

Botryosphaeriaceae occurring on native *Syzygium cordatum* in South Africa and their potential threat to *Eucalyptus*

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Abstract

Eight species of the Botryosphaeriaceae (canker and dieback pathogens) were identified on native *Syzygium cordatum* in South Africa, based on anamorph morphology, ITS rDNA sequence data and PCR-RFLP analysis. The species identified were *Neofusicoccum parvum*, *N. ribis*, *N. luteum*, *N. australe*, *N. mangiferae*, *Botryosphaeria dothidea*, *Lasiodiplodia gonubiensis* and *L. theobromae*. Their pathogenicity on *S. cordatum* seedlings and a *Eucalyptus grandis* × *camaldulensis* clone was determined in glasshouse inoculation trials. Isolates of all identified species, except one of *N. mangiferae*, were more pathogenic on the *Eucalyptus* clone than on *S. cordatum*. Some of the species that cross-infected these hosts, such as *N. ribis*, *N. parvum* and *L. theobromae*, were amongst the most pathogenic on the *Eucalyptus* clone, while *B. dothidea* and *L. gonubiensis* were the least pathogenic. Results of this study illustrate that species of the

Botryosphaeriaceae from native hosts could pose a threat to introduced *Eucalyptus* spp., and *vice versa*.

Introduction

The Botryosphaeriaceae (Dothideales) is comprised of fungal species that have a wide geographic distribution and extensive host range, including *Eucalyptus* spp. (Myrtaceae) (von Arx & Müller, 1954; Crous *et al.*, 2006). These fungi are latent and opportunistic pathogens that occur as endophytes in symptomless plant tissues and they can cause rapid disease development when plants are exposed to unsuitable environmental conditions such as drought, freezing, hot or cold winds, hail wounds or damage caused by insects or other pathogens (Fisher *et al.*, 1993; Smith *et al.*, 1996). Species of the Botryosphaeriaceae cause a wide variety of symptoms on all parts of *Eucalyptus* trees and on trees of all ages, but are mostly associated with cankers and dieback followed by extensive production of kino, a dark-red tree sap, and in severe cases mortality of trees (Smith *et al.*, 1994, 1996; Old & Davison, 2000).

The Myrtaceae is a predominantly southern hemisphere angiosperm family that accommodates more than 3000 species, largely distributed in the tropical and temperate regions of Australasia, as well as Central and South America (Johnson & Briggs, 1981). Species of the Myrtaceae also form an integral part of the Southern African indigenous flora (Palgrave, 1977). In this context, the most widespread myrtaceous tree in South Africa is *Syzygium cordatum* (Palgrave, 1977). *Eucalyptus* species, native Australasian Myrtaceae, are the most widely grown trees in commercial forestry plantations, particularly in the tropics and southern hemisphere, including South Africa.

Movement of pathogens between native and introduced hosts has been recognized as a significant threat to plant communities (Slippers *et al.*, 2005). Because of the potential threat of native pathogens to non-native *Eucalyptus* plantations, various recent studies considered fungal pathogens on native hosts in areas where *Eucalyptus* spp. are intensively planted (Wingfield, 2003; Burgess *et al.*, 2006). These studies showed that pathogens which can cause severe diseases on *Eucalyptus* spp. also occur on native plants and thus pose a threat to *Eucalyptus* spp. Where plantations of non-native *Eucalyptus* spp. are established amongst closely related native myrtaceous trees, pathogens could

cross-infect either the native or introduced host group and cause serious diseases (Burgess & Wingfield, 2001). For example, the rust fungus *Puccinia psidii*, which occurs on a variety of native Myrtaceae in South America, has become one of the main pathogens on exotic *Eucalyptus* spp. in that area (Coutinho *et al.*, 1998).

In South Africa, species of the Botryosphaeriaceae are amongst the most important canker pathogens in plantations of non-native *Eucalyptus* spp., causing twig dieback, branch and stem cankers and mortality of diseased trees (Smith *et al.*, 1994). These fungi have also recently been reported as endophytes from native South African trees closely related to *Eucalyptus*, such as *S. cordatum* and *Heteropyxis natalensis* (Smith *et al.*, 2001). The *Eucalyptus* plantations mostly occur in the eastern part of the country where *S. cordatum* is widely distributed (Palgrave, 1977; Anonymous, 2002; Fig. 1). Thus, Botryosphaeriaceae that occur on this native tree could pose a threat to exotic *Eucalyptus* spp. and *vice versa*. However, there have not been any detailed studies on Botryosphaeriaceae on native hosts closely related to *Eucalyptus* in South Africa. Because of the economic importance of *Eucalyptus* plantations, as well as the need to protect native flora, identification and characterization of Botryosphaeriaceae from *S. cordatum* is of great concern.

Recent studies combined morphological characteristics and DNA sequence data to distinguish and identify species within the Botryosphaeriaceae (Denman *et al.*, 2000; Zhou & Stanosz, 2001; Crous *et al.*, 2006). Molecular approaches most commonly used to study Botryosphaeriaceae are comparisons of sequence data from the internal transcribed spacer (ITS) gene region of the rDNA operon (Denman *et al.*, 2000; Zhou & Stanosz, 2001). However, some closely related or cryptic species of the Botryosphaeriaceae have been difficult to distinguish based on single gene genealogies. Comparisons of sequence data for multiple genes or gene regions were thus used to discriminate between these species (Slippers *et al.*, 2004a, c). Furthermore, identification of large numbers of species has been facilitated by PCR restriction fragment length polymorphism (RFLP) techniques (Slippers *et al.*, 2004b).

The aims of this study were to identify Botryosphaeriaceae occurring on native *S. cordatum* in South Africa, based on ITS rDNA sequence data, PCR-RFLP analysis and anamorph morphology. Isolates belonging to the Botryosphaeriaceae on *S. cordatum* and

Eucalyptus were also compared, with special attention given to overlaps and the potential for cross infection. The pathogenicity of the Botryosphaeriaceae isolates from *S. cordatum* was furthermore tested on both a *Eucalyptus* clone and *S. cordatum* in glasshouse trials.

Materials and methods

Isolates

Isolates used in this study were collected in surveys of Botryosphaeriaceae on native *S. cordatum* in different geographical regions of South Africa, in 2001 and 2002 (Table 1, Fig. 1). The 148 isolates that were collected from 11 *S. cordatum* sites during these surveys form the basis of this study. Between 5 and 45 trees were sampled from each site. From each tree, isolations were made from dying twigs and symptomless, visually healthy twig and leaf tissues. Leaves and twig portions (5 cm in length) were washed in running tap water and surface sterilized by placing them sequentially for 1 min in 96% ethanol, undiluted bleach (3.5–5% available chlorine) and 70% ethanol, then rinsed in sterile water. Treated twig portions were halved and pieces from the pith tissue (2 mm²) and segments of the leaves (3 mm²) were placed on 2% malt extract agar (MEA; 2% malt extract, 1.5% agar; Biolab) in Petri dishes. Following incubation for 2 weeks at 20°C under continuous near-fluorescent light and colonies resembling Botryosphaeriaceae with grey-coloured, fluffy aerial mycelium, were selected. These colonies were transferred to 2% MEA at 25°C and stored at 5°C. All isolates have been maintained in the Culture Collection (CMW) of the Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa, and representative isolates were deposited in the collection of the Centraalbureau voor Schimmelcultures (CBS), Utrecht, the Netherlands.

DNA extraction and ITS rDNA amplification

Single conidial cultures from 21 isolates were grown on MEA for 7 days at 25°C in the dark. Template DNA was obtained from the mycelium using the modified phenol:chloroform DNA extraction method described in Smith *et al.* (2001). DNA was separated by electrophoresis on 1.5% agarose gels, stained with ethidium bromide and

visualized under ultraviolet light. DNA concentrations were estimated against λ standard size markers.

The internal transcribed spacer (ITS) regions ITS1 and ITS2, and the intermediate 5·8S gene of the ribosomal RNA (rRNA), were amplified using the primer pair ITS1 and ITS4 (White *et al.*, 1990). The PCR reactions were performed using the PCR protocol of Slippers *et al.* (2004b). PCR products were separated in a 1·5% agarose gel, stained with ethidium bromide and visualized under UV light. Sizes of PCR products were estimated against a 100 bp molecular weight marker XIV (Roche Diagnostics). The PCR products were purified using the High Pure PCR Product Purification kit (Roche Diagnostics).

DNA sequencing and analysis

Based on conidial morphology, the isolates of Botryosphaeriaceae from *S. cordatum* in South Africa were tentatively separated into eight groups. ITS rDNA sequences were determined for representative samples from all morphological groups (Table 1). To determine the identity and phylogenetic relationships of these isolates, ITS sequences of known species of the Botryosphaeriaceae were obtained from GenBank and included in the analyses (Table 1). The purified PCR products were sequenced using the same primers that were used for the PCR reactions. The ABI PRISM™ Dye Terminator Cycle Sequencing Ready Reaction kit (Perkin-Elmer) was used for sequencing reactions, as specified by the manufacturers. Sequence reactions were run on an ABI PRISM 3100™ automated DNA sequencer (Perkin-Elmer).

Nucleotide sequences were analysed using SEQUENCE NAVIGATOR version 1·0·1. (Perkin-Elmer Applied BioSystems, Inc.) software and alignments were made online using MAFFT version 5·667 (<http://timpani.genome.ad.jp/~mafft/server/>) (Katoh *et al.*, 2002). Gaps were treated as fifth character and all characters were unordered and of equal weight. Phylogenetic analyses of aligned sequences were carried out using PAUP (Phylogenetic Analysis Using Parsimony) version 4·0b8 (Swofford, 1999). Most-parsimonious trees were found using the heuristic search function with 1000 random addition replicates and tree bisection and reconstruction (TBR) selected as the branch swapping algorithm. Branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. Branch support was determined using 1000 bootstrap replicates (Felsenstein, 1985). The trees were rooted using the GenBank sequences of *Guignardia philoprina* and

Mycosphaerella africana, which are closely related to Botryosphaeriaceae. The sequence alignments and phylogenetic tree were deposited in TreeBASE as S1412, M2541.

PCR-RFLP analyses

PCR-RFLP fingerprinting techniques were applied to confirm the identity of isolates that were not sequenced and to identify the isolates that could not be separated based on ITS rDNA sequences. Amplicons obtained using primer pairs ITS1 and ITS4, or BOT15 (5'-CTGACTTGTGACGCCGGCTC-3') and BOT16 (5'-CAACCTGCTCAGCAAGCGAC-3') (Slippers *et al.*, 2004a) were digested with the restriction endonuclease *CfoI*. The RFLP reaction mixture consisted of 10 μ L PCR products, 0.3 μ L *CfoI* and 2.5 μ L matching enzyme buffer (Roche Diagnostics). The reaction mixture was incubated at 37°C overnight. Restriction fragments were separated on 1.5% agarose gel as described for PCR products. The results were compared with those of Slippers (2003).

Morphology and cultural characteristics

Fungal isolates were grown on 2% water agar (WA; Biolab) with sterilized pine needles placed onto the medium, at 25°C under near-UV light, to induce sporulation. Conidia that were released from pycnidia on the pine needles were mounted in lactophenol on glass slides and examined microscopically. Ten measurements of conidia were taken for each isolate. Measurements and digital photographs were taken using a light microscope, a HRc Axiocam digital camera and accompanying software (Carl Zeiss Ltd). Colony morphology and colour were determined from cultures grown on 2% MEA at 25°C under near-UV light. Colony colours (upper surface and reverse) were compared with those in the colour charts of Rayner (1970).

Pathogenicity

Fifteen isolates, representing eight species of Botryosphaeriaceae isolated from native *S. cordatum* in South Africa, were used in this study (Table 1). One isolate of *Botryosphaeria dothidea* and two isolates for each of the other seven species were randomly selected for inoculations. The isolates were grown on 2% MEA at 25°C under continuous near-fluorescent light for 7 days prior to inoculation.

Two-year-old trees of an *E. grandis* × *camaldulensis* clone (GC-540) and 1-year-old saplings of *S. cordatum* were selected for the pathogenicity trials under glasshouse conditions. Saplings of *S. cordatum* were raised from seeds taken from a single tree grown in the Kwambonambi (Kwazulu-Natal province) area. Trees and saplings selected for inoculations were grown in pots outside, and maintained in the glasshouse for acclimatization for 3 weeks prior to inoculation. Trees were inoculated during the spring-summer season (September 2003–February 2004). The glasshouse was subjected to natural day/night conditions and a constant temperature of approximately 25°C. Each of the isolates representing the different species was inoculated into the stems of 10 trees of each host species. Ten trees were also inoculated with sterile MEA plugs to serve as controls. The 160 inoculated trees, 10 for each fungal species and 10 as a control, were arranged in a randomized block design. The entire trial was repeated once under the same conditions, giving a total of 320 trees inoculated for each host species.

For inoculations, wounds were made on the stems of trees using a 6-mm-diameter (*Eucalyptus* clone) or a 4-mm-diameter (*S. cordatum*) cork borer to remove the bark and expose the cambium. Wounds were made between two nodes on the stems of trees approximately 250 mm (*Eucalyptus*) or 150 mm (*S. cordatum*) above soil level. Plugs of mycelium were taken from 7-day-old cultures grown on MEA using the same size cork borer, and were placed into the wounds with the mycelial surface facing the cambium. Inoculated wounds were sealed with laboratory film (Parafilm M, Pechiney Plastic Packaging) to prevent desiccation and contamination. Lesion lengths (mm) were measured 6 weeks after inoculation. The fungi were re-isolated by cutting small pieces of wood from the edges of lesions and plating them on 2% MEA at 25°C. Re-isolations were made from two randomly selected trees per isolate and tree species and from all trees inoculated as controls.

Pathogenicity for all isolates inoculated on the *Eucalyptus* clone and *S. cordatum* was determined based on the length of lesions (mm) that developed after 6 weeks. There was no significant difference between the two repeats of the pathogenicity trials and the data were therefore combined to represent one dataset for the analyses. Statistical analyses of the data were performed using SAS statistical software (version 8, SAS Institute). The 95% confidence limits were determined for all means based on full model analysis of

variance (ANOVA). Differences between means were therefore considered significant at the $P \leq 0.05$ level.

Results

DNA sequence analyses

DNA fragments of approximately 600 bp were amplified. The ITS dataset consisted of 53 ingroup sequences, with *G. philoprina* and *M. africana* as outgroup taxa (Table 1). After alignment, the ITS dataset consisted of 593 characters; 432 uninformative characters were excluded, and 161 parsimony-informative characters were used in the analysis. The parsimony analysis (using heuristic searches) produced 276 most parsimonious trees of 414 steps (consistency index (CI) = 0.702, retention index (RI) = 0.915), one of which was chosen for presentation (Fig. 2).

The isolates considered in the phylogenetic analyses formed 12 clades, designated as groups I to XII (Fig. 2). These groups were resolved in two major clades that corresponded to species of Botryosphaeriaceae with *Fusicoccum*-like or *Diplodia*-like anamorphs. The *Fusicoccum* clade comprised six groups that represented: *Neofusicoccum parvum* and *N. ribis* (group I), *N. mangiferae* (group II), *N. eucalyptorum* (group III), *N. australe* (group IV), *N. luteum* (group V) and *B. dothidea* (group VI). Groups VII and VIII represented species with *Lasiodiplodia* anamorphs: *Lasiodiplodia theobromae* (group VII) and *L. gonubiensis* (group VIII). These two groups (VII and VIII) formed a distinct subclade (supported by 100% bootstrap value) within the *Diplodia* clade. The other major subclade within the *Diplodia* clade contained four groups corresponding to: *D. mutila* (group IX), *D. corticola* (group X), *Diplodia* sp. (= '*Botryosphaeria obtusa*') (group XI) and *Diplodia pinea* (= *Sphaeropsis sapinea*) (group XII) (Fig. 2).

All the isolates obtained from *S. cordatum* in this study resided in seven groups (Fig. 2) as follows: *N. parvum* and *N. ribis* (group I), *N. mangiferae* (group II), *N. australe* (group IV), *N. luteum* (group V), *B. dothidea* (group VI), *L. theobromae* (group VII) and *L. gonubiensis* (group VIII).

PCR-RFLP analysis

Isolates that were not identified using DNA sequence comparisons were subjected to ITS PCR-RFLP analyses. Digests of the PCR products, obtained using primers ITS1 and ITS4, with *CfoI* produced two distinctive banding patterns. These profiles matched those of *N. parvum*/*N. ribis* (99 isolates) and *N. luteum*/*N. australe* (5 isolates) as shown by Slippers *et al.* (2004b). To further distinguish isolates of *N. parvum* from those of *N. ribis*, amplicons obtained using primers BOT15 and BOT16 were digested using the same restriction endonuclease. The two banding patterns obtained matched those of *N. parvum* (42 isolates) and *N. ribis* (57 isolates) as described by Slippers (2003). However, *N. luteum* and *N. australe* could not be separated using this technique.

Morphology and cultural characteristics

All 148 isolates of the Botryosphaeriaceae from *S. cordatum* produced anamorph structures on pine needles on WA within 2–3 weeks. No teleomorph (sexual) structures were observed. Based on conidial morphology, isolates were separated into eight groups. Five of these groups corresponded to Botryosphaeriaceae with *Neofusicoccum* anamorphs (Fig. 3a–f), one with a *Fusicoccum* anamorph (Fig. 3g) and two with *Lasiodiplodia* (*Diplodia*-like) anamorphs (Fig. 4a,b).

Representative samples from the groups emerging from morphological comparisons were identified based on ITS rDNA sequence comparison. As described earlier, isolates of *N. parvum* and *N. ribis* were separated based on PCR-RFLP analyses. Further morphological examination of isolates, identified based on DNA data, provided support for their identity.

Cultures of *N. parvum* were initially white with fluffy, aerial mycelium, becoming pale olivaceous grey from the middle of colony after 3–4 days; columns of the mycelium formed in the middle of colony reaching the lid; margins were regular; reverse sides of the colonies were olivaceous grey. Conidia were hyaline, smooth, aseptate and fusiform to ellipsoid (average of 420 conidia: $18.2 \times 5.5 \mu\text{m}$, l/w 3.3) (Fig. 3a). The 42 isolates were identified as *N. parvum*.

Colonies of *N. ribis* were initially white, becoming pale olivaceous grey from the middle of colony, with thick aerial mycelium reaching the lids of Petri dishes; margins were

regular; reverse sides of the colonies were olivaceous grey. Conidia were hyaline, unicellular, aseptate, fusiform, apices tapered (average of 570 conidia: $21 \times 5.5 \mu\text{m}$, l/w 3.8) (Fig. 3b). The 57 isolates were identified as *N. ribis*.

The culture of the single *B. dothidea* isolate identified in this study produced greenish olivaceous appressed mycelium, its margins regular and the reverse sides of the colonies olivaceous grey to iron-grey. Conidiomata were readily formed in the middle of colonies after 3–4 days of incubation. Conidia were hyaline, smooth with granular contents, aseptate, narrowly fusiform (average of 10 conidia: $27.8 \times 5.4 \mu\text{m}$, l/w 5.1) (). The 30 Fig. 3g).

Isolates of *N. mangiferae* produced pale olivaceous grey appressed mycelium, slightly fluffy on the edges of colonies, with sinuate margins, and the reverse sides of colonies were olivaceous. Conidiomata were readily formed in the middle of colonies after 3–4 days and covered the entire surface of the colonies within 7–10 days. Conidia were hyaline, fusiform (average of 300 conidia: $14.2 \times 6.3 \mu\text{m}$, l/w 2.25) (Fig. 3 isolates were identified as *N. mangiferae*).

Cultures of *N. luteum* were initially white, becoming pale olivaceous grey from the middle of colonies within 3–4 days, with suppressed mycelium, moderately fluffy in the middle and with regular margins. A yellow pigment was noticeable after 3–5 days of incubation and was seen as amber yellow on the reverse side of Petri dishes; after 5–7 days colonies become olivaceous buff to olivaceous grey. Conidiomata were readily formed from the middle of colonies within 3–4 days and covered the whole surface of colonies within 7–10 days. Conidia were hyaline, fusiform to ellipsoid, sometimes irregularly fusiform, smooth with granular contents, unicellular, forming one or two septa before germination (average of 40 conidia: $18.9 \times 6.3 \mu\text{m}$, l/w 3.0) (Fig. 3d,e). The four isolates were identified as *N. luteum*.

Cultures of *N. australe* were very similar in morphology to those of *N. luteum*, but the yellow pigment produced in young cultures was brighter and a honey-yellow colour when viewed from the bottom of the Petri dishes. Conidiomata readily formed at the middle of colonies within 3–4 days and covered the colony surfaces within 7–10 days. Conidia were hyaline, fusiform, apices rounded, aseptate, rarely uniseptate (average of 70 conidia: $20.5 \times 5.7 \mu\text{m}$, l/w 3.6) (Fig. 3c). These conidia were slightly longer and narrower on

average than those of *N. luteum*, which was also reflected in a higher l/w ratio. The seven isolates were identified as *N. australe*.

Isolates of *L. theobromae* produced initially white to smoke-grey fluffy aerial mycelium, becoming pale olivaceous grey within 5–6 days with regular margins; the reverse sides of the cultures were olivaceous grey to iron, becoming dark slate-blue after 7–10 days.

Conidia were hyaline, aseptate, ellipsoid to ovoid, thick-walled with granular contents (average of 50 conidia: $27 \times 14.7 \mu\text{m}$, l/w 1.85) (Fig. 4b). Dark, septate conidia typical for this species were not observed in this study. The five isolates were identified as *L. theobromae*.

Isolates of *L. gonubiensis* were similar in culture morphology to those of *L. theobromae*.

Conidia of *L. gonubiensis* were initially hyaline, unicellular, ellipsoid to obovoid, thick-walled with granular contents, rounded at the apex and occasionally truncate at the base.

Aging conidia became cinnamon to sepia with longitudinal striations, forming one to three septa (average of 20 conidia: $33.9 \times 18.9 \mu\text{m}$, l/w 1.8) (Fig. 4a). The two isolates were identified as *L. gonubiensis*.

Key to species of Botryosphaeriaceae and their anamorphs from *Syzygium cordatum* in South Africa

- | | |
|---|---------------------------------|
| 1. Fusoid to ellipsoid, thin-walled, <i>Fusicoccum</i> -like conidia | 2 |
| 1. Ovoid, thick-walled, <i>Diplodia</i> - or <i>Lasiodyplodia</i> -like conidia..... | 3 |
| 2. Colonies on MEA producing yellow pigment in young cultures | 4 |
| 2. Colonies on MEA not producing yellow pigment in cultures | 5 |
| 3. Conidia on average < 30 μm long; aging conidia becoming dark brown with longitudinal striations and uniseptate as reported by Punithalingam (1976)..... | <i>Lasiodyplodia theobromae</i> |
| 3. Conidia on average > 30 μm long, aging conidia become cinnamon to sepia with longitudinal striations and 1–3 septa..... | <i>L. gonubiensis</i> |
| 4. Colonies producing amber-yellow pigment noticeable between 3–5 days after incubation; conidia on average < 20 μm long | <i>Neofusicoccum luteum</i> |
| 4. Colonies producing honey-yellow pigment noticeable between 3–5 days after incubation; conidia on average > 20 μm long | <i>N. australe</i> |
| 5. Conidia on average > 25 μm long, narrowly fusiform..... | <i>Botryosphaeria dothidea</i> |
| 5. Conidia on average < 25 μm long..... | 6 |
| 6. Conidia on average < 15 μm long, l/w 2–2.5..... | <i>N. mangiferae</i> |
| 6. Conidia on average $\geq 15 \mu\text{m}$ long, l/w 3–5 | 7 |
| 7. Conidia $15\text{--}27 \times 4\text{--}7 \mu\text{m}$, aseptate, fusiform, apices tapered..... | <i>N. ribis</i> |
| 7. Conidia $13\text{--}25 \times 3.5\text{--}6 \mu\text{m}$, aseptate, fusiform to ellipsoid | <i>N. parvum</i> |

Pathogenicity

All Botryosphaeriaceae isolates tested for pathogenicity on the *E.*

grandis \times *camaldulensis* clone (GC-540) produced lesions within 6 weeks. No lesions developed on trees inoculated with sterile MEA plugs as controls. The fungi re-isolated

from the lesions that developed on trees were the same as those used for inoculations. The original Botryosphaeriaceae species were re-isolated from all trees chosen for re-isolations. No Botryosphaeriaceae were re-isolated from the controls.

Statistical analyses showed that the mean lesion length for the majority of isolates used in the trial differed significantly from that of the controls (Fig. 5a). The longest lesions were produced by isolates of *L. theobromae*, while the size of lesions produced by *B. dothidea* and *L. gonubiensis* were not significantly different to those of the controls (Fig. 5a). The mean lesion lengths for different strains of the same Botryosphaeriaceae species were not significantly different, except for the isolates of *L. theobromae*. Thus, *L. theobromae* isolate CMW 14116 was significantly more pathogenic than isolate CMW 14114 (Fig. 5a).

All Botryosphaeriaceae isolates inoculated on *S. cordatum* saplings produced lesions within 6 weeks. However, the mean lesion lengths produced by majority of the isolates were not significantly different from those of the controls (Fig. 5b). Some trees inoculated as controls also developed small lesions, but no Botryosphaeriaceae could be re-isolated from these lesions, which appeared to represent wound reactions. The fungi re-isolated from the lesions on trees inoculated with fungal mycelium were the same as those used for inoculations. The longest lesions were produced by one isolate of *N. mangiferae* (CMW 14034) and the mean lesion length obtained for this isolate was significantly greater than that of the other isolate (CMW 14102) of the same species (Fig. 5b). However, there were no statistically significant differences between the lesion lengths for the different isolates of the other species of Botryosphaeriaceae (Fig. 5b). The mean lengths of lesions produced by one isolate of *N. ribis* (CMW 13992) and one isolate of *L. theobromae* (CMW 14116) were also significantly different from that of the control (Fig. 5b). All the other isolates inoculated onto *S. cordatum* saplings produced lesions that were not significantly different from those of the controls (Fig. 5b).

Isolates of all the Botryosphaeriaceae used in this study, except those of *N. mangiferae*, were more pathogenic on the *Eucalyptus* clone than on *S. cordatum*. Analyses of variance showed that the interactions between mean lesion length produced by the species of Botryosphaeriaceae on the *Eucalyptus* clone and those on *S. cordatum* were statistically significant ($P \leq 0.001$).

Discussion

Eight species of the Botryosphaeriaceae were identified on native *S. cordatum* in South Africa in this study. They were *N. ribis*, *N. parvum*, *N. luteum*, *N. australe*, *N. mangiferae*, *B. dothidea*, *L. theobromae* and *L. gonubiensis*. The isolates were identified based on ITS rDNA sequence data, PCR-RFLP analysis and anamorph morphology. With the exception of *B. dothidea* and *L. gonubiensis*, this is the first report of all of these species of Botryosphaeriaceae on native *S. cordatum*. All eight species had the ability to infect and cause lesions on the stems of a *E. grandis* × *camaldulensis* clone and *S. cordatum* in glasshouse trials. Although lesions produced by most of the isolates on *S. cordatum* saplings were not significantly different from those on the controls, the pathogens could be re-isolated from these lesions. In the case of some species, such as *N. ribis*, *L. theobromae* and *F. mangiferae*, one isolate did not produce lesions that differed from those of the control, while the other isolate did. From these data, and knowledge of the fungi on other hosts, it was concluded that this group of fungi could be regarded as potential pathogens of *Syzygium*. However, apart from the isolates of *B. dothidea* and *L. gonubiensis*, all the other Botryosphaeriaceae in this study produced lesions on the *Eucalyptus* clone that were significantly different from those of the controls. They should be considered as potential threats to plantation grown *Eucalyptus* spp. in South Africa. *Neofusicoccum ribis* was the dominant species collected from native *S. cordatum* in South Africa in this study. This fungus represented 38% of all isolates obtained and was found in most of the areas surveyed. This abundant and wide distribution on a native host might indicate that this species is native to this region. *Neofusicoccum ribis* has been reported from *Eucalyptus* spp. (Myrtaceae) in its native range in Australia and on non-native *Eucalyptus* spp. in plantations (Old & Davison, 2000), but has not been identified on *Eucalyptus* spp. in South Africa (Slippers *et al.*, 2004a). These identifications should, however, be interpreted with caution, as the distinction between *N. parvum* and *N. ribis* had not been recognized at the time of these studies (Slippers *et al.*, 2004a). Furthermore, *N. ribis* as identified in this study (using RFLPs) was also interpreted as representing the *N. ribis sensu lato* group rather than strictly conspecific populations with the type isolates of this species, as identified by Slippers (2003). Further analyses using sequence data for

additional gene regions and other variable markers will be required to more clearly characterize populations and potential cryptic species in this group. *Neofusicoccum ribis* was one of the most pathogenic species of the Botryosphaeriaceae on the *Eucalyptus* clone in this study. This fungus should thus be considered as a potentially important pathogen of *Eucalyptus* spp. in South Africa.

Isolates of *N. parvum* represented 28% of the total number of isolates obtained in this study. Recent studies showed that *N. parvum* is an important and widely distributed pathogen of non-native *Eucalyptus* plantations in South Africa (Slippers *et al.*, 2004b). The wide distribution of *N. parvum* on non-native and native Myrtaceae in South Africa raises intriguing questions, such as whether these populations are native or introduced and how they might be interacting with each other. The movement of this pathogen between these important host groups represents a potential threat for both groups and should be further investigated. Isolates of *N. parvum* used in this study also developed only slightly smaller lesions than those of closely related *N. ribis*, illustrating its potential threat to *Eucalyptus* plantations in South Africa.

Only one isolate obtained from *S. cordatum* was identified as *B. dothidea* (anamorph *Fusicoccum aesculi*). This species is one of the most commonly reported members of the Botryosphaeriaceae from a wide variety of hosts, including *Eucalyptus* spp. (von Arx & Muller, 1954; Smith *et al.*, 2001). While *B. dothidea* was considered to be an important canker pathogen of *Eucalyptus* spp. in South Africa (Smith *et al.*, 1994), some of these isolates that were the most pathogenic (Smith *et al.*, 2001) were re-identified as *N. parvum* (Slippers *et al.*, 2004b). *Botryosphaeria dothidea* was seldom encountered on *Eucalyptus* spp. in other studies on this host (Slippers *et al.*, 2004b) and results of the present study suggest that it is probably not an important pathogen of this tree.

High numbers of isolates from *S. cordatum* were identified as *N. mangiferae*. This species is best known as a pathogen of mango (*Mangifera indica*) worldwide, particularly in Australia (Johnson *et al.*, 1992). *Neofusicoccum mangiferae* was earlier reported under different names from mango in South Africa (Darvas, 1991). Interestingly, however, a recent comprehensive study of Botryosphaeriaceae from mango plantations in South Africa, using a combination of DNA-based techniques and morphological data, did not report this species (Jacobs, 2002). The fact that this fungus is highly pathogenic on *S.*

cordatum might imply that it has been introduced into South Africa on other woody plants. Studies focused on the origin of *N. mangiferae* are likely to yield intriguing results, relevant to commercial forestry and to the protection of natural biodiversity in South Africa.

Neofusicoccum luteum and phylogenetically closely related *N. australe* were identified on *S. cordatum* in this study, but have not been recorded on *Eucalyptus* spp. in South Africa. *Neofusicoccum australe* is a recently described species (Slippers *et al.*, 2004c) and the present study is the first to consider the pathogenicity of this fungus on *Eucalyptus*. *Neofusicoccum luteum* was highly pathogenic to the *Eucalyptus* clone and its occurrence on the related *S. cordatum* in South Africa is of concern. *Neofusicoccum luteum* and *N. australe* were not the most commonly encountered species of the Botryosphaeriaceae on *S. cordatum*, but their presence alone provides sufficient evidence that they are well established in the country.

Two *Lasiodiplodia* species were identified in this study. *Lasiodiplodia theobromae* was isolated from *S. cordatum* in subtropical areas of South Africa. This fungus is an opportunistic pathogen with an extremely wide host range, including more than 500 host plants, mostly in tropical and subtropical regions (Punithalingam, 1976), and has previously been isolated from exotic *Acacia*, *Eucalyptus* and *Pinus* spp. in South Africa (Crous *et al.*, 2000; Burgess *et al.*, 2003). *Lasiodiplodia theobromae* was the most pathogenic species to the *Eucalyptus* clone in this study. Although the two isolates of *L. theobromae* displayed different levels of pathogenicity, both were highly pathogenic. *Lasiodiplodia theobromae* might be considered a potentially important pathogen of *Eucalyptus* in South Africa and studies to consider its pathogenicity to different species and hybrid clones would be warranted. Another *Lasiodiplodia* species isolated from *S. cordatum* was recently described as *L. gonubiensis* (Pavlic *et al.*, 2004) and was isolated from a geographical region with a moderate climate where *L. theobromae* was absent. *Lasiodiplodia gonubiensis* was only very mildly pathogenic to the *Eucalyptus* clone, even though it is most closely related to the highly pathogenic *L. theobromae*.

The results of this study provide an interesting insight into the diversity of Botryosphaeriaceae occurring on native *S. cordatum* in South Africa. Some of these fungi appear to be potentially important pathogens of *Eucalyptus* spp. and future surveys

should recognize this fact. Clearly, additional studies such as the one presented here, considering the pathogenicity of these fungi, will be needed to better understand their importance. This study emphasises the threat of cross-infecting species of the Botryosphaeriaceae to both native and introduced Myrtaceae. In a recent study, Burgess *et al.* (2006) showed that there is no restriction to the movement of *N. australe* between native and planted eucalypts in Western Australia. Population studies on other species of the Botryosphaeriaceae are, therefore, planned to provide further insight into their movement between native and cultivated hosts in South Africa.

References

Anonymous, 2002. *Commercial Timber Resources and Roundwood Processing in South Africa 2000 / 2001*. South Africa: Forestry Economics Services.

von Arx JA, Müller E, 1954. Die Gattungen der amersporen Pyrenomyceten. *Beiträge zur Kryptogamenflora der Schweiz* **11**, 1–434.

Burgess T, Wingfield MJ, 2001. Impact of fungal pathogens in natural forests ecosystems: a focus on *Eucalyptus* . In: Burgess T, Wingfield MJ, eds. *Microorganisms in Plant Conservation and Biodiversity*. Dordrecht, the Netherlands: Kluwer Academic Press, 285–306.

Burgess T, Wingfield MJ, Wingfield BD, 2003. Development and characterization of microsatellite loci for tropical tree pathogen *Botryosphaeria rhodina*. *Molecular Ecology Notes* **3**, 91–4.

Burgess T, Sakalidis M, Hardy GESTJ, 2006. Gene flow of the canker pathogen *Botryosphaeria australis* between *Eucalyptus globulus* plantations and native eucalypt forests in Western Australia. *Austral Ecology* **3**, 559–66.

Coutinho TA, Wingfield MJ, Alfenas AC, Crous PW, 1998. *Eucalyptus* rust: a disease with the potential for serious international implications. *Plant Disease* **82**, 819–25.

Crous PW, Phillips AJL, Baxter AP, 2000. *Phytopathogenic Fungi from South Africa*. Stellenbosch, South Africa: University of Stellenbosch Department of Plant Pathology Press.

Crous PW, Slippers B, Wingfield MJ *et al.*, 2006. Phylogenetic lineages in the *Botryosphaeriaceae*. *Studies in Mycology* **55**, 239–57.

Darvas JM, 1991. *Dothiorella dominicana*, a new mango pathogen in South Africa. *Phytophylactica* **23**, 295–8.

Denman S, Crous PW, Taylor JE, Kang JC, Pascoe I, Wingfield MJ, 2000. An overview of the taxonomic history of *Botryosphaeria* and a re-evaluation of its anamorphs based on morphology and ITS rDNA phylogeny. *Studies in Mycology* **45**, 129–40.

Felsenstein J, 1985. Confidence intervals on phylogenetics: an approach using bootstrap. *Evolution* **39**, 783–91.

Fisher PJ, Petrini O, Sutton BC, 1993. A comparative study of fungal endophytes in leaves, xylem and bark of *Eucalyptus nitens* in Australia and England. *Sydowia* **45**, 1–14.

Jacobs R, 2002. *Characterisation of Botryosphaeria Species from Mango in South Africa*. Pretoria, South Africa: University of Pretoria, MSc thesis.

Johnson GI, Mead AJ, Cooke AW, Dean JR, 1992. Mango stem end rot pathogens – fruit infections by endophytic colonisation of the inflorescence and pedicel. *Annals of Applied Biology* **120**, 225–34.

Johnson LAS, Briggs BG, 1981. Three old southern families – *Myrtaceae*, *Proteaceae* and *Restionaceae*. In: Keast A, ed. *Ecological Biogeography of Australia*.

the Hague, the Netherlands: W. Junk, 427–64.

Katoh K, Misawa K, Kuma K, Miyata T, 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research* **30**, 3059–66.

Old KM, Davison EM, 2000. Canker diseases of eucalypts . In: Keane PJ, Kile GA, Podger FD, Brown BN, eds. *Diseases and Pathogens of Eucalypts*. Collingwood, Australia: CSIRO Publishing, 241–57.

Palgrave KC, 1977. *Trees of Southern Africa*.
Johannesburg, South Africa: C. Struik.

Pavlic D, Slippers B, Coutinho TA, Gryzenhout M, Wingfield MJ, 2004. *Lasiodiplodia gonubiensis* sp. nov., a new *Botryosphaeria* anamorph from native *Syzygium cordatum* in South Africa. *Studies in Mycology* **50**, 313–22.

Punithalingam E, 1976 . *Botryodiplodia theobromae*. Kew, UK: Commonwealth Mycological Institute: CMI descriptions of pathogenic fungi and bacteria no. 519.

Rayner RW, 1970. *A Mycological Colour Chart*. Kew, UK: CMI and British Mycological Society.

Slippers B, 2003. *Taxonomy, Phylogeny and Ecology of Botryosphaeriaceous Fungi Occurring on Various Woody Hosts*. Pretoria, South Africa: University of Pretoria, PhD thesis.

Slippers B, Crous PW, Denman S, Coutinho TA, Wingfield BD, Wingfield MJ, 2004a. Combined multiple gene genealogies and phenotypic characters differentiate several species previously identified as *Botryosphaeria dothidea*. *Mycologia* **96**, 83–101.

Slippers B, Fourie G, Crous PW *et al.*, 2004b. Speciation and distribution of *Botryosphaeria* spp. on native and introduced *Eucalyptus* trees in Australia and South Africa. *Studies in Mycology* **50**, 343–58.

Slippers B, Fourie G, Crous PW, Coutinho TA, Wingfield BD, Wingfield MJ, 2004c. Multiple gene sequences delimit *Botryosphaeria australis* sp. nov. from *B. lutea*. *Mycologia* **96**, 1028–39.

Slippers B, Stenlid J, Wingfield MJ, 2005. Emerging pathogens: fungal host jumps following anthropogenic introductions. *Trends in Ecology and Evolution* **20**, 420–1.

Smith H, Crous PW, Wingfield MJ, Coutinho TA, Wingfield BD, 2001. *Botryosphaeria eucalyptorum* sp. nov., a new species in the *B. dothidea*-complex on *Eucalyptus* in South Africa. *Mycologia* **93**, 277–85.

Smith H, Kemp GHJ, Wingfield MJ, 1994. Canker and die-back of *Eucalyptus* in South Africa caused by *Botryosphaeria dothidea*. *Plant Pathology* **43**, 1031–4.

Smith H, Wingfield MJ, Crous PW, Coutinho TA, 1996. *Sphaeropsis sapinea* and *Botryosphaeria dothidea* endophytic in *Pinus* spp. and *Eucalyptus* spp. in South Africa. *South African Journal of Botany* **62**, 86–8.

Swofford DL, 1999. *PAUP**. *Phylogenetic Analysis Using Parsimony (*and Other Methods)*. Version 4. Sunderland, MA, USA: Sinauer Associates.

White TJ, Bruns T, Lee S, Taylor J, 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics . In: Innis MA, Gelfand DH, Snisky JJ, White TJ, eds. *PCR Protocols: a Guide to Methods and Applications*. San Diego, CA, USA: Academic Press, 315–22.

Wingfield MJ, 2003. Daniel McAlpine Memorial Lecture. Increasing threat of disease to exotic plantation forests in the southern hemisphere: lessons from cryphonectria canker. *Australian Plant Pathology* **32**, 1–7.

Zhou S, Stanosz GR, 2001. Relationships among *Botryosphaeria* species and associated anamorphic fungi inferred from the analyses of ITS and 5·8S rDNA sequences. *Mycologia* **93**, 516–27.

Figures and tables

Figure 1 A map of South Africa indicating the area of natural distribution of *Syzygium cordatum* (left) and sites from where isolates of the Botryosphaeriaceae identified in this study were obtained (stars, right).

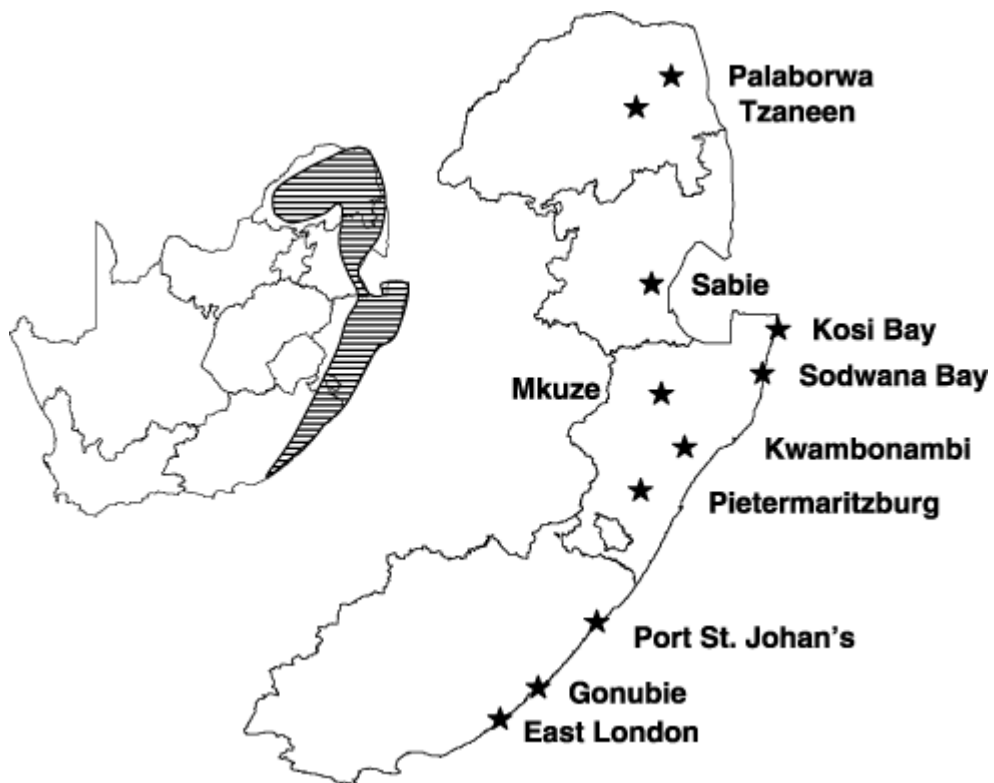


Figure 2 One of 276 most-parsimonious trees obtained from heuristic searches of ITS1, 5·8S and ITS2 rDNA sequence data (tree length = 414 steps, CI = 0·702, RI = 0·915). Branch lengths, proportional to the number of steps, are indicated above the internodes, and bootstrap values (1000 replicates) below the internodes. The tree is rooted to the outgroup taxa *Guignardia philoprina* and *Mycosphaerella africana*. Isolates sequenced in this study are presented in bold.

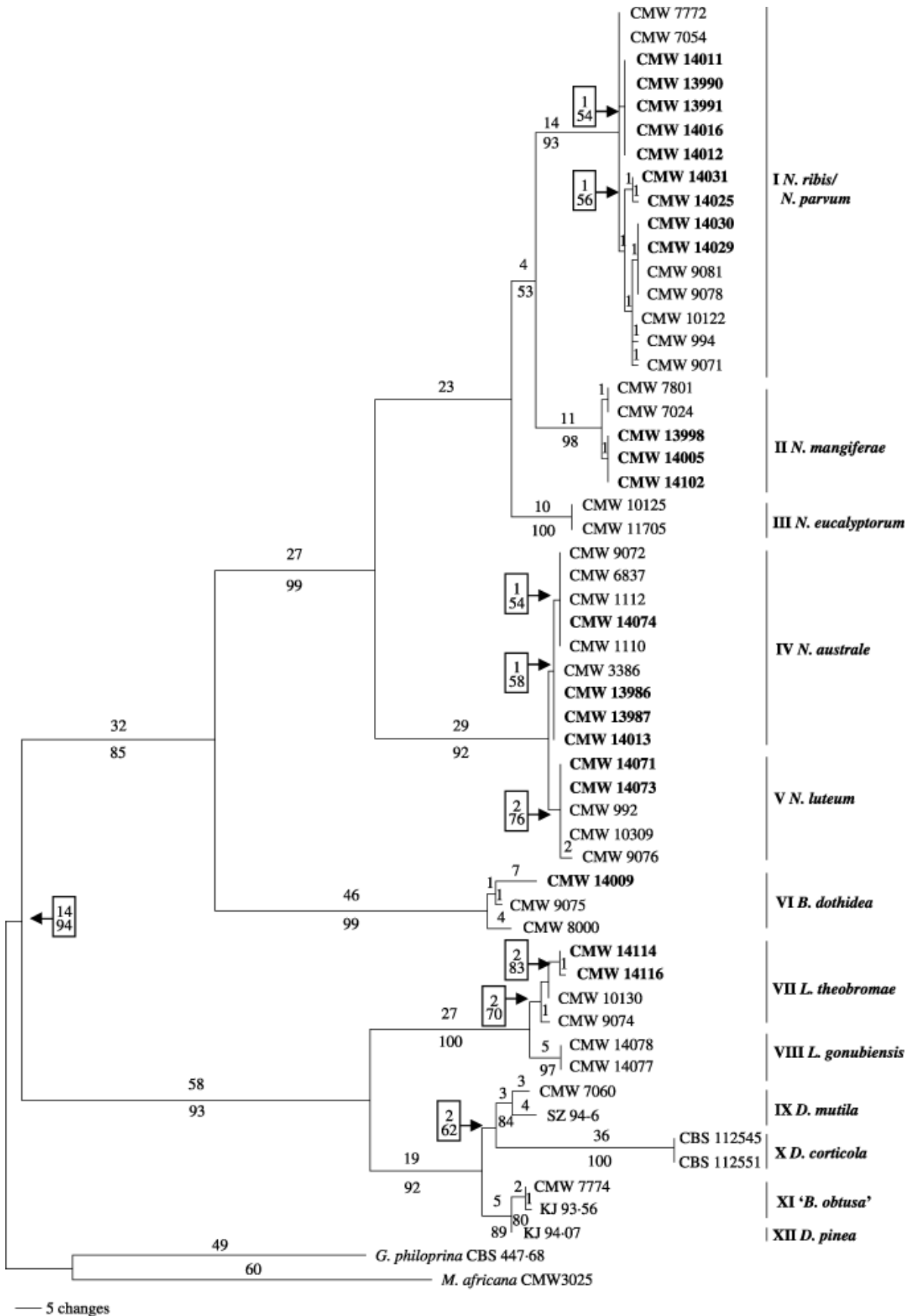


Figure 3 Light micrographs of conidia of six Botryosphaeriaceae species with *Fusicoccum*-like anamorphs: (a) *Neofusicoccum parvum*; (b) *N. ribis*; (c) aseptate and uniseptate conidia of *N. australe*; (d, e) aseptate and germinating uni- and biseptate conidia of *N. luteum*; (f) *N. mangiferae*; (g) *Botryosphaeria dothidea*. Bars = 10 μm .

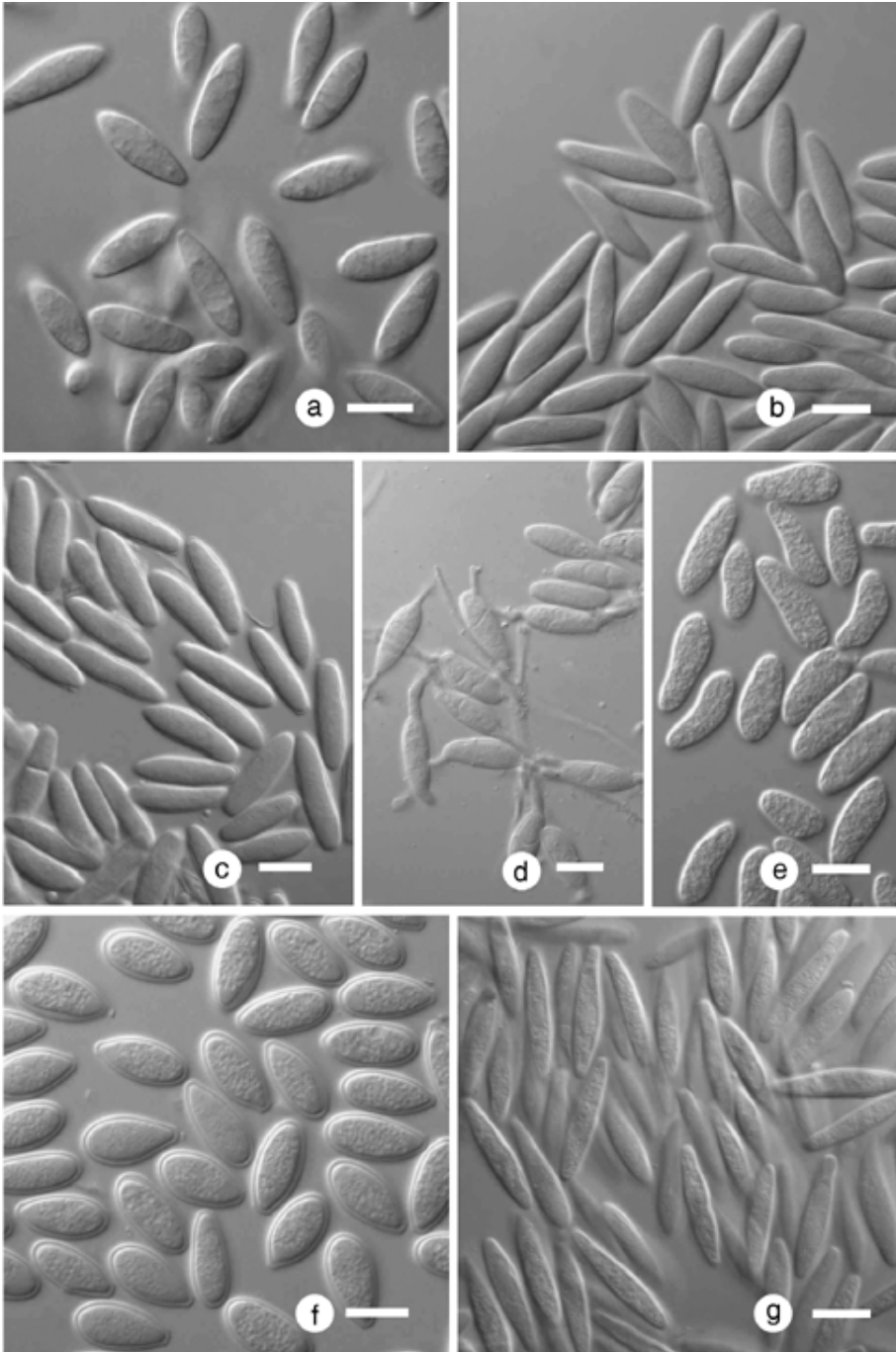


Figure 4 Light micrographs of conidia of two Botryosphaeriaceae species with *Lasiodiplodia* anamorphs: (a) *Lasiodiplodia gonubiensis*; (b) *L. theobromae*. Bars = 10 μm .

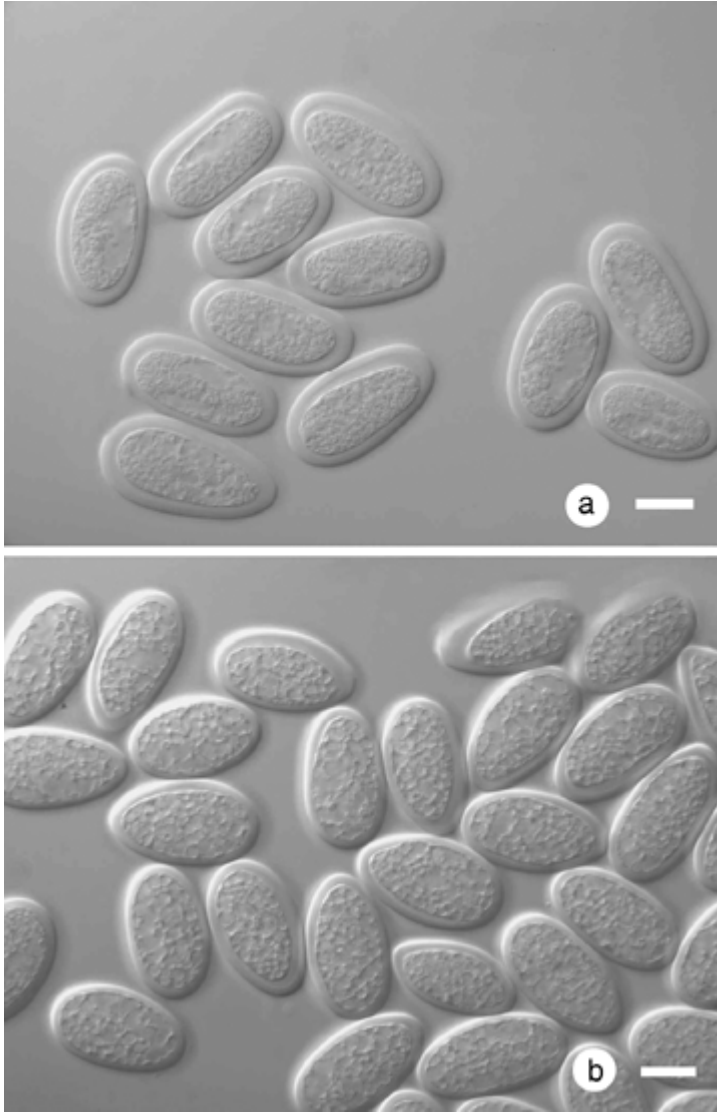


Figure 5 Mean lesion lengths (mm) for each isolate of different species of the Botryosphaeriaceae 6 weeks after inoculations on (a) *Eucalyptus grandis* × *camaldulensis* clone GC-540 and (b) *Syzygium cordatum*. Bars represent 95% confidence limits for each isolate. C = Control; *Botryosphaeria dothidea* (CMW14009), *Neofusicoccum parvum* (CMW14097, 14030); *N. ribis* (CMW13992, 14031); *N. australe* (CMW13987, 14013); *Lasiodiplodia theobromae* (CMW14116, 14114); *L. gonubiensis* (CMW14077, 140780); *N. mangiferae* (CMW14102, 14034); *N. luteum* (CMW14071, 14073).

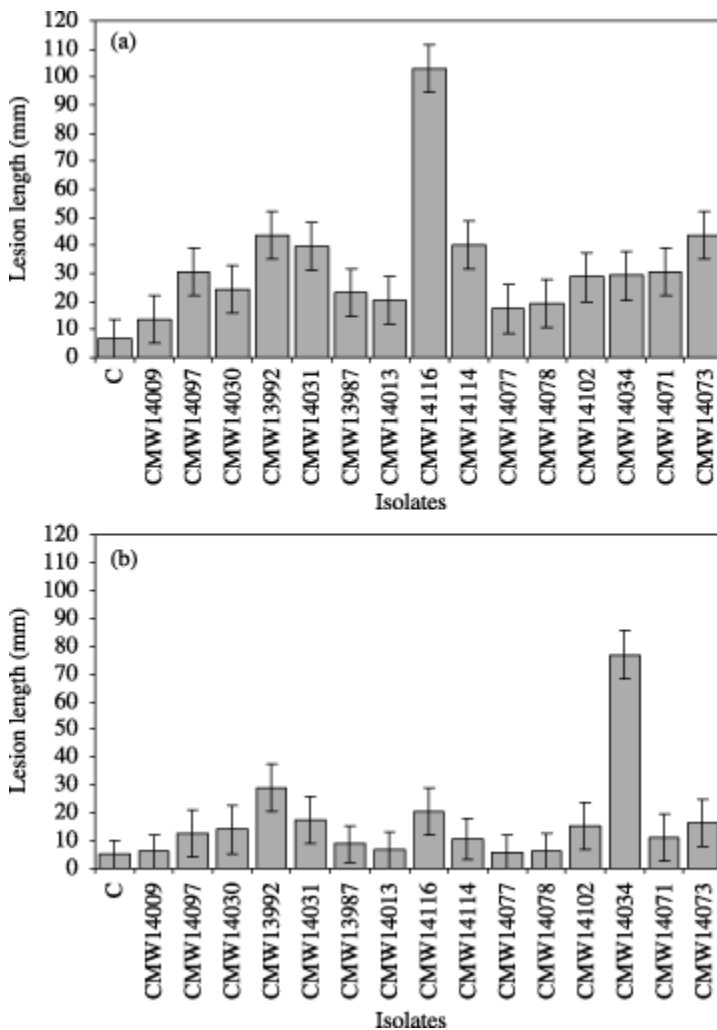


Table 1 Isolates considered in the phylogenetic study and pathogenicity trials

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
CMW 7772		<i>Neofusicoccum ribis</i>	<i>Ribis</i> sp.	New York, USA	B. Slippers & G. Hudler	AY236935
CMW 7054	CBS 121	<i>N. ribis</i> (chromagena)	<i>R. rubrum</i>	New York, USA	N.E. Stevens	AF241177
CMW 14011		<i>N. ribis</i>	<i>Syzygium cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316072
CMW 14012		<i>N. ribis</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316073
CMW 13990		<i>N. ribis</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316074
CMW 13991	CBS 118822	<i>N. ribis</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316075
CMW 14016		<i>N. ribis</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316079
CMW 14031 ^c		<i>N. ribis</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316076
CMW 14025		<i>N. ribis</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316080
CMW		<i>N. ribis</i>	<i>S. cordatum</i>	Sodwana bay, S. Africa	D. Pavlic	

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
13992 ^c						
CMW 9081	ICMP 8003	<i>Neofusicoccum parvum</i>	<i>Populus nigra</i>	New Zealand	G.J. Samuels	AY236943
CMW 9078	ICMP 7925	<i>N. parvum</i>	<i>Actinidia deliciosa</i>	New Zealand	S.R. Pennycook	AY236940
CMW 994	ATCC 58189	<i>N. parvum</i>	<i>Malus sylvestris</i>	New Zealand	G.J. Samuels	AF243395
CMW 9071		<i>N. parvum</i>	<i>Ribes</i> sp.	Australia	M.J. Wingfield	AY236938
CMW 10122		<i>N. parvum</i>	<i>Eucalyptus grandis</i>	Mpumalanga, S. Africa	H. Smith	AF283681
CMW 14030 ^c		<i>N. parvum</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316077
CMW 14029	CBS 118832	<i>N. parvum</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316078
CMW 14097 ^c		<i>N. parvum</i>	<i>S. cordatum</i>	St. John's Port, S. Africa	D. Pavlic	
CMW 7801	BRIP 23396	<i>Neofusicoccum mangiferae</i>	<i>Mangifera indica</i>	Australia	G.I. Johnson	AY615187
CMW 7024	BRIP 24101	<i>N. mangiferae</i>	<i>M. indica</i>	Australia	G.I. Johnson	AY615185
CMW 13998	CBS 118821	<i>N. mangiferae</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316081

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
CMW 14005		<i>N. mangiferae</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316082
CMW 14102 ^c		<i>N. mangiferae</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316083
CMW 14034 ^c		<i>N. mangiferae</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	
CMW 9072		<i>Neofusicoccum australe</i>	<i>Acacia</i> sp.	Melbourne, Australia	J. Roux & D. Guest	AY339260
CMW 6837		<i>N. australe</i>	<i>Acacia</i> sp.	Batemans Bay, Australia	M.J. Wingfield	AY339262
CMW 1110		<i>N. australe</i>	<i>Widdringtonia nodiflora</i>	Cape province, S. Africa	W.J. Swart	AY615166
CMW 1112		<i>N. australe</i>	<i>W. nodiflora</i>	Cape province, S. Africa	W.J. Swart	AY615167
CMW 3386		<i>N. australe</i>	<i>Wollemia nobilis</i>	Queensland, Australia	M. Ivory	AY615165
CMW 14074		<i>N. australe</i>	<i>S. cordatum</i>	East London, S. Africa	D. Pavlic	DQ316089
CMW 13986	CBS 118839	<i>N. australe</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316085
CMW 13987 ^c		<i>N. australe</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316086

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
CMW 14013 ^c		<i>N. australe</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316087
CMW 9076	ICMP 7818	<i>Neofusicoccum luteum</i>	<i>Malus domestica</i>	New Zealand	S.R. Pennycook	AY236946
CMW 992	KJ 93-52	<i>N. luteum</i>	<i>Actinidia deliciosa</i>	New Zealand	G.J. Samuels	AF027745
CMW 10309	CAP 002	<i>N. luteum</i>	<i>Vitis vinifera</i>	Portugal	A.J.L. Phillips	AY339258
CMW 14071 ^c	CBS 118842	<i>N. luteum</i>	<i>S. cordatum</i>	East London, S. Africa	D. Pavlic	DQ316088
CMW 14073 ^c		<i>N. luteum</i>	<i>S. cordatum</i>	East London, S. Africa	D. Pavlic	DQ316090
CMW 10125		<i>Neofusicoccum eucalyptorum</i>	<i>E. grandis</i>	Mpumalanga, S. Africa	H. Smith	AF283686
CMW 11705		<i>N. eucalyptorum</i>	<i>E. nitens</i>	South Africa	B. Slippers	AY339248
CMW 9075	ICMP 8019	<i>Botryosphaeria dothidea</i>	<i>P. nigra</i>	New Zealand	G.J. Samuels	AY236950
CMW 8000		<i>B. dothidea</i>	<i>Prunus</i> sp.	Crocifisso, Switzerland	B. Slippers	AY236949
CMW 14009 ^c	CBS 118831	<i>B. dothidea</i>	<i>S. cordatum</i>	Sodwana Bay, S. Africa	D. Pavlic	DQ316084

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
CMW 10130		<i>Lasiodiplodia theobromae</i>	<i>Vitex donniana</i>	Uganda	J. Roux	AY236951
CMW 9074		<i>L. theobromae</i>	<i>Pinus</i> sp.	Mexico	T. Burgess	AY236952
CMW 14114 ^c	CBS 118843	<i>L. theobromae</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316091
CMW 14116 ^c		<i>L. theobromae</i>	<i>S. cordatum</i>	Kwambonambi, S. Africa	D. Pavlic	DQ316092
CMW 14077 ^c	CBS 115812	<i>Lasiodiplodia gonubiensis</i>	<i>S. cordatum</i>	Eastern Cape, S. Africa	D. Pavlic	AY639595
CMW 14078 ^c	CBS 116355	<i>L. gonubiensis</i>	<i>S. cordatum</i>	Eastern Cape, S. Africa	D. Pavlic	AY639594
CMW 7774		' <i>Botryosphaeria</i> ' <i>obtusa</i>	<i>Ribes</i> sp.	New York, USA	B. Slippers & G. Hudler	AY236953
	KJ 93-56	' <i>Botryosphaeria</i> ' <i>obtusa</i>	Hardwood shrub	New York, USA	G.J. Samuels	AF027759
CMW 7060	CBS 431	<i>Diplodia mutila</i>	<i>Fraxinus excelsior</i>	Netherlands	H.A. van der Aa	AY236955
	ZS 94-6	<i>D. mutila</i>	<i>Malus pumila</i>	New Zealand	N. Tisserat	AF243407
	CBS 112545	<i>Diplodia corticola</i>	<i>Quercus ilex</i>	Spain	M.A. Sanchez & A. Trapero	AY259089

Isolate ^{a,b}	Other no. ^a	Identity	Host	Location	Isolator	GenBank ITS
	CBS 112551	<i>D. corticola</i>	<i>Quercus suber</i>	Portugal	A. Alves	AY259101
	KJ 94-07	<i>Diplodia pinea</i>	<i>Pinus resinosa</i>	Wisconsin, USA	D.R. Smith	AF027758
CMW 3025		<i>Mycosphaerella africana</i>	<i>Eucalyptus viminalis</i>	Stellenbosch, S. Africa	P.W. Crous	AF 283690
CMW 7063	CBS 447-68	<i>Guignardia philoprina</i>	<i>Taxus baccata</i>	Netherlands	H.A. van der Aa	AF312014
^a Culture collections: CMW = Tree Pathology Co-operative Programme, Forestry and Agricultural Biotechnology Institute, University of Pretoria; KJ = Jacobs & Rehner (1998); ATCC = American Type Culture Collection, Fairfax, VA, USA; BRIP = Plant Pathology Herbarium, Department of Primary Industries, Queensland, Australia; CAP = culture collection of A.J.L. Phillips, Lisbon, Portugal; CBS = Centraalbureau voor Schimmelcultures, Utrecht, Netherlands; ICMP = International Collection of Microorganisms from Plants, Auckland, New Zealand; ZS = Zhou & Stanosz (2001).						
^b Isolates sequenced in this study are given in bold.						
^c Isolates used in pathogenicity trials.						