Multiple gene genealogies and phenotypic characters differentiate several novel species of *Mycosphaerella* and related anamorphs on banana

M. Arzanlou¹,², J.Z. Groenewald¹, R.A. Fullerton³, E.C.A. Abeln⁴, J. Carlier⁵, M.-F. Zapater⁵, I.W. Buddenhagen⁶, A. Viljoen⁷, P.W. Crous¹,²

Abstract  Three species of *Mycosphaerella*, namely *M. eumusae*, *M. fijiensis*, and *M. musicola* are involved in the Sigatoka disease complex of bananas. Besides these three primary pathogens, several additional species of *Mycosphaerella* or their anamorphs have been described from *Musa*. However, very little is known about these taxa, and for the majority of these species no culture or DNA is available for study. In the present study, we collected a global set of *Mycosphaerella* strains from banana, and compared them by means of morphology and a multi-gene nucleotide sequence data set. The phylogeny inferred from the ITS region and the combined data set containing partial gene sequences of the actin gene, the small subunit mitochondrial ribosomal DNA and the histone H3 gene revealed a rich diversity of *Mycosphaerella* species on *Musa*. Integration of morphological and molecular data sets confirmed more than 20 species of *Mycosphaerella* (incl. anamorphs) to occur on banana. This study reconfirmed the previously described presence of *Cercospora apiorum*, *M. citri* and *M. thailandica*, and also identified *Mycosphaerella communis*, *M. lateralis* and *Passalora loranthi* on this host. Moreover, eight new species identified from *Musa* are described, namely *Dissoconium musae*, *Mycosphaerella mozambica*, *Pseudocercospora assamensis*, *P. indonesiana*, *P. longispora*, *Stenella musae*, *S. musicola*, and *S. queenslandica*.

**INTRODUCTION**

The genus *Mycosphaerella* is phylogenetically heterogeneous (Crous et al. 2007a), contains more than 3000 names (Aptroot 2006), and has been linked to more than 30 well-known anamorphic genera (Crous et al. 2006a, b, 2007a, b, Arzanlou et al. 2007a). Species of *Mycosphaerella* inhabit different ecological niches as saprobes, plant pathogens or endophytes (Farr et al. 1995, Verkley & Starink-Willemsen 2004, Crous et al. 2004b, 2006a, 2007a, b), and have a worldwide distribution from tropical and subtropical to warm and cool regions (Crous 1998, Crous et al. 2000, 2001). Plant-pathogenic species of *Mycosphaerella* are among the most common and destructive plant pathogens occurring on a wide range of hosts including trees, herbaceous plants, and plantation crops. The invasion of leaf and stem tissue and concomitant distortion of the host plant physiology cause considerable economic losses (Park et al. 2000, Goodwin et al. 2001, Maxwell et al. 2005, Cortinas et al. 2006, Crous et al. 2006a, b, Hunter et al. 2006).

The Sigatoka disease complex, which is the most serious and economically important leaf spot disease of banana, is attributed to species of *Mycosphaerella*. *Mycosphaerella muscula* (anamorph *Pseudocercospora musae*) which causes (yellow) Sigatoka disease, *M. fijiensis* (anamorph *P. fijiensis*) which causes the black Sigatoka disease, and *M. eumusae* (anamorph *P. eumusae*), which causes eumusae leaf spot disease (reviewed in Jones 2000, 2003, Crous & Mourichon 2002) are the major constituents of the Sigatoka disease complex. The disease reduces the photosynthetic capacity of the plant as a consequence of necrotic leaf lesions, and induces physiological alterations of the plant, resulting in reduced crop yield and fruit quality. All three species emerged on bananas during the last century and became major constraints to commercial production worldwide. The chronology of disease records around the world and genetic structure of pathogen population suggests that South-East Asia, where the host genus *Musa* is indigenous, is the centre of origin for all three fungal species (Mourichon & Fullerton 1990, Carlier et al. 1996, Hayden et al. 2003, Rivas et al. 2004).

Yellow Sigatoka disease was first reported on banana in Java in 1902. The disease spread rapidly to all banana-growing regions during the following 20 years, and has since reached the limits of its distribution worldwide (reviewed in Jones 2000, 2003). The fungus responsible for the disease was described as *Cercospora musae*. In 1941 Leach established the connection between *C. musae* and its teleomorph, *Mycosphaerella*...
Table 1  Isolates of Mycosphaerella or its anamorphs used for DNA analysis and morphological studies.

<table>
<thead>
<tr>
<th>Species</th>
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<th>Source</th>
<th>Origin</th>
<th>GenBank numbers (ITS, ACT, HIS, mtSSU)</th>
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The identity and distribution of the various *Mycosphaerella* species associated with leaf spots of banana are not yet fully understood, which is mainly due to the difficulties experienced by scientists who have to identify them by conventional methods and without specialist taxonomic support. Furthermore, because these species are morphologically highly similar and frequently co-occur on the same lesion, pathogen recognition and subsequent disease management have proven to be rather difficult. To enable the development of specific molecular-based diagnostic tools for pathogen recognition, all related species present on the same host have to be considered. Recently, Arzanlou et al. (2007a) developed a highly sensitive set of Taqman probes to distinguish *M. fijiensis* from *M. musicola* and *M. eumusae* in leaf material. Little attention has been given to date, however, to other species of *Mycosphaerella* that occur on *Musa* spp. Because several *Mycosphaerella* species can co-occur in the same lesion (Crous 1998), it is quite possible that there may be other species of *Mycosphaerella* associated with the Sigatoka disease complex. The aim of the present study was, therefore, to employ a multi-gene DNA sequence typing approach on a global set of *Mycosphaerella* isolates to distinguish the various species occurring on banana. To this end morphological and cultural growth data were integrated with DNA sequence data from the internal transcribed spacer region of the rDNA operon, and partial actin, histone H3, and small subunit mitochondrial ribosomal DNA gene sequences.
MATERIALS AND METHODS

Isolates

Isolates (Table 1) were obtained by isolation from infected symptomatic banana leaves, or supplied as pure cultures by the following departments and institutes: The Horticulture and Food Research Institute of New Zealand, Auckland, New Zealand; Centre de coopération internationale en recherche agronomique pour le développement (CIIRAD, Montpellier, France); University of Florida, Tropical Research & Education Centre (USA); Forestry and Agricultural Biotechnology Institute (FABI, Pretoria, South Africa). Isolates were recovered from infected banana leaves as single ascospores or conidia. Germinating spores were examined 24 h after germination on 2 % malt extract agar (MEA, Sigma-Aldrich Chemie, Zwijndrecht, The Netherlands) plates under a stereomicroscope, and single-sporo cultures were established on fresh MEA plates following the protocol of Crous (1998).

DNA phylogeny

Genomic DNA was isolated from fungal mycelia grown on MEA, using the FastDNA kit (BIO101, Carlsbad, CA, USA) according to the manufacturer’s protocol. The primers ITS1 and ITS4 (White et al. 1990) were used to amplify part of the internal transcribed spacer region (ITS) of the nuclear ribosomal RNA operon, including the 3’ end of the 18S rRNA gene, the first ITS region, the 5.8S rRNA gene, the second ITS region, and the 5’ end of the 28S rRNA gene. A part of the actin gene (ACT) was amplified with primers ACT-512F and ACT-783R (Carbone & Kohn 1999), a part of the small subunit mitochondrial ribosomal DNA (mtSSU) with primers MNS1 and MNS2 (Li et al. 1994), and a part of the histone H3 (HIS) gene with primers CYLH3F and CYLH3R (Crous et al. 2004b). Amplification reactions were performed with each primer set in a total reaction volume of 25 µl, which was composed of 1 × PCR Buffer (Applied Biosystems, Foster City, USA), variable MgCl₂ concentrations, 60 µM dNTPs, 0.2 µM of each forward and reverse primer, 1.5 U of Taq DNA polymerase (Roche Diagnostics, Indianapolis, USA) and 1–10 ng of genomic DNA. PCR cycle conditions were 5 min of 95 °C, followed by 36 cycles of 94 °C for 30 s, 55 °C for 30 s, 72 °C for 60 s, and a final elongation at 72 °C for 7 min. Amplicons were sequenced using both PCR primers with a DYEnamic ET Terminator Cycle Sequencing kit (Amersham Biosciences, Roosendaal, the Netherlands) according to the manufacturer’s recommendations, and sequences were analysed on an ABI Prism 3700 DNA Sequencer (Perkin-Elmer, Norwalk, Foster City, CA).

The resulting nucleotide sequences were analysed and automatically aligned using BioNumerics v. 4.5 (Applied Maths, Kortrijk, Belgium) followed by manual improvement by eye where necessary. Phylogenetic analyses were performed with PAUP (Phylogenetic Analysis Using Parsimony) v. 4.0b10 (Swofford 2003), using the neighbour-joining algorithm with the uncorrected (‘p’), the Kimura 2-parameter and the HKY85 substitution models. Alignment gaps longer than 10 bases were coded as single events for the phylogenetic analyses; the remaining gaps were treated as missing data. Any encountered ties were randomly broken. Phylogenetic relationships were also inferred with the parsimony algorithm using the heuristic search option with simple (ITS alignment) or 100 random taxa additions (combined alignment) and tree bisection and reconstruction (TBR) as the branch-swapping algorithm; alignment gaps were treated as missing (combined alignment) or as a fifth character state (ITS alignment) and all characters were unordered and of equal weight. Branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. Other measures calculated included tree length, consistency index, retention index and rescaled consistency index (TL, CI, RI and RC, respectively). The robustness of the obtained trees was evaluated by 10 000 000 fast stepwise (ITS alignment) or 1000 bootstrap heuristic bootstrap replications (combined alignment). Sequences were deposited in GenBank (Table 1) and the alignments in TreeBASE (www.treebase.org).

RESULTS

DNA phylogeny

Two alignments of DNA sequences were subjected to phylogenetic analyses. The first alignment consisted of ITS sequences generated in this study as well as sequences obtained from the NCBI GenBank nucleotide sequence database. The ITS alignment consisted of a total number of 113 sequences (including one outgroup); 508 characters including alignment gaps were subjected to the analyses. Of these characters, 224 were parsimony-informative, 42 variable and parsimony-uninformative, and 242 were constant. Trees supporting the same clades were obtained irrespective of the analysis method used. The parsimony analysis yielded 11 780 equally most parsimonious trees that mainly differed in the order of taxa at the terminal nodes; one of the trees is presented in Fig. 1 (TL = 881 steps; CI = 0.569; RI = 0.934; RC = 0.532). The sequence data in the second alignment were analysed as one combined set consisting of 1648 characters (incl. alignment gaps) (number of included characters: ITS: 509, ACT: 188, HIS: 375; mtSSU: 576). This second alignment included 54 sequences (including the outgroup) and of the 1648 characters, 517 were parsimony-informative, 93 were variable and
parsimony-uninformative, and 1038 were constant. Trees supporting the same clades were obtained irrespective of the analysis method used. The parsimony analysis yielded eight equally most parsimonious trees that mainly differed in the order of taxa at the terminal nodes; one of the trees is presented in Fig. 2 (TL = 1513 steps; CI = 0.654; RI = 0.901; RC = 0.589). Similar to the results obtained for the ITS alignment, the same clades were found with the combined alignment. The ACT and HIS data were found to be more variable within species than the ITS and mtSSU data (data not shown for individual loci, variation within clades in Fig. 2). The phylogenetic results obtained are discussed where applicable in the descriptive notes below.

Taxonomy

The results of this study showed a rich diversity of Mycosphaerella spp. on Musa. Phylogenetic analyses revealed that more than 20 species of Mycosphaerella or its anamorphs occur on banana, including species known from hosts other than banana, namely Cercospora asii, Mycosphaerella citri, M. communal, M. lateralis, M. thailandica, and Passalora ioranthi (Fig. 1). Furthermore, eight species proved to be morphologically and phylogenetically distinct from the species presently known from banana. These new species are described below.

Fig. 1 One of 11 780 equally most parsimonious trees obtained from a heuristic search with simple taxon additions of the ITS sequence alignment. The scale bar shows 10 changes, and bootstrap support values (65% and higher) from 10 000 000 fast stepwise replicates are shown at the nodes. Thickened lines indicate the strict consensus branches. The tree was rooted to sequences of Davidiella tassiana strain CPC 11600 (GenBank accession number DQ228900). M. = Mycosphaerella and P. = Pseudocercospora.
Cercospora apii Fresen., Beitr. Mykol. 3: 91. 1863


Notes — In their treatment of the genus Cercospora, Crous & Braun (2003) considered C. hayi to be a synonym of the older name, Cercospora apii, which is known to have a wide host range. Based on a comparison of DNA sequence data with the ex-type strain of C. apii (GenBank AY840519; Groenewald et al. 2006), this synonymy appears to be correct.

Dissoconium musae Arzanlou & Crous, sp. nov. — MycoBank MB505972; Fig. 3, 4

Dissoconium commun simile, sed coloniis in vitro tarde crescentibus (usque ad 10 mm diam post 30 dies ad 24 °C in agarō maltōso).

Etymology. Named after its host plant, Musa.

In vitro on MEA: Mycelium submerged and superficial; submerged hyphae hyaline to subhyaline, thin-walled, smooth, forming a dense network with numerous anastomoses, 2–3 µm wide; aerial hyphae subhyaline, smooth, 2–3 µm wide.

Fig. 2 One of eight equally most parsimonious trees obtained from a heuristic search with 100 random taxon additions of the combined (ITS, ACT, HIS, mtSSU) sequence alignment. The scale bar shows 10 changes, and bootstrap support values (65 % and higher) from 1000 replicates are shown at the nodes. Thickened lines indicate the strict consensus branches. The tree was rooted to sequences of Davidiella tassiana strain CPC 11600 (GenBank accession number DQ269800, DQ269867, EF679665, EUS14455, respectively). M. = Mycosphaerella.
**Conidiophores** arising orthotropically from vegetative hyphae, often reduced to conidiogenous cells and continuous with supporting hyphae, thin-walled, smooth, pale brown, unbranched, straight, subulate to lageniform, tapering towards the apex, (10–)19–25(–53) × (2.5–)3–5 µm. **Conidiogenous cells** terminal, proliferating sympodially (but appearing as annellides under the light microscope), giving rise to a short conidium-bearing rachis, loci somewhat darkened and thickened. **Conidia** forming in sympodial order in pairs on a conidiogenous cell; the primary conidium is 2-celled, while the secondary conidium is aseptate; primary conidia pale olivaceous-brown, thin-walled, smooth, ellipsoidal to obclavate, 1-septate, apex obtuse, base obconically-truncate, (11–)22–26(–35) × (3–)4–5 µm, hilum unthickened; about 1 µm diam. Secondary conidia 1-celled, pale olivaceous-brown, pyriform to turbinate, 4–5 × 3–4 µm, base truncate, flat, unthickened, about 0.5 µm diam. Both conidial

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**Fig. 3** *Dissoconium musae* (CBS 122453). a–d. Conidiophores with sympodially proliferating conidiogenous cells, which produce primary and secondary conidia in pairs; e–g. primary conidia with truncate base; h–l. anastomoses between hyphae, primary and secondary conidia and primary conidia. — Scale bar = 10 µm.
types are discharged forcibly in pairs and then anastomose on
the agar surface. Anastomosis between primary conidia occurs
as well and primary conidia may show multiple anastomoses.
Primary conidia germinate from both ends and produce sev-
eral conidiogenous cells and conidia (microcyclic conidiation).
Germination of secondary conidia was not observed.

Cultural characteristics — Colonies on MEA slow-growing,
reaching 10 mm diam after 30 d at 24 °C, erumpent, unevenly
folded, with sparse aerial mycelium, colonies with granulate
margin; surface hazel to isabelline in centre, and vinaceous-buff
in outer region; brown-vinaceous in reverse. Colonies on OA
reaching 25 mm diam after 30 d at 24 °C, effuse, with moder-
ate aerial mycelium, later become powdery in centre, surface
hazel; olivaceous in reverse.

Specimen examined. INDIA, Tamil Nadu, Tiruchirapalli, Musa cv. Nendran
(Plantain) AAB, 2005, I. Buddenhagen, holotype CBS H-20036, culture ex-
type X1021 = CBS 122453.

Notes — The genus **Dissoconium** is characterised by pro-
ducing pairs of forcibly discharged primary and secondary
conidia on sympodially proliferating conidiogenous cells.
Sympodial proliferation of the conidiogenous cells gives rise to
a conidium-bearing rachis, which resembles that encountered
in the genus **Ramichloridium**. The recent revision of the genus
**Ramichloridium** and allied genera (Arzanlou et al. 2007b)
revealed that *R. apiculatum*, the type species of the genus,
is phylogenetically close to the species in the genus **Dissocon-
imus**. However, **Dissoconium** is morphologically distinct
from **Ramichloridium** by producing two types of forcibly discharged
conidia. So far, seven species of **Dissoconium** have been de-
scribed from different substrates (de Hoog et al. 1991, Jackson
et al. 2004). **Dissoconium musae** is phylogenetically distinct
from the other species of this genus, but morphologically similar
to *D. commune* and *D. dekkeri* (teleomorph: **Mycosphaerella
lateralis**), from which it differs based on its slower growth rate
in culture.

**Mycosphaerella eumusae** Crous & Mour., Sydowia 54: 36.
2002

*Anamorph. Pseudocercospora eumusae* Crous & Mour., Sydowia 54: 36.
2002.

*Specimen examined. RéUNION, on leaves of Musa sp., 2001, J. Cardier,
PREM 57314 (holotype of teleomorph), PREM 57315 (holotype of anamorph),
cultures ex-type (CIRAD 1156, 1157 = CPC 4579, 4580 = CBS
114824, CBS 114825).

Notes — Based on the DNA sequence data obtained in this
study (Fig. 2), it appears that *M. eumusae* is heterogeneous
as presently circumscribed. Further studies would be required
to determine if the phylogenetic variation also correlates with
differences in morphology.


1979.


≡ *Paracercospora fijiensis* var. *difformis* (J.L. Mulder & R.H. Stover)

*Specimens examined. CAMERON, on leaves of Musa sp., D.S. Meredith & J.S.
Lawrence, holotype IMI 136696. – CAMERON, date and collector unknown,
epitype designated here CBS H-20037, culture ex-epitype CIRAD 86 = CBS
120258.

Note — The specimen and associated strain designated
here as epitype, represent the strain that was selected by the
**Mycosphaerella** consortium to obtain the full genome sequence
of *M. fijiensis* (www.jgi.doe.gov/sequencing/why/CSP2006/
mycosphaerella.html).

**Mycosphaerella mozambica** Arzanlou & Crous, sp. nov.
— MycoBank MB505973; Fig. 5, 6

*Anamorph. Ramichloridium*-like.

Ascosporae rectae vel curvatae, fusideo-ellipsoidae utrinque obtuse ubusae, ad
septum medianum vix constrictae, (9–)10–11(–12) × 3–3.5(–4) µm.

*Etymology.* Named after the country of origin, Mozambique.

In vivo: *Leaf spots* amphigenous, irregular to subcircular, 1–7
mm diam, grey to pale brown on adaxial surface, grey on abaxial
surface, with dark brown margins. *Ascomata* amphigenous,
intermingled among those of *M. musicola*, dark brown, subepi-
dermal, becoming erumpent, globose, 70–90 µm diam; wall
consisting of 2–3 layers of medium brown textura angularis.
Asci aparaphysate, fasciculate, bitunicate, subsessile, obovoid
to broadly ellipsoid, straight to slightly curved, 8-spored, 28–35
× 7–9 µm. Ascosporae bi- to tri-seriate, overlapping, hyaline,
non-guttulate, thin-walled, straight to curved, fusoid-ellipsoidal
with obtuse ends, widest in middle of apical cell, medianly
1-septate, not to slightly constricted at the septum, tapering
M. Arzanlou et al.: Mycosphaerella

Fig. 5 Mycosphaerella mozambica (CBS 122464). a. Verruculose hyphae; b–e. unbranched or loosely branched conidiophores with sympodially proliferating conidiogenous cells; f–g. sympodially proliferating conidiogenous cells give rise to short conidium-bearing rachis; h. conidia with truncate base. — Scale bars = 10 µm.

Fig. 6 Mycosphaerella mozambica (CBS 122464). a. Ascus with biseriate ascospores; b. ascospore germination pattern; c. conidiophores with sympodially proliferating conidiogenous cells, which give rise to short conidium-bearing rachis; d. conidia. — Scale bar = 10 µm.

towards both ends, but more prominently towards the lower end, (9–)10–11(–12) × 3–3.5(–4) µm; ascospores becoming distorted upon germination after 24 h on MEA, becoming constricted at the septum, 6–7 µm wide with irregular, wavy germ tubes, growing 90 ° to the long axis, and not arising from the polar ends of the spore.

In vitro on MEA: Mycelium submerged and superficial; submerged hyphae hyaline to subhyaline, thin-walled, smooth or slightly rough, 2–4 µm wide; aerial hyphae pale olivaceous, smooth or finely verruculose. Conidiophores arising from unbranched or loosely branched hyphae, occasionally reduced to conidiogenous cells or integrated, hyaline, subcylindrical, 2–2.5 µm wide and up to 35 µm long. Conidiogenous cells integrated, terminal, polyblastic, sympodial, loci aggregated, flat, not protuberant (not denticle-like), unthickened, but somewhat darkened. Conidia solitary, obovoid, ellipsoidal, obclavate 0(–1)-septate, hyaline, thin-walled, smooth, (5–)9–12(–22) × 2–2.5(–3) µm; hilum truncate, flat, broad, unthickened, slightly darkened, about 1 µm diam. Although rarely observed, older conidia can become elongated, obclavate, and up to 4-septate.

Cultural characteristics — Colonies on MEA reaching 45 mm diam after 30 d at 24 °C; erumpent, folded, with moderate velvety to hairy aerial mycelium, with smooth, entire margins; surface pale vinaceous to mouse-grey; brown-vinaceous in reverse. Colonies on OA reaching 51 mm diam after 30 d at 24 °C; effuse, with sparse aerial mycelium and entire edge; surface vinaceous-buff to vinaceous, and pale vinaceous in reverse.

Notes — Sympodially proliferating conidiogenous cells are somewhat confusing with other morphologically similar genera such as *Ramichloridium* and *Veronaea*. The type species and most of the taxa referred to these genera are dematiaceous. The scars in *Ramichloridium* are subhyaline and slightly prominent. *Veronaea* has pigmented, truncate, flat loci and conidia with truncate bases. A recent revision of *Ramichloridium* and allied genera (Arzanlou et al. 2007b) revealed the type species of *Ramichloridium*, *R. apiculatum*, to be allied to the *Dissoconium* clade in Capnodiales, while the type species of *Veronaea*, *V. botryosa*, resides in Chaetothyriales. *Mycosphaerella mozambica* appeared to occur quite commonly on the banana samples investigated from Mozambique. Based on DNA sequence data, the ex-type strain appears similar to an isolate collected in Australia (CBS 121391 = X884). Unfortunately, however, the latter strain was sterile, so this could not be confirmed based on morphology.

**Mycosphaerella musae** (Speg.) Syd. & P. Syd., Philipp. J. Sci., C 8: 482. 1913


*Specimen examined.* **Argentina**, Jujuy, Orán, on leaves of *Musa sapientum*, Mar. 1905, holotype LPS, slide ex-type IMI 91165.

Notes — *Mycosphaerella musae* is reported to be the causal organism of *Mycosphaerella* speckle disease. However, as shown in the present study (Fig. 1), several distinct species appear to be able to induce these symptoms. Further collections would thus be required to recollect this species. All cultures examined in the present study were sterile.


*Basionym.* *Mycosphaerella musicola* R. Leach, Trop. Agric. (Trinidad) 18: 92. 1941 (nom. nud.).


*Specimens examined.* **Jamaica**, on leaves of *Musa sapientum*, Jan. 1959, R. Leach, holotype IMI 75804; — **Cuba**, on leaves of *Musa* sp., epitype designated here CBS H-20038, culture ex-epitype IMI 123823 = CBS 116634.

**Pseudocercospora assamensis** Arzanlou & Crous, sp. nov. — MycoBank MB505974; Fig. 7, 8

*Pseudocercosporae musae* similis, sed conidiis longioribus et angustioribus, (30–)59–70(–83) × 2–3 µm.

*Etymology.* Named after the locality of origin, India, Assam.

In vitro on MEA: *Mycelium* submerged and superficial; submerged hyphae smooth, branched, septate, medium brown, 2.5–4 µm wide; aerial hyphae thin-walled, smooth, medium brown. *Conidiophores* solitary, arising from superficial hyphae, medium brown, thin-walled, smooth, unbranched or branched above, 0–1-septate, subcylindrical, straight, up to 20 µm long, 2–3 µm wide. *Conidiogenous cells* integrated, terminal, or conidiophores reduced to conidiogenous cells, subcylindrical, tapering to truncate or bluntly rounded apices, medium brown, smooth, proliferating sympodially; conidial scars inconspicuous. *Conidia* solitary, pale brown, smooth, subcylindrical, with truncate bases and bluntly rounded apices, thin-walled with irregular swellings in older conidia, straight or curved, pluriseptate, (30–)59–70(–83) × 2–3 µm; hilar about 1 µm wide, neither thickened nor darkened-refractive; microcyclic conidiation observed.

Cultural characteristics — Colonies on MEA reaching 47 mm diam after 30 d at 24 °C. Colonies elevated at the centre, with

![Fig 7](image-url) **Pseudocercospora assamensis** (CBS 122467). a. Conidiophore with sympodial and percurrent growth of conidiogenous cell; b–c. conidia. — Scale bar = 10 µm.
abundant aerial mycelium, and entire, smooth margin; surface pale mouse-grey to mouse-grey, olivaceous in reverse. Colonies on OA reaching 35 mm diam after 30 d at 24 °C; effuse, with moderate, velvety aerial mycelium, and entire, smooth margins; surface pale mouse-grey, and iron-grey in reverse.

Specimen examined. India, Assam, Naojan, on leaf of Musa cv. Nanderan (Plantain), 2005, I. Buddenhagen, holotype CBS H-20044, culture ex-type X988 = CBS 122467.

Notes — Based on its characteristic conidial shape and dimensions, *P. assamensis* appears distinct from those species presently known from this host. *Pseudocercospora musae* conidia are shorter and above all wider (10–80 × 2–6 µm; Carlier et al. 2000) than in *P. longispora*. *Pseudocercospora longispora* has much longer and somewhat wider conidia.

*Pseudocercospora indonesiana* Arzanlou & Crous, sp. nov. — MycoBank MB505975; Fig. 9, 10

*Pseudocercosporae longisporae similis, sed conidiis modice brunneis, hyphis tenuitunicatis, modice brunneis, non inflatis et non monilioidibus-muriformibus, colonis in vitro celeriter crescentibus (usque ad 27 mm diam post 30 dies ad 24 °C in agarō maltoso).*

*Etymology.* Named after its country of origin, Indonesia.

In vitro on MEA: *Mycelium* submerged and superficial; submerged hyphae thin-walled, smooth, branched, septate, medium brown, 2.5–4 µm wide; aerial hyphae, thin-walled, smooth, medium brown. *Conidiophores* solitary, arising from superficial hyphae, medium brown, smooth, unbranched, 0–2-septate, subcylindrical, straight, up to 30 µm long, 2–2.5 µm wide. *Conidiogenous cells* integrated, terminal, subcylindrical, tapering to truncate or bluntly rounded apices, medium brown, smooth, proliferating sympodially, frequently reduced to conidiogenous loci; conidial scars inconspicuous. *Conidia* solitary, pale brown, smooth, subcylindrical, bases truncate, apices bluntly rounded, thin-walled, straight or curved, guttulate, 3–7-septate,
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Fig. 10 Pseudocercospora indonesiana (CBS 122473). — Scale bar = 10 µm.

**Pseudocercospora indonesiana** (CBS 122473). — Scale bar = 10 µm.

(40–)78–95(–120) × 2–3 µm; hila unthickened, neither darkened nor refractive.

Cultural characteristics — Colonies on MEA reaching 27 mm diam after 30 d at 24 °C. Colonies low convex, with abundant aerial mycelium, and entire, smooth margin; surface pale mouse-grey to mouse-grey; in reverse dark mouse-grey. Colonies on OA reaching 35 mm diam after 47 d at 24 °C; effuse, with moderate aerial mycelium, and entire, smooth margins; surface pale mouse-grey; in reverse olivaceous-black.

Specimen examined. **Indonesia**, Western Sumatra, Kumango, on leaf of Musa cv. Buai, 2004, I. Buddenhagen, holotype CBS H-20045, culture ex-type X992 = CBS 122473.

Notes — *Pseudocercospora indonesiana* is phylogenetically distinct from the other species of *Pseudocercospora* occurring on *Musa*. Morphologically it has longer conidia than *P. musae* (teleomorph *M. musicola*) and *P. assamensis*, though they are very similar to those of *P. longispora*; it can, however, be distinguished from the latter by having medium brown conidia (those of *P. longispora* being pale brown), and its faster growth rate on MEA and OA.

**Pseudocercospora longispora** Arzanlou & Crous, sp. nov. — MycoBank MB505976; Fig. 11, 12

*Pseudocercosporae musae similis, sed conidiis longioribus, 82–120 × 2.5–4 µm.*

Etymology. Named after its characteristically long conidia.

In vitro on OA: Mycelium submerged and superficial; submerged hyphae smooth, branched, septate, medium brown, thin-walled, 2–3 µm wide; aerial hyphae smooth, medium brown; hyphal cells become thick-walled, swollen, forming dark-brown moniloid, muriform cells, 5–17 × 7–12 µm. Conidiophores solitary, arising from superficial hyphae; conidiophores medium brown, smooth, unbranched or branched above, 0–2-septate, subcylindrical, straight, up to 30 µm long, 2–3 µm wide. Conidiogenous cells integrated, terminal, subcylindrical, tapering to truncate or

Fig. 11 Pseudocercospora longispora (CBS 122469). a–e. Conidia. — Scale bar = 10 µm.
bluntly rounded apices, medium brown, smooth, forming conidia by sympodial proliferation, rarely by means of percurrent proliferation; conidial scars inconspicuous. Conidia solitary, pale brown, thin-walled, smooth, cylindrical to subcylindrical, widest in the middle of conidium, tapering towards the apex, bases truncate, straight, multi-septate, 82–120 × 2.5–4 µm; hila about 1 µm diam, neither thickened nor darkened-refractive.

Cultural characteristics — Colonies reaching 15 mm diam after 30 d at 24 °C. Colonies erumpent, with moderate aerial mycelium, and entire, smooth edges; surface buff to rosy-buff, mouse-grey to dark grey; in reverse dark mouse-grey. Colonies on OA reaching 15 mm diam after 30 d at 24 °C, effuse, with abundant aerial mycelium, and entire, smooth margins; surface pale mouse-grey; in reverse dark mouse-grey.


Notes — *Pseudocercospora longispora* resembles *P. musae* (teleomorph *Mycosphaerella musicola*) in its colony morphology on MEA and OA. However, in *P. musae* conidia are much shorter (10–80 × 2–6 µm; Carlier et al. 2000) than in *P. longispora*.

**Stenella musae** Arzanlou & Crous, sp. nov. — MycoBank MB505977; Fig. 13, 14a

Conidiophora ex hyphis superficialibus oriunda, modice brunnea, tenui-tunicata, verruculosa vel verrucoosa, 0–3-septata, subcylindrica, recta vel geniculata-sinuosa, non ramosa, ad 30 µm longa et 2–2.5 µm lata. Cellulae conidiogenae integratae, terminales, interdum intercalares, modice brunneae, verruculosa, subcylindrice, apicem versus attenuatae, sympodiadis, locis truncatis, subdenticulatis, 1–1.5 µm diam, inspissatis et fuscatis-refringentibus praeditae. Conidia solitaria, dilute brunnea, verruculosa, tenuitunicata, subcylindrica vel obclavata, recta vel curvata, 0–7-septata, (7–)27–40(–70) × 1.5–3 µm, hilo inspissato obscuriore refringente, 1–1.5 µm diam praedita.

Etymology. Named after its host, *Musa*.

In vitro on MEA: *Mycelium* submerged and superficial; submerged hyphae smooth to verrucose, thin-walled, subhyaline to medium brown, 2–3 µm wide, with thin septa; aerial hyphae coarsely verrucose, olivaceous-brown to medium brown, rather
thick-walled, 2–2.5 µm wide, with thin septa. *Conidiophores* arising from superficial hyphae, medium brown, rather thick-walled, finely verruculose to verrucose, 0–3-septate, subcylindrical, straight to geniculate-sinuous, unbranched, up to 30 µm long, 2–2.5 µm wide. *Conidiogenous cells* integrated, terminal, sometimes intercalary, unbranched, medium brown, finely verruculose, subcylindrical, tapering towards flat-tipped, subdenticulate apical loci, 1–1.5 µm diam, proliferating sympodially; loci thickened, darkened, refractive. *Conidia* solitary, thin-walled, pale brown, finely verrucose, subcylindrical to obclavate, with subobtuse apex, and long obconically subtruncate to obconically subtruncate base, straight to curved, 0–7-septate, (7–)27–40(–70) × 1.5–3 µm; hilum thickened, darkened, refractive, 1–1.5 µm diam.

Cultural characteristics — Colonies on MEA reaching 30 mm diam after 30 d at 24 °C. Colonies erumpent, unevenly folded, with moderate aerial mycelium, and entire, smooth margin; surface pale mouse-grey to mouse-grey; in reverse dark mouse-grey. Colonies on OA reaching 48 mm diam after 30 d at 24 °C; effuse, with moderate aerial mycelium, and entire margins; surface pale mouse-grey to mouse-grey, and dark mouse-grey in reverse.


Notes — Stover (1994) discussed and illustrated a *Stenella* sp. from banana, and named it *Cercospora non-virulentum*, which was considered as a prevalent co-inhabitant with Black Leaf Streak and Sigatoka. *Mycosphaerella musae* is the causal agent of Mycosphaerella Speckle disease of banana (Carlier et al. 2000). A comparison made between strains isolated from Mycosphaerella Speckle disease symptoms (presumed *M. musae*), and *Cercospora non-virulentum* isolates in culture, suggested that the two species are identical, both producing brown, verruculose conidia with thickened scars on agar medium (Stover 1994). An inoculation assay carried out by using a mixture of conidia and mycelium of *Cercospora non-virulentum* on banana ‘Cavendish Valery’ leaves resulted in leaf spot symptoms after 70 d incubation, resembling those obtained using ascospores derived from *M. musae* strains.

Because *Cercospora non-virulentum* was never validly published, it is difficult to make a comparison with *Stenella musae*. However, based on the description provided by Stover (1994), *S. musae* has shorter conidia (7–70 × 1.5–3 µm) than *Cercospora non-virulentum* (55–200 × 2.6–3.2 µm).

A further complication lies in the fact that several phylogenetically distinct species of *Mycosphaerella* have in the past been isolated from Mycosphaerella Speckle disease symptoms of banana. All the *M. musae* isolates examined in this study were sterile, and thus could not be used for morphological comparison. *Mycosphaerella musae* was originally described from *Musa sapientum* leaves collected in Argentina. An examination of the type (IMI 91165) shows ascospores to be straight to slightly curved, fusoid-ellipsoidal with narrowly obtuse ends, being widest at the median septum (Fig. 15). Further collections would thus be required to clarify the identity of this species.
**Stenella musicola** Arzanlou & Crous, *sp. nov.* — MycoBank MB505978; Fig. 14c, 16

*Stenellae musae* similis, sed conidiophoris leviter longioribus et latioribus, (18–)30–36(–45) × (2–)2.5–3(–4) µm, conidiis saepe longioribus, (7–)37–57(–120) × 2–4 µm. A *Stenellae queenslandica* conidiophoris 0–2-septatis et conidiis 2–4 µm latis differt.

**Etymology.** Named after its host, *Musa*.

In vitro on MEA: Mycelium submerged and superficial; submerged hyphae smooth to verrucose, thin-walled, subhyaline to olivaceous brown, 2–3 µm wide, with thin septa; aerial hyphae coarsely verrucose, olivaceous-brown, rather thick-

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![Fig. 16 Stenella musicola (CBS 122479). a–e. Conidiophores with sympodially proliferating conidiogenous cells and darkened, thickened loci; f–g. hyphal anastomoses; h–i. conidia. — Scale bar = 10 µm.](image)
walled, 2–2.5 µm wide, with thin septa. *Conidiophores* arising from superficial hyphae, pale brown, rather thick-walled, finely verruculose, 0–2-septate, occasionally continuous with supporting hyphae, subcylindrical, straight to geniculate-sinuous, unbranched, (18–)30–36(–45) × (2–)2.5–3(–4) µm. *Conidiogenous cells* integrated, terminal, sometimes intercalary, unbranched, pale brown, smooth or finely verruculose, cylindrical to subcylindrical, sometimes swollen at the apex, with flat-tipped apical loci, proliferating sympodially; 1–1.5 µm diam, loci thickened, darkened, refractive. *Conidia* solitary, rarely in unbranched chains, medium brown, thin-walled, finely verruculose subcylindrical to obclavate, with subobtuse apex, and long obconically subtruncate to obconically subtruncate base, straight to curved, 0–pluri-septate, (7–)37–57(–120) × 2–4 µm; hilum thickened, darkened, refractive, 0.5–1 µm wide.

*Cultural characteristics* — Colonies on MEA reaching 28 mm diam after 30 d at 24 °C; effuse, slightly raised at the centre, with moderate, velvety to hairy aerial mycelium; folded, with entire smooth margin; surface pale mouse-grey to mouse-grey; in reverse dark mouse-grey. Colonies on OA reaching 39 mm diam after 30 d at 24 °C; effuse, with moderate velvety to hairy aerial mycelium, and entire, smooth margins; surface pale mouse-grey to mouse-grey, and olivaceous in reverse.

Specimen examined. _India_, Tamil Nadu, Tiruchirapally, on leaf of Musa cv. Grand Nain AAA (Cav.), 2005, I. Buddenhagen, holotype CBS H-20046, culture ex-type X1019 = CBS 122479.

Notes — *Stenella musicola* morphologically also resembles _S. citri-grisea_ (teleomorph *Mycosphaerella citri*), which is known from *Citrus* (Pretorius et al. 2003). It differs from the later species, however, based on its conidial dimensions. In _S. muscicola_ conidia range from (7–)37–57(–120) × 2–4 µm, while in _S. citri-grisea_ conidia are longer and narrower, namely 25–200 × 1.5–3 µm. The three new *Stenella* species on *Musa* spp. are morphologically very similar and only gradually differentiated in the size and septation of the conidiophores and conidia.

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**Stenella queenslandica** Arzanlou & Crous, _sp. nov._ — MycoBank MB505979; Fig. 14b, 17

*Stenellae musae* similis, sed conidiis longioribus, 51–83 × 2–2.5 µm. A *Stenella muscicola* conidiophoris 1–4-septatis et conidiis saepe longioribus et angustioribus, 51–83 × 2–2.5 µm, differt.

*Etymology.* Named after Queensland, the state in Australia where this fungus was collected.

In vitro on MEA: *Mycelium* submerged and superficial; submerged hyphae smooth, thin-walled, subhyaline to olivaceous-brown, 2–3 µm wide, with thin septa; aerial hyphae coarsely verruculose, olivaceous-brown, rather thick-walled, 2–2.5 µm wide, with thin septa. *Conidiophores* arising from superficial hyphae, pale brown, thin-walled, finely verruculose, 1–4-septate, occasionally reduced to conidiogenous cells, subcylindrical, straight to geniculate-sinuous, unbranched, up to 40 µm long and 2–3 µm wide. *Conidiogenous cells* integrated, terminal, sometimes intercalary, unbranched, pale brown, smooth or finely verruculose, cylindrical, tapering to a bluntly rounded apex with flat-tipped apical loci that proliferate sympodially; loci thickened, darkened, refractive about 1 µm diam. *Conidia* solitary, medium brown, thin-walled, verruculose, subcylindrical to obclavate, with subobtuse to obtuse apex and long obconically subtruncate to obconically subtruncate base, straight to curved, 0–multi-septate, 51–83 × 2–2.5 µm; hilum thickened, darkened, refractive, 0.5–1 µm wide.

*Cultural characteristics* — Colonies on MEA reaching 24 mm diam after 30 d at 24 °C. Colonies effuse, slightly elevated at the centre with abundant aerial mycelium, and entire, smooth margins; surface mouse-grey to dark mouse-grey; dark mouse-grey in reverse. Colonies on OA reaching 41 mm diam after 30 d at 24 °C, colonies effuse, with moderate aerial mycelium, and entire, smooth margin; surface olivaceous-grey; iron-grey in reverse.

Specimen examined. **Australia**, Queensland, Mount Lewis, Mount Lewis Road, 16° 34’ 47.2” S, 145° 19’ 7” E, 538 m alt., on *Musa banksii* leaf, Aug. 2006, P. W. Crous, W. Gams & B. Summerell, holotype CBS H-20050, culture ex-type CBS 122475.

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**Fig. 17** _Stenella queenslandica_ (CBS 122475). a. Conidiophore with terminal conidiogenous cell; b–d. conidia. — Scale bar = 10 µm.
Notes — The ITS sequence of *Stenella queenslandica* is identical to that of *Mycosphaerella obscuris* (Burgess et al. 2007), a pathogen of *Eucalyptus* known from Vietnam and Indonesia. However, the latter fungus is a species of *Teratosphaeria* with a *Readerella* anamorph (CBS 119973), which appears to be a synonym of *T. suttonii* (Crous & Wingfield 1997, Crous et al. 2007a, b), and the deposited sequences (DQ632676, DQ632677) belong to another species.

**DISCUSSION**

The present study is the first multi-gene DNA phylogenetic study of a global set of *Mycosphaerella* isolates associated with the Sigatoka disease complex of banana. Considering that Sigatoka diseases are the economically most important diseases of banana and the main constraint for banana production worldwide (reviewed in Jones 2000), there was a huge paucity of knowledge relating to the identity of other *Mycosphaerella* species occurring on banana. Even though several species of *Mycosphaerella* have in the past been described from *Musa*, the majority has never been known from *Pandanus*, the majority has never been known from *Musa* (Pont 1960, Stover 1963, 1969, 1977, 1980, 1994, Mulder & Stover 1976, Pons 1987, Crous et al. 2003, Aptroot 2006, Arzanlou et al. 2007a). The integration of DNA analyses and morphology in the present study revealed more than 20 species of *Mycosphaerella* to occur on banana. Five of these species were shown to have wider host ranges than banana only, and we described a further eight new species of *Mycosphaerella* from various *Musa* collections.

The three primary agents of the Sigatoka disease complex, *M. eumusae*, *M. fijiensis*, and *M. musicola* can be distinguished based on their conidial morphology and ascospore germination patterns (reviewed in Jones 2000, Crous & Mourichon 2002). Conidia of *M. fijiensis* are medium brown, and have a characteristic thickening along the basal rim of the hilum, which is absent in *M. musicola* and *M. eumusae*. These two species have medium and pale brown conidia, respectively. Ascospores of *M. fijiensis* and *M. musicola* germinate from both polar ends, do not become distorted (4–5 µm wide), with a germ tube parallel to the long axis of the spore. However, in *M. musicola* a mucoid sheath surrounds the germinating ascospores, and the germ tubes are more irregular in width than in *M. fijiensis*. Ascospores of *M. eumusae* show some distortion upon germination (5–6 µm wide), and frequently germinate by means of 3–4 germ tubes, which grow parallel or lateral to the long axis of the spore (Fig. 18, 19). Thus, all of these species can be identified based on a combination of morphology and cultural characteristics, but proper identification remains problematic to the non-specialist. Hence the DNA barcodes generated in this study, along with the Taqman probes (Arzanlou et al. 2007a) is an alternative method of identification.

Besides the three primary agents of the Sigatoka complex disease, which have *Pseudocercospora* anamorphs, three additional *Pseudocercospora* species were described from *Musa* in the present study. One of these, *Pseudocercospora longispora*, has in the past been confused with *P. musae* (teleomorph *M. musicola*) and has been isolated from similar Sigatoka disease lesions. Although these species can be distinguished based on differences in conidial size and shape, these characters overlap among the various *Pseudocercospora* species, making explicit identification solely possible by means of additional markers such as DNA sequence data (Fig. 2).

Much confusion still surrounds the identity of *M. musae*. According to Stover (1994), *M. musae* is identical to a *Stenella* species called ‘*Cercospora non-virulentum*’. This species was considered as a prevalent co-inhabitant with black Sigatoka and yellow Sigatoka. A comparison made between isolates isolated from *Mycosphaerella* Speckle disease symptoms, revealed several phylogenetically distinct species to be associated with this disease. In the present study we treated four *Stenella* species, three of which proved to be new on banana. None of these three new species fit with the description provided for ‘*Cercospora non-virulentum*’ by Stover (1994), which appears to represent yet another undescribed species of *Stenella*. Further collections would thus be required to resolve the status of ‘*Cercospora non-virulentum*’ and *M. musae*.

Data obtained in the present study revealed three species of *Dissoconium on Musa*, of which one is described as new. The recent revision of the genus *Ramichloridium* and allied genera (Arzanlou et al. 2007b) revealed that *R. apiculatum*, type spe-

![Fig. 18](image-url) a–c. Conidia in *Pseudocercospora eumusae*, *P. fijiensis*, and *P. musae*, respectively; d–f. ascospore germination pattern in *M. eumusae*, *M. fijiensis* and *M. musicola*, respectively. — Scale bar = 10 µm.
cies of Ramichloridium, has phylogenetic affinity with the genus Dissoconium. However, the latter genus is morphologically distinct from Ramichloridium by producing forcibly discharged pairs of primary and secondary conidia. Thus far seven species of Dissoconium have been described from different substrates, and as in the Pseudocercospora species occurring on Musa, identification is best achieved by means of molecular sequence data.

It is interesting to note that up to six species have been reported during the course of the present study as occurring on hosts other than Musa. Although our present data suggest the causal agents of Sigatoka to be highly specific to banana, no information is presently available to elucidate the ecology and possible pathology of the wide host range species, and inoculation studies would now be required to fully resolve their status as foliar pathogens of banana. The possibility exists that some of the species described here as new have been described previously on hosts other than banana. However, none of the sequences presently in GenBank, or in the MycoBank database, match any known comparable species.

From the data presented in this study, it is clear that the Sigatoka disease complex is caused by a multitud of Mycosphaerella species. However, the exact contribution of each of these species to the disease complex remains unclear. The multi-locus DNA sequence data set established in this study can be used to develop species-specific molecular detection tools, which is a good alternative for traditional diagnostics. These tools can subsequently be implemented in disease management programmes.

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