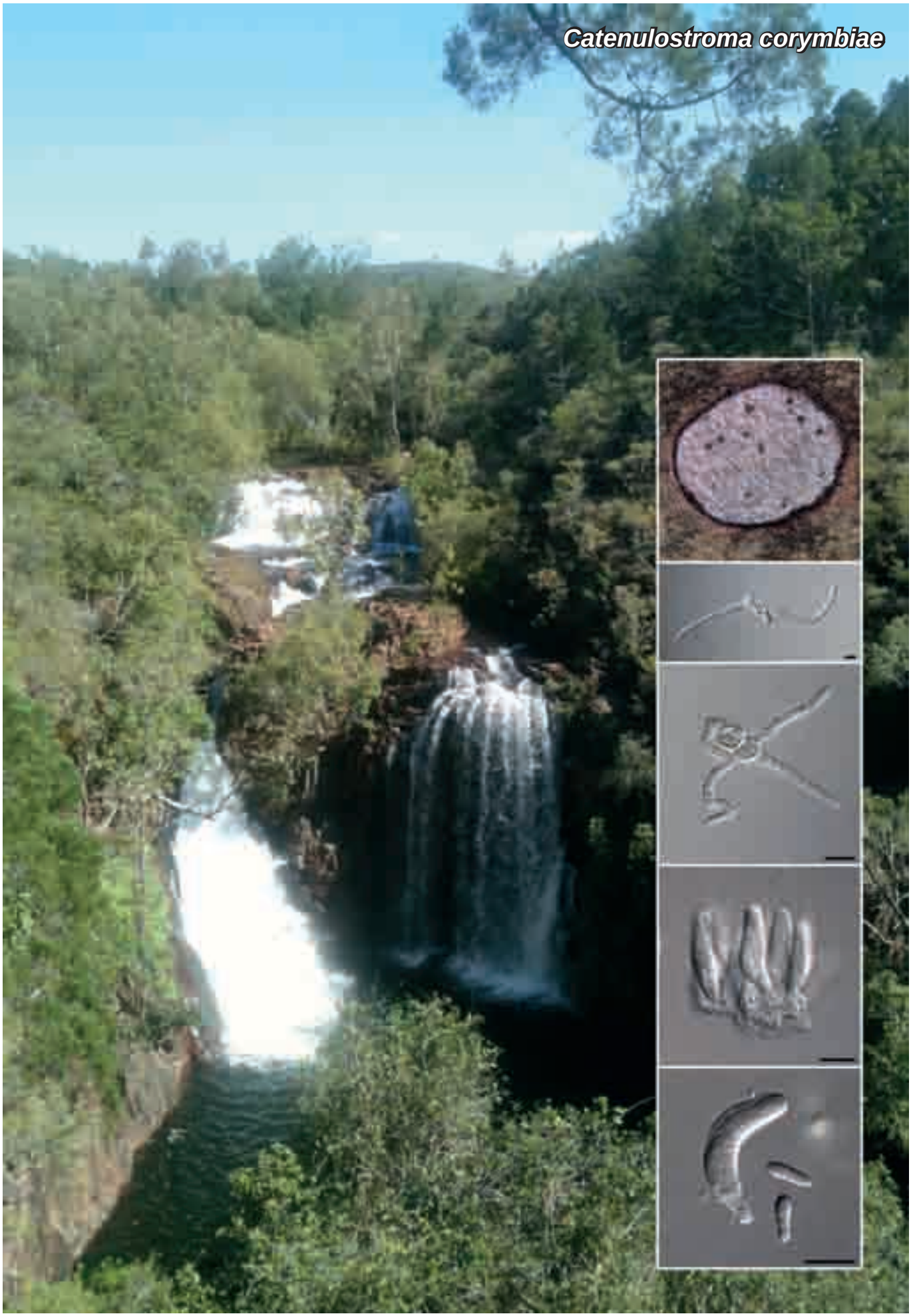
Catenulostroma corymbiae

Fungal Planet 145 – 20 December 2012

Catenulostroma corymbiae Crous & Summerell, *sp. nov.*

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

Leaf spots amphigenous, subcircular, 2–3 mm diam, grey-brown with a dark brown, raised border. *Ascomata* pseudothecial, amphigenous, black, subepidermal, erumpent, globose, up to 120 µm diam; central ostiole 10–20 µm diam; wall consisting of 2–3 layers of medium brown *textura angularis*. *Asci* aparaphysate, fasciculate, bitunicate, subsessile, obovoid to subcylindrical, straight to curved, 8-spored, 20–30 × 7–9 µm. *Ascospores* multiseriate, overlapping, hyaline, guttulate, thin-walled, straight, obovoid with obtuse ends, widest in middle of apical cell, medianly 1-septate, not or slightly constricted at septum, tapering towards both ends, but more prominently towards lower end, 7–8(–10) × (2–)3(–3.5) µm. *Ascospores* become distorted upon germination, brown, verruculose, 7–10 µm diam; initial germ tubes parallel to the long axis, but additional tubes at various angles to the long axis. *Colonies* on SNA. *Mycelium* consisting of septate, branched, smooth, pale brown, 2–3 µm diam hyphae, that give rise to globose or elongated sclerotial-like bodies of brown, multiseptate, thick-walled cells (variously shaped and branched, up to 25 µm diam). *Conidiophores* developing mostly on terminal hyphal ends, subcylindrical, brown, straight or variously curved, with multiple septa, up to 80 µm tall, and 4–6 µm wide. *Conidiogenous cells* subcylindrical, brown, smooth, terminal and lateral, 5–15 × 4–6 µm, with flattened, truncate locus, 2–3 µm diam, mono- to polyblastic. *Conidia* brown, smooth, subcylindrical to fusoid-ellipsoidal, straight to variously curved, at times with lateral branches, 0–3 transversely septate, apex obtuse or truncate, base truncate, 2 µm diam, somewhat darkened, not thickened, 8–20 × 3.5–4 µm; commonly arranged in branched chains that branch irregularly below or near apex of conidial chain.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margins. On malt extract agar (MEA) centre olivaceous-grey, outer region iron-grey, reverse iron-grey. On oatmeal agar surface olivaceous-grey. On potato-dextrose-agar same as MEA, reaching 13 mm diam.

Typus. Australia, Northern Territory, Darwin, just off Arnhem Highway, S12°44.839' E131°31.558', on leaves of *Corymbia* sp. (*Myrtaceae*), 9 May 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-21087, cultures ex-type CPC 19435, CPC 19437 = CBS 133584, ITS sequence GenBank KC005783, LSU sequences GenBank KC005805–KC005805, MycoBank MB801781.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Teratosphaeria encephalarti* (GenBank FJ372417; Identities = 836/850 (98 %), Gaps = 0/850 (0 %)), *Catenulostroma chromoblastomycosum* (GenBank EU019251; Identities = 877/892 (98 %), Gaps = 0/892 (0 %)) and *Penidiella rigidophora* (GenBank EU019276; Identities = 833/853 (98 %), Gaps = 0/853 (0 %)). Closest hits using the ITS sequence yielded highest similarity to *Catenulostroma protearum* (GenBank GU214628; Identities = 600/668 (90 %), Gaps = 29/668 (4 %)), *Catenulostroma hermanusense* (GenBank JF499833; Identities = 599/668 (90 %), Gaps = 29/668 (4 %)) and *Teratosphaeria encephalarti* (GenBank FJ372400; Identities = 592/661 (90 %), Gaps = 21/661 (3 %)). Although phylogenetically closely related to *C. protearum* (conidia 12–45 × 7–25 µm; Crous & Groenewald 2011), *C. corymbiae* has much smaller conidia.

Colour illustrations. *Corymbia* and *Eucalyptus* spp. in Northern Territory, Darwin; symptomatic *Corymbia* leaf; germinating ascospores; asci and ascospores. Scale bars = 10 µm.

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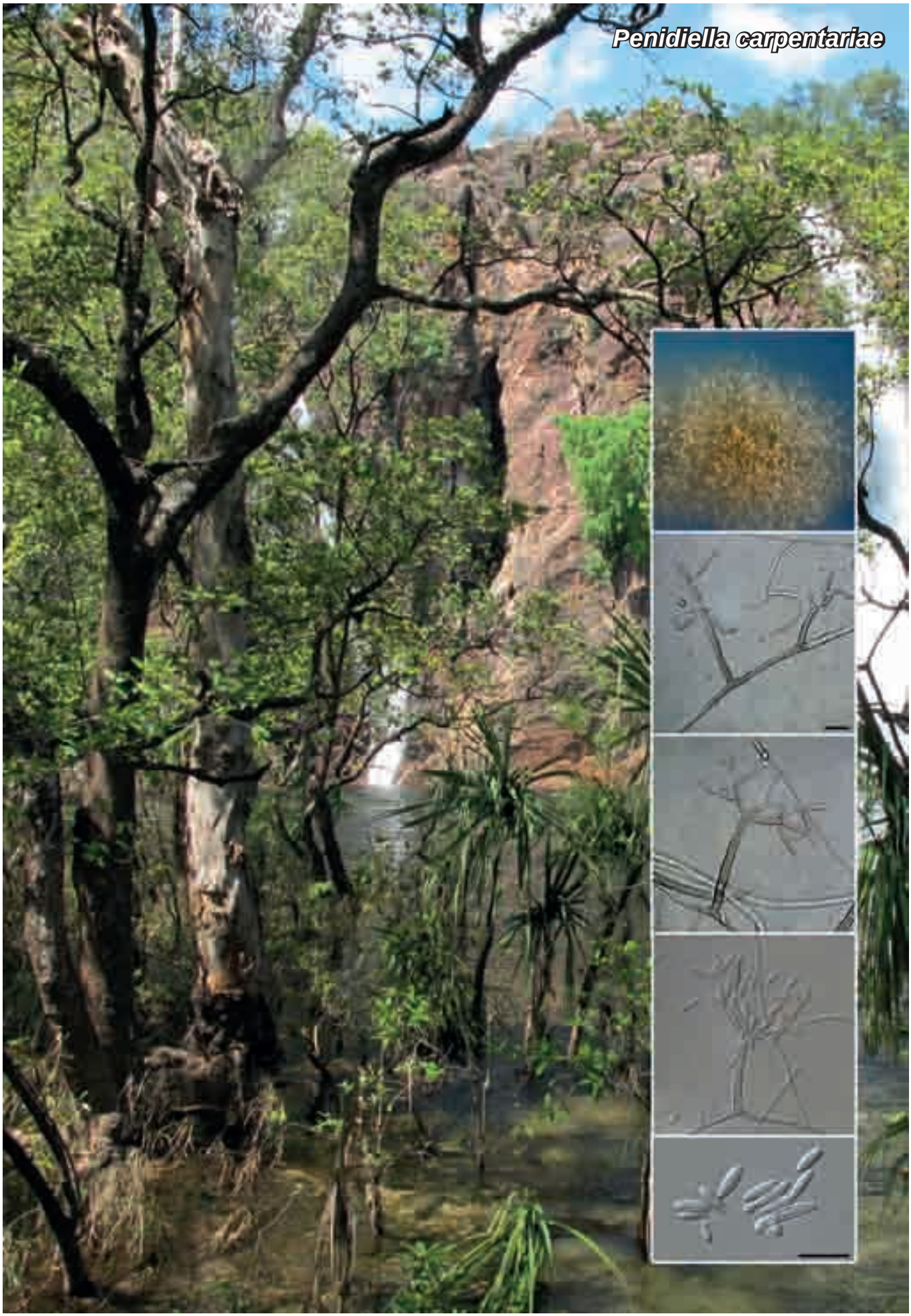
Penidiella carpentariae

Fungal Planet 146 – 20 December 2012

Penidiella carpentariae Crous & Summerell, *sp. nov.*

Etymology. Named after the host genus from which it was isolated, *Carpentaria*.

Colonies on synthetic nutrient-poor agar. *Mycelium* consisting of smooth, pale brown, septate, branched, 2–3 µm diam hyphae. *Conidiophores* erect, subcylindrical, pale brown, smooth to finely verruculose, straight or flexuous, unbranched, 1–3(–7)-septate, 20–90 × 2–4 µm. *Conidiogenous cells* terminal, integrated, subcylindrical, smooth, pale brown, proliferating sympodially, 15–25 × 2–3 µm; numerous scars aggregated at apex, flattened, thickened, somewhat darkened, 0.5–1.5 µm diam. *Ramoconidia* 0(–1)-septate, granular to guttulate, subcylindrical to fusoid-ellipsoidal, smooth, pale brown, 10–18 × 2–3 µm, with one to numerous loci at apex (especially on OA); hila somewhat thickened and darkened, 0.5–1 µm diam. *Conidia* fusoid-ellipsoidal, pale brown, smooth, guttulate, (6–)7–8(–10) × (1.5–)2(–2.5) µm, aseptate; hila flattened, truncate, somewhat thickened and darkened, 0.5–1 µm diam. *Chlamydospores* not observed.

Culture characteristics — (in the dark, 25 °C after 2 wk): Colonies erumpent, spreading, with smooth, lobate margins and sparse to moderate aerial mycelium. On potato-dextrose agar, malt extract agar and oatmeal agar surface and reverse iron-grey, colonies reaching 20 mm diam.

Typus. Australia, Northern Territory, Litchfield National Park, Wangi Falls, on leaves of *Carpentaria acuminata* (*Arecaceae*), 24 Apr. 2011, *P.W. Crous & B.A. Summerell*, holotype CBS H-21088, cultures ex-type CPC 19439 = CBS 133586, ITS sequence GenBank KC005784, LSU sequence GenBank KC005806, MycoBank MB801782.

Notes — Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Parapenidiella tasmaniensis* (GenBank GU214452; Identities = 865/895 (97 %), Gaps = 2/895 (0 %)), *Parapenidiella pseudotasmaniensis* (GenBank GQ852625; Identities = 859/889 (97 %), Gaps = 2/889 (0 %)) and *Phacellium paspali* (GenBank GU214669; Identities = 863/895 (96 %), Gaps = 3/895 (0 %)). Closest hits using the ITS sequence had highest similarity to *Devriesia tardicrescens* (GenBank JF499840; Identities = 453/527 (86 %), Gaps = 21/527 (4 %)), *Teratosphaeria associata* (GenBank EU707857; Identities = 360/391 (92 %), Gaps = 9/391 (2 %)) and *Teratosphaeria parva* (GenBank AY626980; Identities = 458/534 (86 %), Gaps = 32/534 (6 %)). *Penidiella carpentariae* clusters basal to a clade that contains *Parapenidiella tasmaniensis* and *P. pseudotasmaniensis*.

Parapenidiella Crous & Summerell, *gen. nov.*

Etymology. *Para* (= close to) + its morphological similarity to *Penidiella*.

Mycelium consisting of branched, septate, smooth subhyaline to pale brown hyphae. *Conidiophores* macronematous, occasionally micronematous; macronematous conidiophores arising from superficial mycelium, solitary, erect, pale brown, thin-walled, smooth to finely verruculose; terminally penicillate, unbranched in terminal part; conidiogenous apparatus composed of a series of conidiogenous cells and/or ramoconidia. *Conidiogenous cells* integrated, terminal or intercalary, unbranched, pale brown, smooth, tapering to a flattened or rounded apical region, mono- or polyblastic, sympodial, giving rise to a single or several sets of ramoconidia on different levels; with relatively few conidiogenous loci, slightly thickened, slightly darkened. Conidia in branched acropetal chains. *Ramoconidia* 0–1-septate, pale brown, smooth, thin-walled, fusoid-ellipsoidal to subcylindrical. *Conidia* subcylindrical, fusoid to ellipsoid-ovoid, aseptate, pale olivaceous to pale brown, smooth, thin-walled, catenate; hila truncate, slightly thickened, somewhat darkened.

Type species. *Parapenidiella tasmaniensis* (Crous & M.J. Wingf.) Crous. MycoBank MB801783.

Parapenidiella pseudotasmaniensis (Crous) Crous, *comb. nov*.

Penidiella pseudotasmaniensis Crous, Persoonia 23: 126. 2009. MycoBank MB801784.

Parapenidiella tasmaniensis (Crous & M.J. Wingf.) Crous, *comb. nov.*

Basionym. Mycovellosiella tasmaniensis Crous & M.J. Wingf., Mycol. Res. 102: 527. 1998.

≡ *Passalora tasmaniensis* (Crous & M.J. Wingf.) Crous & U. Braun, in *Mycosphaerella* and its anamorphs. 1. Names published in *Cercospora* and *Passalora*: 472. 2003.

= *Mycosphaerella tasmaniensis* Crous & M.J. Wingf., Mycol. Res. 102: 527. 1998.

Notes — *Parapenidiella* represents a genus between *Devriesia* (Seifert et al. 2004) and *Penidiella* (Crous et al. 2007), which are known to be paraphyletic (Crous et al. 2009a, b). All three genera have *Teratosphaeria*-like teleomorphs (Crous et al. 2008, 2012). *Parapenidiella* is distinguished from *Penidiella* and *Devriesia* by having pale brown, unbranched, penicillate conidiophores, with olivaceous to pale brown, branched conidial chains. *Penidiella carpentariae* strongly resembles *Parapenidiella* in morphology, yet appears to represent a different lineage in this generic complex.

MycoBank MB801785.

Colour illustrations. Wangi Falls, Litchfield National Park, Northern Territory; colony sporulating on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Seiridium phylicae

Fungal Planet 147 – 20 December 2012

Seiridium phylicae Crous & M.J. Wingf., *sp. nov*.

Etymology. Name refers to the host genus, *Phylica*.

Caulicolous. *Conidiomata* stromatic, pycnidia, scattered to aggregated, erumpent, conical, up to 350 µm diam, uniloculate, dark brown to black, opening by irregular rupture; basal stroma of dark brown *textura angularis*. *Conidiophores* lining cavity, filamentous, creating impression of paraphyses, septate, branched, hyaline, smooth, up to 80 µm long, and 3.5 µm wide. *Conidiogenous cells* subcylindrical, terminal and lateral, integrated, smooth, hyaline, 10–20 × 1.5–3 µm; proliferating percurrently. *Conidia* fusoid to ellipsoid, dark to golden brown, granular, 5-septate, not constricted at septa, with visible central septal pore, (23–)28–30(–35) × (9–)10(–11) µm; basal cell conical with truncate hilum, pale brown to hyaline, 3–5 µm long; 4 median cells doliiform to subcylindrical, brown, with wall and septa being darker, cells together 17–23 µm long; apical cell broadly conical, apex rounded, hyaline, 2–4 µm long. Apical appendages tubular, unbranched, eccentric, 6–8 µm long; basal appendages unbranched, centric, 2–5 µm long.

Culture characteristics — (in the dark, 24 °C after 2 wk): Colonies erumpent, spreading, with moderate aerial mycelium and even, lobate margins. On malt extract agar surface pale olivaceous-grey, with patches of dirty white; reverse cinnamon. On potato-dextrose agar surface dirty white with patches of black sporulation; reverse dirty white. On oatmeal agar surface pale grey-olivaceous with patches of dirty white, reaching 30 mm diam.

Typus. UK, British Overseas Territory of Saint Helena, Ascension and Tristan da Cunha, Inaccessible Island, Blenden Hall, S37°17'41" W12°42'08", stems of *Phylica arborea* (*Rhamnaceae*), Sept. 2011, *P.G. Ryan*, holotype CBS H-21089, cultures ex-type CPC 19962–19965 (CPC 19964 = CBS 133587), β-tubulin (TUB) sequence GenBank KC005819–KC005821, TEF1-α sequences GenBank KC005815–KC005817, ITS sequences GenBank KC005785–KC005785, LSU sequences GenBank KC005807–KC005810, MycoBank MB801788.

Notes — Conidia of *Seiridium cardinale* are 21–30 × 8–10 µm, with basal appendage being 1 µm long when present, and apical appendage 0.5–1.5 µm (Sutton 1980), which clearly distinguishes it from *Seiridium phylicae*. Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Seiridium eucalypti* (GenBank DQ414533; Identities = 833/833 (100 %), Gaps = 0/833 (0 %)), *Seiridium unicorne* (GenBank DQ414532; Identities = 833/833 (100 %), Gaps = 0/833 (0 %)) and *Lepteutypa cupressi* (GenBank AF382379; Identities = 872/875 (99 %), Gaps = 3/875 (0 %)). Closest hits using the ITS sequence had highest similarity to *Seiridium cardinale* (GenBank AF409995; Identities = 552/558 (99 %), Gaps = 2/558 (0 %)), *Seiridium cupressi* (GenBank FJ430600; Identities = 558/567 (98 %), Gaps = 4/567 (1 %)) and *Seiridium unicorne* (GenBank AF377299; Identities = 567/578 (98 %), Gaps = 2/578 (0 %)). Closest hits using the TUB sequence had highest similarity to *Seiridium cardinale* (GenBank DQ926973; Identities = 353/366 (96 %), Gaps = 3/366 (1 %)) and *Seiridium cupressi* (GenBank AF320495; Identities = 385/401 (96 %), Gaps = 2/401 (0 %)). Only distant hits (e.g. Identities = 218/249 (88 %), Gaps = 12/249 (5 %)) with *Pestalotiopsis* spp. were obtained when the TEF sequences were used in a megablast search.

Colour illustrations. *Phylica arborea* growing on Inaccessible Island; colony on synthetic nutrient-poor agar; conidiophores, conidiogenous cells and conidia. Scale bars = 10 µm.

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Microcyclospora rhoicola

Fungal Planet 148 – 20 December 2012

Microcyclospora rhoicola Tanney, *sp. nov.*

Etymology. Named after the host from which it was collected, *Rhus typhina*.

Colonies on *Rhus typhina* forming dark, sometimes slimy, crust on petiole and twig surfaces, forming a stroma-like sheath on trichomes, *textura prismatica* in surface view. *Mycelium* consisting of pale brown, branched, thick-walled (c. 1 µm), septate hyphae, (2–)4–6.5(–7.5) µm diam, smooth. Micromorphology identical to that in culture, described below.

Colonies on malt extract agar (MEA). *Mycelium* consisting of pale brown, branched, septate hyphae, 1.5–3.5 µm diam, smooth. In older cultures, hyphae becoming darker, thick-walled (c. 1 µm), ossiform, and fragmenting to form a yeast-like colony. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* integrated, lateral on hyphae, solitary, subdenticulate, 3–5 µm tall, 2–3 µm wide, pale brown, smooth. *Conidia* (0–)1–3(–6)-septate, 3-septate conidia most frequent, 5–6-septate conidia rarely observed, aseptate conidia (8–)9–17.5(–29.5) × (2–)2.5–3 µm, 1-septate conidia (10.5–)11.5–22.5(–36) × (2–)2.5–3(–3.5) µm, 2-septate conidia (17–)19–28(–32) × (2.5–)3–3.5(–4), 3-septate conidia (19–)26–35.5(–40) × (2–)2.5–3(–3.5) µm, 4-septate conidia (36–)37.5–44(–47.5) × (2.5–)2.5–3(–3.5) µm, 5-septate conidia (47–)48.5–56(–57) × 2.5–3 µm, 6-septate conidia 48.5 × 3 µm, hyaline, smooth, cylindrical, straight to variously curved, apex obtuse, base truncate, older conidia somewhat constricted at septa, guttulate, aggregated in mucoid masses; hila neither thickened nor darkened; anastomosis among conidia sometimes observed; microcyclic conidiation commonly observed.

Culture characteristics — (in the dark, 25 °C after 2 wk on MEA): Colonies convex, with moderate to woolly aerial mycelium; surface irregular, slimy, dark grey to olive (1F1–1F3) (Kornerup & Wanscher 1978), aerial mycelium greyish off-white to pastel grey (1B2–1B3), margin diffuse; reverse dark grey (1F1); diam up to 4 mm. In older colonies (> 6 wk), aerial mycelium becoming yellowish brown to tobacco brown (5E8–5F6), collapsing, centre carbonaceous, slimy and yeast-like, margin lobate.

Typus. Canada, Ontario, Ottawa, Dominion Arboretum, on twigs of *Rhus typhina* var. *laciniata* (*Anacardiaceae*), 20 Oct. 2011, *J.B. Tanney*, holotype DAOM 242272, dried culture ex-type DAOM 242276, ITS sequence GenBank KC012605, LSU sequence GenBank KC012606, TEF1 sequence GenBank KC012604, MycoBank MB801439.

Notes — *Microcyclospora* was first described in 2010, with three species causing sooty blotch on *Malus domestica* fruit (Frank et al. 2010). The genus is characterised by 1–multiseptate, smooth, pale brown, scolecosporous to cylindrical conidia borne from reduced and integrated mono- to polyblastic conidiogenous cells. Conidia occur in mucoid masses and microcyclic conidiation is common (Frank et al. 2010). Morphologically, *M. rhoicola* conforms with the generic concept of *Microcyclospora* and can be differentiated from other species by its shorter conidia with fewer septa (Table 1). The discovery of *M. rhoicola* represents the first record of *Microcyclospora* in North America and on its host, *Rhus typhina*.

The phylogenetic analysis below is based on internal transcribed spacer (ITS) sequences derived from two *M. rhoicola* isolates (specimens collected c. 250 km apart) and previously published data (Frank et al. 2010, Crous et al. In press). *Microcyclospora rhoicola* has distinct ITS sequences from those sequenced to date and appears to be rather distant from the currently described species.

Several cercosporoid fungi are described from *Rhus* spp. in North America (Farr et al. 1989), including *Cercosporella toxicodendri* and *Pseudocercospora rhoina*. Both species occur as leaf spots and have more complex conidiophores compared to the reduced and integrated conidiogenous cells characterising *M. rhoicola*.

Fig. 1 Consensus phylogram (50 % majority rule) of 15 002 trees resulting from a Bayesian inference analysis of an ITS sequence alignment using MrBayes v. 3.1.2. Posterior probabilities indicated with colour-coded branches (see legend).

Table 1 Comparison of hosts, distribution and micromorphology of currently described *Microcyclospora* species.

Species	Host	Origin	Morphology		Reference
			Conidial dimensions (µm)	Conidial septation	
M. malicola	*Malus*	Germany, Slovenia	45–75 × 2.5	(1–)5–7(–13)	Frank et al. (2010)
M. pomicola	*Malus*	Germany	50–75 × 2.5–3	1–13	Frank et al. (2010)
M. quercina	*Quercus*	Netherlands	30–45 × 2.5–3	(1–)3–4(–11)	Crous et al. (In press)
M. rhoicola	*Rhus*	Canada	26–36 × 2.5–3	(0–)1–3(–6)	Present study
M. rumicis	*Rumex*	Iran	37–54 × 2.5	1–10	Arzanlou & Bakhshi (2011)
M. tardicrescens	*Malus*	Slovenia	35–55 × 2	1–9	Frank et al. (2010)

Colour illustrations. *Rhus typhina* var. *laciniata* at the Dominion Arboretum, Ottawa, Ontario, Canada (type host, photo K. Seifert); mycelium on individual trichomes (scale bar = 100 µm); conidiogenous cells and conidia exhibiting microcyclic conidiation. Scale bars = 10 µm.

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Collembolispora aristata

Fungal Planet 149 – 20 December 2012

Collembolispora aristata Marvanová & J.Z. Groenew., *sp. nov*.

Etymology. *aristatus* (L.) = with bristles.

Conidia isolated from foam according to the methodology of Marvanová et al. (2003). *Colonies* on malt agar medium fast growing, reaching 25 mm after 20 d at 12 °C, dark grey, reverse black. Aerial mycelium abundant, lanose to funiculose. Hyphae glabrous, hyaline, thin-walled, 1–3 µm wide or dark brown, thicker-walled, up to 5 µm wide. Sporulation initially directly on agar, in subcultures after submergence in standing distilled water at 15 °C within a few days. *Conidiophores* intercalary, lateral or terminal, simple to profusely branched; stipes, if present, cylindrical or distally slightly widening up to 32 × 1.5–3.5 µm, with branches on various levels along the stipes or in a penicillate head; often concurrent with conidiogenous cells, sometimes verticillate, cylindrical or subclavate, 4–8 × 2–3 µm. *Conidiogenous cells* subclavate to narrow-doliiform, usually 1–3 per conidiophore branch, polyblastic sympodial, 5–11 × 1.5–3 µm, with one to few denticles at the apex, scars flat. *Conidia* in slimy masses when formed outside water, appearing in close sequence. Axis 31–46 × 2–3.5 µm, proximal part obclavate and unequilateral, mildly curved or straight, 3(–5)-septate, basal scar truncate, sometimes eccentric, apex with an integrated, setose extension sometimes slightly curved away; branch single (exceptionally two), typically ventral, rarely dorsal, usually arising from the second suprabasal cell of the axis, often strongly retrorse, but also perpendicular to the axis, straight or often slightly curved abaxially, rarely adaxially, proximal part obclavate, base often slightly sinuous, 16–30 × 1.5–2.7 µm, insertion unequally constricted, distally protracted into setose extension. Some considerably swollen conidia are usually present in submerged cultures after several weeks. Hyphopodia-like outgrowths may appear in aged, submerged cultures on hyphae, and also on conidia.

Typus. Czech Republic, South Moravian region, between the villages Ochoz uTišnova and Lomnice, c. 440 m alt., isolated from foam in an unnamed left tributary of the Křeptovský potok stream (the streamlet is shallow, 80–100 cm wide, slow-flowing, with grasses on the banks and *Typha latifolia* and *Glyceria maxima* in the littoral zone), Mar. 1984, *L. Marvanová*, holotype CBS H-21090, culture ex-type CPC 21145 = CCM F-01585 = CBS 115662; ITS sequence GenBank KC005789, LSU sequence GenBank KC005811, MycoBank MB491201.

Notes — The hyphomycete genus *Collembolispora* is based on *C. barbata*, isolated from *Alnus glutinosa* leaf baits submerged in a slow-flowing, oligotrophic softwater stream in North Portugal (Marvanová et al. 2003). *Collembolispora aristata* has similar colonies, conidiogenesis as well as conidia like *C. barbata*, but the conidia of the latter differ from those of *C. aristata* by having a branched, terminal, setose extension on the conidial axis and on the conidial branch, and by the presence of a hyphomycetous, phialidic (?spermatial) morph.

As far as we know, there is thus far only one other report on conidia of *C. aristata* (Roldán & Puig 1992, f. 3C, as *Gyoerffyella* sp.). These authors collected detached conidia in a stream in the river Esva basin in the Asturias Province of Northern Spain, 285 m alt., in a site where the riparian vegetation consists predominantly of grasses.

Conidia of *C. aristata* resemble those of *Ramulispora bromi*, which is a grass parasite causing spots on *Bromus* spp. In fact the conidia illustrated by Sprague (1950, f. 76), resemble underdeveloped conidia of *C. aristata*, without long extensions. According to Braun (1995), *R. bromi* is an insufficiently known species, with conidia resembling those of *Mycocentrospora* or *Spermospora*. *Ramulispora* is based on *R. andropogonis*, which according to Braun (1995) is a facultative (taxonomic) synonym of *R. sorghi*, based on *Septorella sorghi*. Conidia of *R. sorghi* are filiform to narrow obclavate, sometimes with 1–2 lateral branches. *Ramulispora sorghi* is anamorphic *Mycosphaerellaceae*, *Dothideomycetes* (Crous et al. 2009a, c).

Collembolispora aristata conidia are superficially also similar to those of two *Gyoerffyella* species with single-branched non-coiled conidia (*G. entomobryoides* and *G. tricapillata*). However, members of this holoanamorphic genus have pale colonies and polyblastic, clavate conidiogenous cells, which do not proliferate.

Phylogenetically *Collembolispora* clusters in the *Helotiales*, with the nearest group formed by strains of *Leptodontidium orchidicola*. *Leptodontidium* was established for dematiaceous endophytes in roots of various plants growing in cool soils rich in humus (Fernando & Currah 1995). Based on a megablast search of NCBIs GenBank nucleotide database, the closest hits using the LSU sequence are *Cadophora luteo-olivacea* (GenBank HM116760; Identities = 907/913 (99 %), Gaps = 0/913 (0 %)) and *Mollisia dextrinospora* (GenBank HM116757; Identities = 906/913 (99 %), Gaps = 0/913 (0 %)). Closest hits using the ITS sequence had highest similarity to *Collembolispora barbata* (GenBank GQ411302; Identities = 559/576 (97 %), Gaps = 7/576 (1 %)) and *Leptodontidium orchidicola* (GenBank GU586841; Identities = 555/580 (96 %), Gaps = 10/580 (2 %)).

There is little information on the ecology of species of *Collembolispora*. It is not known whether they should be considered indwellers, residents or transients (in the sense of Park 1972) in the water environment. In both localities of *C. aristata*, *Poaceae* were present on the stream banks or in the littoral zone. Although the occurrence of *Poaceae* at the type locality may support the hypothesis about relationships between *R. bromi* and *C. aristata,* the phylogenetic affinity suggests this not to be the case.

Colour illustrations. Left tributary of the stream Křeptovský potok between the villages Ochoz u Tišnova and Lomnice; conidiophores, conidiogenous cells and appendaged conidia. Scale bars = 10 µm.

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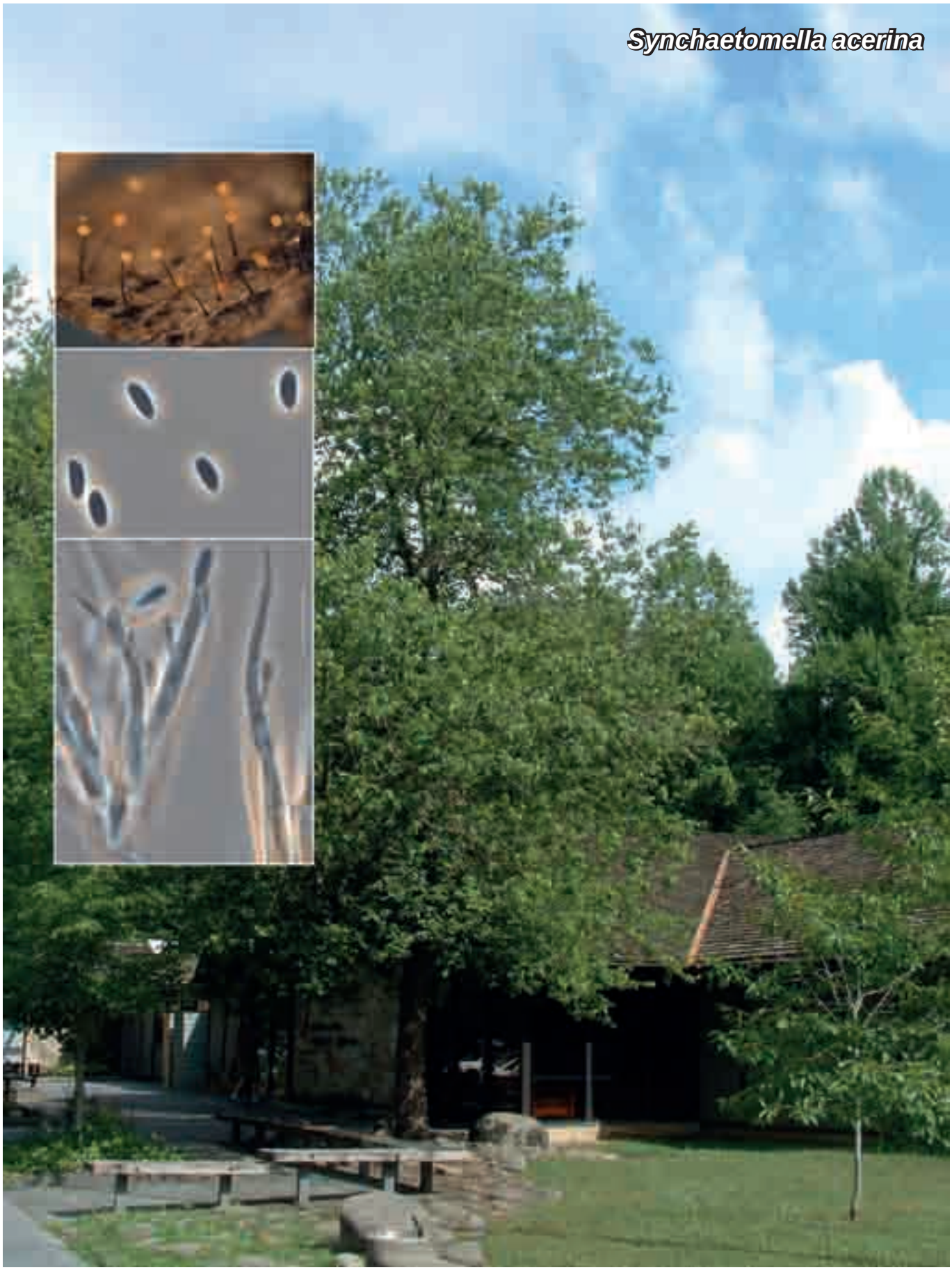
Synchaetomella acerina

Fungal Planet 150 – 20 December 2012

Synchaetomella acerina Seifert, *sp. nov.*

= *Stilbella acerina* Overh., Mycologia 35: 253. 1943. nom. inval. Art. 36.

Etymology. Named after the genus of its host, duplicating the epithet proposed by the original discoverer of this species.

Synnemata 250–825 µm tall, subulate, capitate, slender, 30–50 µm wide at the base, narrowing to 20–40 µm wide, black or dark brown, fading below the capitulum, usually unbranched, solitary, scattered or gregarious, sometimes associated with necrotic leaf spots of a *Phyllosticta* sp. Hyphae of stipe in two zones: marginal hyphae 2–3 µm wide, golden brown, unbranched, with walls up to 1 µm thick, sometimes seta-like and projecting into the capitulum and supporting the conidial mass; core hyphae 2–2.5 µm wide, hyaline, branching in the capitulum to give rise to the conidiophores. *Conidiophores* biverticillate or terverticillate, with terminal branches comprising 2–3 conidiogenous cells in an acropleurogenous chain; metulae 7–11 × 1.5–2 µm. *Conidiogenous cells* phialidic; terminal phialides 7–13 × 1–2 µm, subulate or acerose; intercalary phialides 6–9 × 1–2.5 µm, cylindrical with a lateral, apically directed, terminal conidiogenous extension, 1–11.5 µm long, usually longest near the base of the chain; periclinal thickening and collarettes not seen. *Conidial mass* globose, at first hyaline, becoming white, usually orange when dry, sometimes white, yellow, or red, about 75–125 µm diam when dry. *Conidia* 5–7.5(–9.5) × 1.5–2.5(–3) µm (6.53 ± 0.06 × 2.37 ± 0.02, n = 25), aseptate, allantoid to ellipsoidal, hyaline.

Culture characteristics — Typical synnemata develop on oatmeal agar, as do sessile conidiomata with identical conidiophores and conidia. Mononematous conidiophores, similar to those in conidiomata, are produced on the agar surface. There is more variation in conidial size than is seen on the natural substrate. On 2 % malt extract agar, parts of the colony are yeast-like, with irregularly shaped yeast cells. Other parts of the colony have a mycelial, micronematous anamorph, perhaps a degenerated version of conidiophores seen in conidiomata. Synnemata that develop in a damp chamber are often apically branched 1–4 times.

Typus. USA, Tennessee, Gatlinburg, Great Smokey Mountains National Park, Cataloochee Campground, on leaves of *Acer rubrum,* 15 July 2004, *R. Bennett* (holotype DAOM 242271, culture ex-type CCFC 242271); ITS sequence GenBank JX989830, LSU sequence GenBank JX989831, SSU sequence GenBank JX989832, *Cox1* sequence GenBank JX989833, MycoBank MB801762.

Additional material examined. Same location and host, Park Headquarters Building, *L.O. & F.M. Overholts*, 18 Aug. 1939 (PAC 22851, holotype of *Stilbella acerina* nom. inval.); Park Headquarters Building, *D.H. DeFoe*, 27 June 1984 (culture CBS 543.84).

Colour illustrations. *Acer rubrum* near the Park Headquarters of the Great Smokey Mountains National Park (*Andrew Miller*), with synnemata, conidiophores and conidia from the type of *Synchaetomella acerina*.

Notes — The hyphomycete genus *Synchaetomella* is based on *S. lunatospora,* a species with falcate, 1-septate conidia, which was originally isolated from leaf-litter collected in Singapore (Decock et al. 2005). *Synchaetomella acerina* has similar conidiomata and conidiophore branching and is phylogenetically closely related, but differs by having aseptate, allantoid conidia, and occurs on living leaves of *Acer rubrum*. The lignicolous *Exophiala calicioides* also has acropleurogenous conidiogenous cells terminating in dark synnemata, but they have distinct annellations, and other characters are dissimilar to those of *S. acerina* (Ellis 1971, as *Graphium*).

Stilbella acerina was invalidly described by Overholts (1943) without a Latin diagnosis, and excluded from *Stilbella* by Seifert (1985) without redisposition. In 1984, park rangers at Great Smokey Mountains National Park sent us living leaves of *Acer rubrum* from near the park headquarters, where Overholts reported finding the fungus. To our surprise, the synnematous fungus emerged from the leaves when damp chambered, and was easily cultured. Twenty years after that, K. Hodge and her student R. Bennett of Cornell University recollected the fungus again during a foray of the Mycological Society of America in the same park, providing the specimen used as the holotype of the species here.

Synchaetomella belongs to the complex of anamorph genera including *Chaetomella, Hainesia, Pilidium* and *Sphaerographium* (Rossman et al. 2004). These genera have species with similar conidia and phialidic conidiogenous cells that develop in acropleurogenous chains. They differ primarily in the nature of their conidiomata, which in the other genera are coelomycetous. The addition of *S. acerina* to the complex calls into question the monophyly of these genera as presently circumscribed, but the species clearly belongs to *Synchaetomella* morphologically, based on its synnematous conidiomata.

Supplementary material in MycoBank includes line drawings of *S. acerina* and its yeast-like form in vitro.

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Devriesia imbrexigena

Fungal Planet 151 – 20 December 2012

Devriesia imbrexigena A.J.L. Phillips & M.L. Coutinho, *sp. nov.*

Etymology. Name derived from the Latin word for tile (*imbrex*) relating to the habitat where it was found.

On half-strength potato-dextrose agar. *Mycelium* immersed or superficial, consisting of dark brown, branched, septate, 4–5 µm diam hyphae. *Arthroconidia* brown, smooth, barrel-shaped or globose, thick-walled, irregular, (5–)7–9(–10) × (4.5–)5–6(–6.5) µm, occurring in branched chains, buds arising at intervals along the chain. *Chlamydospores* intercalary or terminal, thick-walled, brown, 5–6.5 × 4.5–5 µm.

Culture characteristics — (In the dark, 25 °C after 4 wk): Colonies spreading with mostly appressed mycelium and lobate margins, reaching 35 mm diam, olivaceous to brown.

Typus. Portugal, Sintra, Palácio da Pena, on glazed decorative tiles in association with *Trebouxia* sp. (*Chlorophyta*), 29 Oct. 2011, *M.L. Coutinho* (holotype LISE 96109, culture ex-type CAP1373), ITS sequence GenBank JX915746, LSU sequence GenBank JX915750, MycoBank MB801761.

Additional material examined. Same collection: CAP1371, ITS sequence GenBank JX915745, LSU sequence GenBank JX915749; CAP1374, ITS sequence GenBank JX915747, LSU sequence GenBank JX915751; CAP1375, ITS sequence GenBank JX91574, LSU sequence GenBank JX915752.

Notes — *Devriesia* is paraphyletic (Frank et al. 2010), comprising at least four lineages, three of which are distantly related to *D. staurophora*, the type species of the genus. In the LSU phylogeny *Devriesia imbrexigena* clusters in one of these lineages, but not with the typical cluster of soil-inhabiting, heat resistant strains. In the nutrient-poor habitat where *D. imbrexigena* was found it seems to derive nutrition by parasitizing algae that colonise tiles (Coutinho et al. 2012).

A megablast search of NCBIs GenBank nucleotide sequence database with the LSU sequence revealed highest similarities to *Devriesia hilliana* (GenBank GU214414; Identities = 913/920 (99 %), Gaps = 0/920 (0 %)), *Passalora* sp. (GenBank GQ852622; Identities = 912/920 (99 %), Gaps = 0/920 (0 %)) and *Devriesia queenslandica* (GenBank JF951168; Identities = 911/920 (99 %), Gaps = 0/920 (0 %)). Closest hit with the ITS sequence is *Teratosphaeria capensis* (GenBank JN712501; Identities = 436/471 (93 %), Gaps = 12/471 (3 %)), followed by *Devriesia* sp. (GenBank HQ914861; Identities = 434/476 (91 %), Gaps = 14/476 (3 %)) and *Devriesia lagerstroemiae* (GenBank GU214634; Identities = 427/471 (91 %), Gaps = 15/471 (3 %)).

Colour illustrations. Pena National Palace, Sintra, Portugal. Branched chain of arthroconidia, buds developing on the chain of arthroconidia, multiple buds, detail of a budding cell. Scale bars = 5 µm.

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Passalora lobeliae-fistulosis

Fungal Planet 152 – 20 December 2012

Passalora lobeliae-fistulosis J.L. Alves & R.W. Barreto, *sp. nov.*

Etymology. Named after the host species from which it was collected, *Lobelia fistulosa*.

Leaf spots circular, centrally white greyish, with distinct dark brown margins, becoming subcircular to irregular, tissue collapsing in the necrotic areas and often torn, 2–16 × 3–20 mm. *Internal mycelium*, inter- and intracellular, 1.5–2 µm wide, branched, septate, pale brown, smooth. *External mycelium* absent. *Stromata* subepidermal, globose to subglobose, 25–85.5 × 28–63.5 µm, composed of dark brown *textura angularis*. *Conidiophores* amphigenous, aggregated in dense erect synnemata, subcylindrical, straight to slightly sinuous at apex, up to 330 µm long, 2–4 µm wide, multiseptate, unbranched, chestnut-brown at base becoming yellowish brown at apex, geniculate, smooth. *Conidiogenous cells* integrated, terminal, slightly sinuous, tapering to flat-tipped apical loci, subcylindrical 6–25 × 1.5–4 µm, pale brown. *Conidiogenous loci* conspicuous, 1–3 per cell, truncate to slightly convex, 1.5–2 µm diam, thickened and darkened. *Conidia* brown, smooth, dry, guttulate, solitary or catenulate, forming branched chains, cylindrical to subcylindrical, 10–59 × 1.9–5.5 µm, apex rounded, base obconically truncate, (1–)2–3(–4)-septate; hilum thickened and darkened.

Culture characteristics — Colonies slow growing (reaching 10 mm diam after 15 d) on vegetable broth agar (VBA; Pereira et al. 2003) at 25 °C; circular or irregular, raised centrally of dense cottony aerial mycelium, olivaceous-black, with black-grey uneven margins. Reverse on VBA iron-grey, alternate with olivaceous-black; sporulation abundant.

Typus. Brazil, Rio de Janeiro, Nova Friburgo, Riograndina, Alto dos Micheis, on leaves of *Lobelia fistulosa*, 9 July 2011, *R.W. Barreto* (holotype VIC 31840, culture ex-type COAD 1116), LSU sequence GenBank JX171142, ITS sequence GenBank JX494388, MycoBank MB800217.

Notes — *Passalora lobeliae-fistulosis* was found associated with distinct leaf spotting of *Lobelia fistulosa* (*Campanulaceae*). There is only one species of *Passalora* described on a member of the genus *Lobelia*, namely *P. lobeliae-cardinalis* (http://nt.ars-grin.gov/fungaldatabases/index.cfm). The presence of long synnemata, conidial chains and also conidial size allows for an easy distinction of *P. lobeliae-fistulosis* from *P. lobeliae-cardinalis* and the other species of *Passalora* described hitherto on members of the *Campanulaceae*, namely: *P. codonopsis*, *P. effusa, P. ferruginea, P. isotomae* and *P. lobeliae-cardinalis.* These species were originally treated as members of *Cercospora* or *Mycovellosiella* but have been transferred to *Passalora* (Braun 1995, Braun & Crous 2003). The closest species of *Passalora* as compared by LSU sequences available in public databases is *P. brachycarpa.* Nevertheless, this is a pathogen of *Solanum* spp. (*Solanaceae*) which is both phylogenetically and morphologically distinct from *P. lobeliae-fistulosis.* No sexual morph was observed on the leaves, nor were we able to induce any in culture. BLASTn results of the LSU sequence of *P. lobeliae-fistulosis* (VIC 31840, VIC 31841) had an E-value of 0.0 with the LSU sequence of *P. brachycarpa* (GenBank GU214664, 100 % query coverage).

Colour illustrations. *Lobelia fistulosa* growing on a humid slope at type locality in the Atlantic rainforest at Nova Friburgo, state of Rio de Janeiro, Brazil. Close-up of leaf spot; dense and erect synnema; conidia with thickened and darkened hila. Scale bars = 10 um

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Clitopilus austroprunulus

Fungal Planet 153 – 20 December 2012

Clitopilus austroprunulus Morgado, G.M. Gates & Noordel., *sp. nov.*

Etymology. austro (L) = southern, being a southern counterpart of *Clitopilus prunulus*.

Macroscopic description — *Pileus* 40–90 mm diam, convex when young, expanding to concave or infundibuliform, with involute margin, becoming irregularly shaped with age with undulating marginal zone. Not hygrophanous, not translucently striate, uniformly pale grey, sometimes with a slight brown tinge at the centre (10YR 7/3–4), adpressed-tomentose all over. *Lamellae* arcuate-decurrent, grey-pink with entire, concolorous or more or less hyaline edge, crowded. *Stipe* 30–60 × 10–15 mm (apex), usually central, rarely eccentric, tapering towards base, white or with a greyish brown tinge like pileus, tomentose. *Context* white, firm and rather thick in pileus. *Odour* very strongly farinaceous-rancid. *Taste* farinaceous-rancid.

Microscopic description — *Spores* (8–)9–11 × 4.5–6 µm, Q = 1.7–2.1, Qav = 1.9, slender fusiform occasionally amygdaliform, thin-walled, distinctly ribbed lengthwise with 5–8 longitudinal ribs, angular in polar view. *Basidia* 20–30 × 4–8 µm, 4-spored. *Lamella* edge fertile or with scattered subcylindrical cheilocystidia, 20–40 × 4–11 µm. *Pileipellis* a cutis of densely packed, narrow cylindrical, 4–8 µm wide hyphae with dark brown coloured walls, and scattered fine encrustations. Clamp-connections absent.

Habitat — Terrestrial in litter on wet sclerophyll forest of *Eucalyptus regnans* with an understorey of *Acacia*, *Olearia*, *Bedfordia*, *Pomaderris* and *Phebalium*.

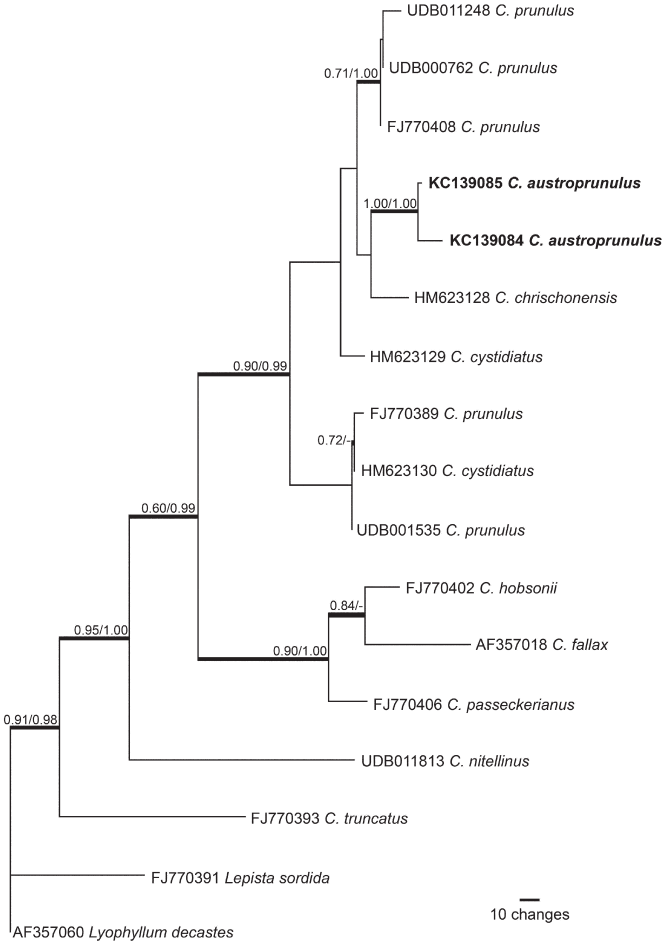
Typus. Australia, Tasmania, Kermandie Falls, Lower Track, S43°12' E146°52', 24 Mar. 2009, *M.E. Noordeloos* 2009062 (L); ITS sequence GenBank KC139085, MycoBank MB802264.

Additional collections Australia, Tasmania, Kermandie Falls, Lower Track, S43°12' E146°52', 16 Mar. 1999, *G. Gates* E 226; ibid., 23 May 2000, *G. Gates* E 936; ibid., 5 Apr. 2001, *G. Gates* E 1072; ibid., 16 May 2002, *G. Gates* E 1508; ibid., 10 Apr. 2003, *G. Gates* E 1694; ibid., Upper Track, 26 Apr. 2001, *G. Gates* E 1131; Reuben Falls, 15 May 1999, *G. Gates* E 507; Tahune, hanging bridges walk, S43°06', E146°43', 14 Mar. 2009, *M.E. Noordeloos* 2009001 (L), ITS sequence GenBank KC139084.

Notes — The morphospecies *Clitopilus prunulus* is widespread in Europe and North America. A number of closely related species have been described in literature (Hausknecht & Noordeloos 1998, Yang 2007, Vizzini et al. 2011). Species limits are however often difficult to define due to the lack of good morphological characters. Recent studies confirm that the current concept of *C. prunulus* is polyphyletic (Hartley et al. 2009, Vizzini et al. 2011). *Clitopilus austroprunulus* is very similar morphologically to *C. prunulus* from Europe, and therefore Noordeloos & Gates (2012) initially listed it as *Clitopilus* cf. *prunulus.* However, a phylogenetic analysis based on internal transcribed spacer (ITS) sequences derived from two *C. austroprunulus* isolates and previously published data (Co-David et al. 2009, Hartley et al. 2009, Vizzini et al. 2011) clearly showed that the collections of *C. austroprunulus* cluster together as a clade of their own, phylogenetically distinct from the rest of the *C. prunulus* clade. The other closely related species, *C. cystidiatus* and *C. chrischonensis* are phylogenetically distinct and differ from *C. austroprunulus* in morphology by the abundant presence of cheilocystidia. Although judging from the phylogeny presented here, the occurrence of cheilocystidia may well be of limited value in the systematics of this group. *Clitopilus amygdaliformis* described from China (Yang 2007) is also closely related, but differs in spore and stipe morphology. Unfortunately, sequences for this species are not available in public databases and therefore it was not included in the phylogenetic analysis.

A multi-gene maximum-likelihood phylogeny based on four independent genetic markers (data not shown) yielded the same conclusions as the ITS phylogeny presented here. Therefore *C. austroprunulus* is phylogenetically distinct from all sequenced species and morphologically distinct from all described species without available sequences.

Maximum-likelihood phylogram (-ln L = 3770.9401) of ITS sequence analysis with general-time-reversible model using Garli 2.0 (Zwickl 2006), showing the phylogenetic position of *Clitopilus austroprunulus* (in **bold**) generated in this study among representatives of closely related taxa with sequences deposited in GenBank and the UNITE database. Branches with bootstrap support (BS) ≥ 0.70 (based on 100 replicates) and/or bayesian posterior probability (PP) ≥ 0.95 (based on 5 000 generations) (Ronquist et al. 2012) are thickened with BS/PP values indicated above the branches. The tree was rooted with *Lepista sordida* and *Lyophyllum decastes.*



Colour illustrations. Australia, Tasmania, Kermandi Falls, Lower Track, type-locality. *Clitopilus austroprunulus*, holotype (photo's M.E. Noordeloos).

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REFERENCES

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

Arzanlou M, Bakhshi M. 2011. Microcyclospora rumicis, a new species on Rumex crispus from Iran. Mycotaxon 118: 181–186.

Arzanlou M, Crous PW. 2006. Strelitziana africana. Fungal Planet No. 8. Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands.

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

Berbee ML, Pirseyedi M, Hubbard S. 1999. Cochliobolus phylogenetics and the origin of known, highly virulent pathogens, inferred from ITS and glyceraldehyde-3-phosphate dehydrogenase sequences. Mycologia 91: 964–977.

Braun U. 1995. A monograph of Cercosporella, Ramularia and allied genera (Phytopathogenic Hyphomycetes). IHW Verlag, München, Germany.

Cannon PF, Hawksworth DL, Sherwood-Pike MA. 1985. The British Ascomycotina. An annotated checklist. Commonwealth Mycological Institute, Kew, Surrey, England.

Cheewangkoon R, Groenewald JZ, Summerell BA, Hyde KD, To-anun C, Crous PW. 2009. Myrtaceae, a cache of fungal biodiversity. Persoonia 23: 55–85.

Chomnunti P, Ko Ko TW, Chukeatirote E, Hyde KD, Cai L, et al. 2012. Phylogeny of the Chaetothyriaceae in northern Thailand including three new species. Mycologia 103: 382–395.

Co-David D, Langeveld D, Noordeloos M. 2009. Molecular phylogeny and spore evolution of Entolomataceae. Persoonia 23: 147–176.

Constantinescu O, Holm K, Holm L. 1989. Teleomorph-anamorph connections in Ascomycetes. 1–3. Stanhughesia (Hyphomycetes) new genus, the anamorph of Ceramothyrium. Studies in Mycology 31: 69–84.

Coutinho ML, Miller AZ, Gutierrez-Patricio S, Hernandez-Marine M, Gomez-Bolea A, et al. 2012. Microbial communities on deteriorated artistic tiles from Pena National Palace (Sintra, Portugal). International Biodeterioration & Biodegradation. doi.org/10.1016/j.ibiod.2012.05.028.

Crous PW. 1999. Species of Mycosphaerella and related anamorphs occurring on Myrtaceae (excluding Eucalyptus). Mycological Research 103: 607–621.

Crous PW, Braun U. 2003. Mycosphaerella and its anamorphs. 1. Names published in Cercospora and Passalora. CBS Biodiversity Series 1: 1–571. Utrecht, The Netherlands.

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

Crous PW, Braun U, Hunter GC, Wingfield MJ, Verkley GJM, et al. In press. Phylogenetic lineages in Pseudocercospora. Studies in Mycology 75: 37–114.

Crous PW, Groenewald JZ. 2011. Why everlastings don't last. Persoonia 26: 70–84.

Crous PW, Groenewald JZ, Shivas RG. 2010a. Devriesia fraseriae. Fungal Planet 65. Persoonia 25: 150–151.

Crous PW, Groenewald JZ, Shivas RG. 2010b. Strelitziana eucalypti. Fungal Planet 62. Persoonia 25: 144–145.

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

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

Crous PW, Summerell BA, Carnegie AJ, Wingfield MJ, Groenewald JZ. 2009b. Novel species of Mycosphaerellaceae and Teratosphaeriaceae. Persoonia 23: 119–146.

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

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

Crous PW, Wingfield MJ, Groenewald JZ. 2009d. Niche sharing reflects a poorly understood biodiversity phenomenon. Persoonia 22: 83–94.

Crous PW, Wood AR, Okada G, Groenewald JZ. 2008. Foliicolous microfungi occurring on Encephalartos. Persoonia 21: 135–146.

Decock C, Delgado Rodriguez G, Seifert KA. 2005. Phylogeny of Synchaetomella lunatospora, a new genus and species of synnematous fungi from Southeast Asia. Antonie van Leeuwenhoek 88: 231–240.

Ellis MB. 1971. Dematiaceous hyphomycetes. CAB International, Kew, UK.

Farr DF, Bills GF, Chamuris GP, Rossman AY. 1989. Fungi on plants and plant products in the United States. APS Press, USA.

Fernando AA, Currah RS. 1995. Leptodontidium orchidicola (Mycelium radicis atrovirens complex): Aspects of its conidiogenesis and ecology. Mycotaxon 54: 287–294.

Flory SL, Kleczewski N, Clay K. 2011. Ecological consequences of pathogen accumulation on an invasive grass. Ecosphere 2, 120: 1–12.

Frank J, Crous PW, Groenewald JZ, Oertel B, Hyde KD, et al. 2010. Microcyclospora and Microcyclosporella: novel genera accommodating epiphytic fungi causing sooty blotch on apple. Persoonia 24: 93–105.

Glienke C, Pereira OL, Stringari D, Fabris J, Kava-Cordeiro V, et al. 2011. Endophytic and pathogenic Phyllosticta species, with reference to those associated with Citrus Black Spot. Persoonia 26: 47–56.

Groenewald JZ, Nakashima C, Nishikawa J, Shin H-D, Park JH, et al. In press. Species concepts in Cercospora: spotting the weeds among the roses. Studies in Mycology 75: 115–170.

Hartley AJ, Mattos-Shipley K, Collins CM, Kilaru S, Foster GD, Bailey AM. 2009. Investigating pleuromutilin-producing Clitopilus species and related basidiomycetes. FEMS Microbiology Letters 297: 24–30.

Hausknecht A, Noordeloos ME. 1998. Neue oder seltene arten der Entolomataceae (Agaricales) aus Mittel- und Südeuropa. Österreichische Zeitschrift für Pilzkunde 8: 199–221.

Hoog GS de. 1977. Rhinocladiella and allied genera. Studies in Mycology 15: 1–140.

Hoog GS de, Weenink XO, Gerrits van den Ende AHG. 1999. Taxonomy of the Phialophora verrucosa complex with the description of two new species. Studies in Mycology 43: 107–121.

Hyde KD, Frölich J, Taylor JE. 1998. Fungi from palms XXXVI. Sydowia 50: 21–79.

Kang JC, Crous PW, Old KM, Dudzinski MJ. 2001. Non-conspecificity of Cylindrocladium quinqueseptatum and Calonectria quinqueseptata based on beta-tubulin gene phylogeny and morphology. Canadian Journal of Botany 79: 1241–1247.

Kang JC, Hyde KD, Kong RYC. 1999. Studies on the Amphisphaeriales 1. The Clypeosphaeriaceae. Mycoscience 40: 151–164.

Kang JC, Kong RYC, Hyde KD. 1998. Studies on the Amphisphaeriales 1. Amphisphaeriaceae (sensu stricto) and its phylogenetic relationships inferred from 5.8SrDNA and ITS2 sequences. Fungal Diversity 1: 147–157.

Kleczewski NM, Flory SL. 2010. Leaf blight disease of the invasive grass Microstegium vimineum caused by a Bipolaris sp. Plant Disease 94: 807–811.

Kleczewski NM, Flory SL, Clay K. 2012. Variation in pathogenicity and host range of Bipolaris sp. causing leaf blight disease on the invasive grass Microstegium vimineum. Weed Science 60: 486–493.

Kobayashi T. 2007. Index of fungi inhabiting woody plants in Japan. Host, distribution and literature. Zenkoku-Noson-Kyoiku Kyokai Publishing Co., Ltd., Japan.

Kornerup A, Wanscher JH. 1978. Methuen handbook of colour. Eyre Methuen Ltd., UK.

Lombard L, Crous PW, Wingfield BD, Wingfield MJ. 2010a. Species concepts in Calonectria (Cylindrocladium). Studies in Mycology 66: 1–14.

Lombard L, Crous PW, Wingfield BD, Wingfield MJ. 2010b. Phylogeny and systematics of the genus Calonectria. Studies in Mycology 66: 31–69.

Lombard L, Zhou XD, Crous PW, Wingfield BD, Wingfield MJ. 2010c. Calonectria species associated with cutting rot of Eucalyptus. Persoonia 24: 1–11.

Manamgoda DS, Cai L, McKenzie EHC, Crous PW, Madrid H, et al. 2012. A phylogenetic and taxonomic re-evaluation of the Bipolaris – Cochliobolus – Curvularia complex. Fungal Diversity 56: 131–144.

Marvanová L, Pascoal C, Cássio F. 2003. New and rare hyphomycetes from streams of Northwest Portugal. Part I. Cryptogamie Mycologie 24: 339–358.

Noordeloos ME, Gates GM. 2012. The Entolomataceae of Tasmania. Fungal Diversity Research Series, vol. 22.

Overholts L. 1943. Mycological notes for 1939–40. Mycologia 35: 243–254.

Park D. 1972. On the ecology of heterotrophic micro-organisms in freshwater. Transactions of the British Mycological Society 58: 291–299.

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

Pereira JM, Barreto RW, Ellison AC, Maffia LA. 2003. Corynespora casiicola f. sp. lantanae: a potential biocontrol agent from Brazil for Lantana camara. Biological Control 26: 21–31.

Pisetta M, Montecchio L, Longa CMO, Salvadori C, Zottele F, Maresi G. 2012. Green alder decline in the Italian Alps. Forest Ecology and Management 281: 75–83.

Quaedvlieg W, Kema GHJ, Groenewald JZ, Verkley GJM, Seifbarghi S, et al. 2011. Zymoseptoria gen. nov.: a new genus to accommodate Septoria-like species occurring on graminicolous hosts. Persoonia 26: 57–69.

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

Roldán A, Puig MA. 1992. Hifomycetos acuáticos en la cuenca del río Esva (Asturias, norte de Espana). Anales del Real Jardín Botánico de Madrid 17: 3–11.

Ronquist F, Teslenko M, Mark P, Ayres D, Darling A, Hohna S, Larget B, Liu L, Suchard M, Huelsenbeck J. 2012. MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542.

Rossman AY, Aime MC, Farr DF, Castlebury LA, Peterson KR, Leahy R. 2004. The coelomycetous genera Chaetomella and Pilidium represent a newly discovered lineage of inoperculate discomycetes. Mycological Progress 4: 275–290.

Saccardo PA. 1882. Sylloge fungorum omnium hucusque cognitorum I. Patavii, Italy.

Seifert KA. 1985. A monograph of Stilbella and some allied hyphomycetes. Studies in Mycology 27: 1–235.

Seifert KA, Nickerson NL, Corlett M, Jackson ED, Lois-Seize G, Davies RJ. 2004. Devriesia, a new hyphomycete genus to accommodate heat-resistant, cladosporium-like fungi. Canadian Journal of Botany 82: 914–926.

Shimizu K, Tanaka C, Peng Y-L, Tsuda M. 1998. Phylogeny of Bipolaris inferred from nucleotide sequences of Brn1, a reductase gene involved in melanin biosynthesis. Journal of General and Applied Microbiology 44: 251–258.

Shivas RG, Alcorn JL. 1996. A checklist of plant pathogenic and other microfungi in the rainforests of the wet tropics of northern Queensland. Australasian Plant Pathology 25: 158–173.

Sivanesan A. 1987. Graminicolous species of Bipolaris, Curvularia, Drechslera, Exserohilum and their teleomorphs. Mycological Papers 158: 1–261.

Sprague R. 1950. Diseases of cereals and grasses in North America. Ronald Press Co., New York, USA.

Stukenbrock EH, Quaedvlieg W, Javan-Nikhah M, Zala M, Crous PW, McDonald BA. 2012. Zymoseptoria ardabiliae and Z. pseudotritici, two progenitor species of the septoria tritici leaf blotch fungus Z. tritici (synonym: Mycosphaerella graminicola). Mycologia 104: 1397–1407.

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

Swofford DL. 2003. PAUP* 4.0b10. Phylogenetic Analysis Using Parsimony (*and other methods). Version 4. Sinauer Associates, Sunderland, MA, USA.

Tomlinson PB. 2006. The uniqueness of palms. Botanical Journal of the Linnean Society 151: 5–14.

Vizzini A, Musumeci E, Ercole E, Contu M. 2011. Clitopilus chrischonensis sp. nov. (Agaricales, Entolomataceae), a striking new fungal species from Switzerland. Nova Hedwigia 92: 425–434.

Yang ZL. 2007. Clitopilus amygdaliformis, a new species from tropical China. Mycotaxon 100: 241–246.

Zhang R, Yang HL, Sun GY, Li HY, Zhuang JL, Zhai XR, Gleason ML. 2009. Strelitziana mali, a new species causing sooty blotch on apple fruit. Mycotaxon 110: 477–485.

Zwickl D. 2006. Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD thesis, The University of Texas at Austin.