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A New Ceratocystis Species Defined Using Morphological and Ribosomal DNA Sequence Comparisons

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Summary

A Ceratocystis Ell. & Halst. species has recently been reported from Acacia mearnsii De Willd. in South Africa showing symptoms of die-back and gummosis. The fungus was tentatively identified as Ceratocystis fimbriata Ell. & Halst. that is a well-known and notorious pathogen of many plants of the world. The fungus from A. mearnsii, however, differs morphologically from authentic C. fimbriata isolates. In this study, isolates from A. mearnsii in South Africa were compared with C. fimbriata isolates from different geographic areas on the basis of morphology and ribosomal RNA (rRNA) sequence data. Morphological comparisons showed that the Ceratocystis isolates from A. mearnsii have light-coloured perithecial bases and divergently arranged ostiolar hyphae compared with entirely black perithecia and convergently arranged ostiolar hyphae of typical C. fimbriata isolates. Comparisons of rDNA confirmed the morphological differences and grouped the South Africa isolates apart from C. fimbriata originating from other areas. This important pathogenic fungus is consequently described as new.

Key words: Ceratocystis - Chalara - Acacia Wilt disease - C. fimbriata - Ribosomal RNA sequence

Introduction

Ceratocystis sensu lato includes the genera, Ceratocystis sensu stricto, Ceratocystiopsis Upad. & Kendr. and Ophiostoma H. & P. Sydow (De Hoog and Scheffer, 1984; Wingfield et al., 1993). These fungi are known to be closely associated with insects (Whitney, 1982) and include important plant pathogens (Wingfield et al., 1993). Pathogens range from being weak; such as C. paradoxa (Dade) C. Moreau to aggressive primary pathogens as in the case of O. ulmi (Buism.), O. novo-ulmi Brasier and C. fimbriata (Kile, 1993).

Ceratocystis fimbriata is a well known pathogen with a world-wide distribution and causes diseases on a wide range of hosts. It is sometimes referred to as the sweet potato black rot fungus (Kojima and Uritani, 1974; Kojima et al., 1982; Kawakita and Kojima, 1983; Kawakita and Kojima, 1986; Yasuda and Kojima, 1986) due to the fact that it was first isolated from sweet potatoes (Ipomoea batatas [L.] Lam.), causing dark circular spots on the roots (Halsted, 1890). Other hosts include, rubber (Olson and Martin, 1949), coffee (Pontis, 1951), quaking aspen (Wood and French, 1963), prune, apricot and peach trees (De Vay et al., 1963; De Vay et al., 1968), apsen (Zalasky, 1965; Manion and French, 1967), pimento (Leather, 1966), poplar (Gremmen and De Kam, 1977), plane (Anonymous, 1986; Grosclaude and Olivier, 1988), mango (Ribeiro et al., 1986), syngonium (Vogelzang and Scott, 1990) and almond (Teviotdale and Harper, 1991).

A fungus tentatively identified as C. fimbriata has recently been isolated from A. mearnsii (black wattle) in South Africa (Morris et al., 1993). In this situation, the fungus causes gummosis and die-back of trees. This was the first report of C. fimbriata attacking A. mearnsii but was not the first record of the fungus in South Africa. The fungus was previously isolated from a diseased Protea L. plant in the Transvaal Province (Gorter, 1977).

Isolates of the purported *C. fimbriata* are being obtained from black wattle in South Africa regularly. These, however, differ morphologically from authentic isolates occurring elsewhere in the world and from various descriptions of the fungus. The aim of this study was, therefore, to compare South African isolates of *C. fimbriata* from black wattle with those from other parts of the world using conventional mycological techniques as well as partial ribosomal RNA sequence comparisons.

Materials and Methods

Sources of isolates

Isolates used for morphological and molecular comparisons are listed in Table 1. Cultures of *C. fimbriata* from plane trees (PREM 51642, PREM 51644) were supplied by Prof. C. Grosclaude, INRA, Station de Pathologie Vègètale, 84143 Montfavet cedex, France. The isolate from sweet potato in Papua New Guinea (PREM 51643) was obtained from the culture collection of the DSIR, Auckland New Zealand (8579); isolates from Italy were supplied by Dr. P. Capretti, Instituto di Patologi E Zoologia Forestale, Piazzale Delle Casine 28, Firenze and isolated by Dr. Panconesi. The isolate of *C. moniliformis* (Hedgc.) C. Moreau from Japan originates from the culture collection of the Institute for Fermentation, Osaka (IFO 8667).

Morphological comparisons

Isolates PREM 51641 and PREM 51645 of the Ceratocystis sp. from black wattle in South Africa and PREM 51643 and PREM 51642 from Papua New Guinea and France respectively, were cultured on malt extract agar (20 g Difco malt extract; 20 g Difco Bacto agar/1000 ml water) at 25 °C and studied by means of light microscopy. Measurements were taken for the different structures and analyzed with SAS/Stat system for personal computers (SAS Institute Inc. SAS Campus Drive, Cary, NC 27513). These were then compared with morphological characteristics from a herbarium specimen identified as C. fimbriata from a *Protea* sp. in South Africa (PREM 48263) as well as characteristics of this fungus previously recorded in the literature.

For scanning electron microscopy (SEM), cultures were grown on 2% malt extract agar. Agar blocks were cut from cultures and

| fixed in glutaraldehyde (3%) for 4 h and then in osmium (1%) for |
|--|
| 1,5 h. Dehydration of the material followed via a graded acetone |
| series. The material was critical point dried, mounted on stubs, |
| coated with gold/palladium and examined with a JEOL WIN- |
| SEM (ISM 6400) scanning electron microscope. |

The growth rates of isolates of the South African Ceratocystis sp. (PREM 51641, PREM 51645) were compared with two authentic isolates from Papua New Guinea (PREM 51643) and France (PREM 51642). Three plates containing 2% MEA were inoculated with 4 mm discs from two week old cultures of each and were incubated at temperatures ranging from 15 °C to 30 °C at 5 °C intervals. Growth rates were recorded after eight days and two measurements of the colony diameter were made at right angles to each other. For each isolate, the average of six measurements was therefore taken.

Molecular comparisons

Cultures used for molecular comparisons included PREM 51639, PREM 51829, PREM 51645, PREM 51643, IFO 8667, PREM 51644, PREM 51830, PREM 51831 (Table 1). Sterile cellophane discs (8 cm diameter) were placed on 2% MEA in Petri dishes and inoculated with the test fungi. Strains were grown at 25 °C until the mycelia covered the cellophane discs which were then removed and lyophilised.

Fungal mycelium was scraped from the cellophane surface and the DNA isolated according to the methods described by Viljoen et al. (1993). The internal transcribed spacer regions (ITS1 and ITS2), as well as the 5.8S gene of the ribosomal RNA operon were amplified using the Polymerase Chain Reaction (PCR) [Saiki et al., 1988] with primers ITS1 and LR1 (Table 2). DNA fragments were purified using Magic PCR Preps (Promega Cor-

| Species ² | Source | Origin |
|-------------------------------|--------------------|------------------|
| Ceratocystis sp. (PREM 51641) | Acacia mearnsii | South Africa |
| Ceratocystis sp. (PREM 51639) | A. mearnsii | South Africa |
| Ceratocystis sp. (PREM 51829) | A. mearnsii | South Africa |
| Ceratocystis sp. (PREM 51645) | A. mearnsii | South Africa |
| C. fimbriata (PREM 48263) | Protea sp. | South Africa |
| C. fimbriata (PREM 51643) | Ipomoea batatas | Papua New Guinea |
| C. fimbriata (PREM 51642) | Platanus hybrida | France |
| C. fimbriata (PREM 51644) | P. hybrida | France |
| C. fimbriata (PREM 51830) | P. orientalis | Italy, Sicily |
| C. fimbriata (PREM 51831) | P. orientalis | Italy |
| C. moniliformis (IFO 8667) | a Anna compania | Japan |

¹ The isolate from *Protea* sp. represents a dried culture used in light microscopy

² PREM is the official designation of the National Collection of Fungi, Pretoria, South Africa and IFO refers to the culture collection of the Institute for Fermentation, Osaka, Japan

| Primers | Sequence | Source |
|---------|----------------------|---------------------------|
| ITS1 | TCCGTAGGTGAACCTGCGG | White et al., 1990 |
| LR1 | GGTTGGTTTCTTTTCCT | Vilgalys and Hester, 1990 |
| 5.8SR | GCATCGATGAAGAACGCAGC | Vilgalys and Hester, 1990 |
| CS21 | CGAATCTTTGAACGCACATG | Dr. B. D. Wingfield |

¹ Based on the 5.8S gene of several ophiostomatoid fungi sequenced in our laboratory Table 1. Isolates of Ceratocystis spp. used in morphological and molecular comparisons¹

Table 2. Primers used to amplify and to sequence the desired region of the rDNA operon poration, Madison, USA). Both strands of the purified PCR fragment were sequenced using the fmol DNA Sequencing System (Promega Corporation, Madison, USA). The ITS1, CS2, 5.8SR and LR1 primers (Table 2) were used for sequencing.

The nucleotide sequences were aligned using CLUSTAL (PC-Gene, IntelliGenetics, Inc., Mountain View, California). Phylogenetic relations of the fungal isolates were determined with PAUP (Phylogenetic Analysis Using Parsimony, Swofford, 1993) and UPGMA (unweighted group-pair method with arithmetic mean, Sneath and Sokal, 1973). The DNA sequence of Neurospora crassa Shear & Dodge was used as an outgroup for the phylogenetic analyses (Chambers et al., 1986). C. moniliformis was included in this study to provide a measure of the relative distance from the other Ceratocystis species.

| Table 3. Comparison of morphological characteristics of the Ceratocystis sp. from | black wattle in South Africa, authentic isolates of |
|---|---|
| C. fimbriata from various geographic regions, herbarium material from Protea sp. | in South Africa and published descriptions1 |

| Character | Halsted and Fairchild 1891 | Hunt 1956 | Upadhyay 1981 | PREM 51641 | PREM 51645 | PREM 51642 | PREM 51643 | PREM 48263 |
|--------------------------------|----------------------------------|---|--|---------------------------------|---------------------------------|-----------------------------|--------------------|---------------------------------|
| Perithecial base width | 96-224 | 130-200 | 121-255 | 104–200 (158)d | 160–368 (245)b | 208–320 (270)a | 88-200 (157)d | 112-280 (176)c |
| Neck length | 395-608 | -800 | 950-1200 | 208840 (510)d | 440–1000 (685)a | 495–688 (595)c | 480–736 (628)bc | 416848 (645)b |
| Neck width, base | 24-34 | 20-35 | 18-40 | 20-32 (27)c | 32-64 (44)a | 32—40 (33)b | 24-40 (31)b | 16-32 (26)c |
| Neck width, tip | 14-20 | 10-20 | 10-18 | 16–24 (17)c | 16-32 (25)a | 16-32 (24)a | 16-20 (17)c | 16-32 (19)b |
| Ascospore length | | 4.5-8 | 3.5-8 | 46.5 (5.2)a | 56 (5.6)ab | 4→6 (5.1)ab | 5-7 (5.8)ab | 3.5-5 (4.6)b |
| Ascospore width | - | 2.5-5.5 | 2-2.5 | 3.5–5 (4.2)a | 35 (3.7)b | 3-5 (3.7)b | 35 (4)a | 3-3.5 (3)c |
| Cylindrical conidia, length | 16-30 | 11-16 | 9-21 | 8–24 (14.6)bc | 7-20 (13.8)c | 12-32 (18)a | 9–23 (14.3)bc | 9-19 (15)b |
| Cylindrical conidia, width | 4-9 | 4-5 | 2-6.5 | 3 -4 (3.5)a | 3-4 (3.3)a | 2.5 -4 (3.8)a | 3-5 (3.9)a | 24 (3.1)a |
| Barrel conidia, length | 12-19 | 9–16 | 9–17 | 6–10 (7)b | 6-12 (9)a | <u>8</u> 8 | 5-13 (8)b | - |
| Barrel conidia, width | - | 6-13 | 5-13 | 4—8 (6)a | 4-10 (7)a | <u>8</u> | 4-9 (8)a | - |
| Hyphal diameter | 2.0-6.0 | 2.0-6.0 | 1.5-5 | 2–5 | 2.3-3.1 | 1.5-2 | 2-3 | 2 |
| Perithecial colour | - | brown- black | brown-dark brown/ black | yellowish with black neck | yellowish with black neck | black | black | yellowish with black neck |
| Colony colour | H | hyaline – light brown, greenish brown | hyaline – subhyaline, greyish brown – dark brown | creamy – light brown | creamy – light brown | greenish brown | greenish brown | 2 |
| Hyphal colour | - | aerial: hyaline, submerged: darker | hyaline — pale brown | hyaline | hyaline | hyaline | hyaline | hyaline |
| Ostiolar hyphae arrangement | 12 | - | straight/ flexuous | divergent | divergent | convergent | convergent | - |
| Odour | - | banana oil/ fruit-like | 카 | fruit-like | fruit-like | banana oil | banana oil | - |

¹ For each isolate, the ranges of measurements are given in µm, followed by the mean value of 50 measurements in brackets. Corresponding alphabetical letters in rows indicate no significant difference for that particular character



Figs. 1–4. Light micrographs of teleomorph and anamorph characteristics of *Ceratocystis albofundus*. Fig. 1. Perithecium with light coloured base (Bar = 100 μ m). Fig. 2. Divergent ostiolar hyphae with hat-shaped ascospore extruding from the tip. Rectangular conidia in the background (Bar = 10 μ m). Fig. 3. Barrel-shaped conidia (Bar = 10 μ m). Fig. 4. Hat-shaped ascospores (Bar = 10 μ m).

Results

Morphological comparisons

Morphological comparisons of the purported C. fimbriata isolates from black wattle with those from other sources and with characteristics reported in the literature are presented in Table 3. Characteristics of isolates from A. mearnsii in South Africa (Figs. 1-5) differed morphologically from C. fimbriata (Figs. 6-9) in various ways. South African isolates including those from Protea had light coloured colonies that were distinguishable from the dark colonies of the C. fimbriata isolates from other georaphic areas. This was to some extent influenced by differences in peripheral colour between the sets of isolates. The South African isolates including herbarium specimens from Protea had light perithecial bases with black necks that formed flattened areas where the necks extruded from the bases (Figs. 1, 5a). In contrast, the C. fimbriata isolates had entirely black perithecia (Fig. 8). Isolates from A.



Fig. 5. Perithecium, conidiophores with conidia and ascospores of *Ceratocystis albofundus*. Fig. 5a. Perithecium with light coloured base and dark neck terminating in divergent ostiolar hyphae (Bar = 100 μ m). Figs. 5b, c. Barrel-shaped and cylindrical conidia produced enteroblastically through ring wall building (Bar = 10 μ m). Fig. 5d. Hat-shaped ascospores from side and end view (Bar = 10 μ m).

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mearnsii in South Africa also differed from authenticated isolates in that they had divergent ostiolar hyphae (Fig. 9) compared with the convergent ostiolar hyphae for the authenticated isolates of *C. fimbriata* (Fig. 7). Measurements of various structures varied greatly in all isolates and there were also significant differences amongst isolates known to represent the same fungus (Table 3). These were thus not considered as taxonomically useful.

Scanning electron microscopy showed that the hatshaped ascospores of the South African isolates (Fig. 6) had double brims. The same was true for the authentic *C. fimbriata* isolates as has previously been observed (*De Beer* et al., 1995). One of these brims was around the spore whereas the other was discontinuous and occurred only at opposite ends of the ascospores.

Growth characteristics on agar of the South African Ceratocystis sp. from A. mearnsii differend from the authentic C. fimbriata isolates (Table 4). South African isolates had an optimum growth at 30 °C. Isolates of C. fimbriata grew optimally between 20–25 °C.

Table 4. Comparative growth rates of *Ceratocystis albofundus* from *Acacia mearnsii* in South Africa and *C. fimbriata* at different temperatures¹

| Source of isolates | Temperature (°C) | | | | |
|--------------------|------------------|-----------|------------------------|------------------------|------------|
| | | 15 Col | 20 ony dia after | 25 imeter 8 days | 30 (mm) |
| Platanus hybrida | (PREM 51642) | 16 | 22 | 20 | 13 |
| Ipomoea batatas | (PREM 51643) | 10 | 24 | 25 | 19 |
| Àcacia mearnsii | (PREM 51641) | 10 | 18 | 20 | 27 |
| A. mearnsii | (PREM 51645) | 9 | 11 | 20 | 24 |
| | | | | | |

Growth rates determined on 60 mm Petri dishes containing 15 ml 2% MEA

Molecular comparisons

The amplified fragments obtained for the South African isolates from A. mearnsii and the authentic C. fimbriata isolates included approximately 620 and 520 base pairs respectively (Fig. 10). Rooted phylogenetic trees from PAUP analysis (Fig. 11) grouped the South African isolates apart from authentic C. fimbriata isolates. Ceratocystis moniliformis which is morphologically similar to C. fimbriata grouped apart from all other isolates. The C. fimbriata isolate from Papua New Guinea, although grouping in the greater C. fimbriata group, was more distant from the European isolates of C. fimbriata than they were from each other. Bootstrap values gave 67-100% confidence intervals for branching patterns obtained with PAUP. Distance matrix analysis [UPGMA] (unweighted pair group method using arithmetic averages) yielded the same results as obtained using PAUP analysis and are therefore not presented.



Figs. 6–9. Perithecial and ascospore characteristics of *Ceratocystis albofundus* and *C. fimbriata*. Fig. 6. Scanning electron micrograph of hat-shaped ascospores of *C. albofundus* with double brims above the continuous brims and on opposite ends of the spores (Bar = 1 μ m). Fig. 7. Scanning electron micrograph of convergent arrangement of ostiolar hyphae for *C. fimbriata* (Bar = 1 μ m). Fig. 8. Light micrograph of the entirely black perithecium of *C. fimbriata* (Bar = 100 μ m). Fig. 9. Scanning electron micrograph of divergent ostiolar hyphae in *C. albofundus* (Bar = 1 μ m).

Discussion

Based on detailed morphological and molecular comparisons in this study, we conclude that the *Ceratocystis* species from black wattle in South Africa and tentatively identified as *C. fimbriata* (Morris et al., 1993) is a distinct taxon. The following description is therefore provided for the fungus:

Ceratocystis albofundus Wingfield, De Beer and Morris, sp. nov. Coloniae in 2% MEA tarde crescentes, incremento optimo ad 30°C, attingentes diametrum 2.7 cm 8 diebus, initio albae, maturae cremescentes. Nullum incrementum ad 10°C. Perithecia nata superficialiter in superficie texti hospitis et in laminis primarii secernendi in cultura in laminis 2% MEA. Bases peritheciales 104–200 (158) µm, fulvae, globosae, inornatae; colla perithecialia, 208–840 (510) µm longa, 20–32 (27) µm lata ad basim, 16–24 (17) µm lata proxime infra hyphas ostiolares, atra ad basim pallescentia prope apicem, glabro-tunicata, extendentia in basim perithecialem cum collari (modo lato). Hyphae os-

tiolares 40-60 (49) µm, hyalinae, dispositione digrediente. Asci evanescentes. Ascosporae unicellulares, hyalinae, ellipsoideae visae a fronte, similes petasorum visae a latere 4-6 (5.2) µm longae, 3.5-5 (4) µm latae accumulatae in guttulis mucosis ad apicem colli, costula gemina praesente ad extrema opposita ascosporarum supra costulam continuam, sine vagina gelatinosa. Conidia nata et in hospite et in 2% MEA. Duae in mycelio superficiali formae conidiorum, vel cylindrica 8-24 (15) µm longa, 3-4 (3.5) µm lata; vel doliiformia 6-10 (7.4) µm longa, 4-8 (6.2) µm lata; ambo hyalina, extremis truncatis, nata parietibus annuliformibus constructis, unicellularia, nata concatenata, aliquando aggregatis massis mucosis. Conidiophora 24-104 (54) µm longa, 3-5 (3.8) µm lata, septata, mononematosa, hyalina, glabro-tunicata. Hyphae 2-5 (3.2) µm, hyalinae, septatae.

Specimina explorata: In ramis A mearnsii monstrantibus in Valle Fluminis "Mkomasi", Provinica Natali, Africa Australi, 1992, M. Morris, PREM 51641 HOLO-TYPUS. Paratypi in A. mearnsii, in Valle Fluminis "Mkomasi", Provincia Natali, Africa Australi, 1992, M. Morris, PREM 51637, PREM 51639; Isotypi in A. mearnsii, "East London" 1993, M. Morris, PREM 51645.

Ceratocystis albofundus Wingfield, De Beer and Morris, sp. nov.

Colonies on 2% MEA slow growing, with optimum growth at 30 °C, reaching a diameter of 2.7 cm in 8 days, white at first, becoming creamy at maturity. No growth at 10 °C. Perithecia (Figs. 1, 5a) produced superficially on surface of host tissue and on primary isolation plates in

| | | 10 | 20 | 30 | 40 | 50 |
|---|------|--|--------------------------|---|---------------------|---------------------|
| PREM 5 | 1639 | CTGTNTTTTG | GTGAAGACGG | AAAGCTGCCT | TGGTGGGTGT | NTOTACTOOT |
| PREM 5 | 1829 | G | | | | C |
| PREM 5 | 1645 | T | G | | | C |
| PREM 5 | 1644 | AT.C | TA.TGAGAT. | | та | |
| PREM 5 | 1831 | TAT.C | TA.TGAGAT. | T | | |
| PREM 5 | 1830 | TAT.C | TA. TGAGAT. | | - 4T | |
| PREM 5 | 1643 | T AT. C | TA. TGAGAT. | | - AT | |
| IFO 86 | 67 | TGTAA.CCAT | TTGA | | | |
| N. cra | ssa | | TAC. | GTTCT.GG | C.CCG | CC.G.AA |
| | | | 120 | 2/2/ | 1226 | |
| DDDD DA | | 60 | 70 | 80 | 90 | 100 |
| PREM 5. | 1639 | GTTAACCT-C | TTTTTTATAAG | GGGGCAGCCC | ACTACCGCTA | GCCACCAGCA |
| PREM 5. | 1829 | · · · · · · · · · · · · · · · · · · · | | * * * * * * * * * * | | |
| PREM 5. | 1645 | | | • • • • • • • • • • | ******* | ******* |
| PREM 5. | 1031 | GG | C.G.AGG. | | G | |
| PREM 5. | 1831 | GG | C.G.AGG. | | G | |
| PREM 5. | 1830 | GG | C.G.AGG. | | G | |
| FREM 5. | 1043 | GG, | C.G.AGG. | A | G | |
| IFO 866 | 67 | T=== | A.CA | T.AA.T | AT.GGG | .T.T |
| N. crai | ssa | | C | CT | GGATT.GG | .T.TC |
| PREM 51 | 1639 | 110 GCATACAAGT |) 120 CTTTTACCAC |) 130 TATAAACCTT |) 14(CTGTATATTT |) 150 TTTAAAATTT |
| PREM 51 | 1829 | | | | ****** | |
| PREM 51 | 1645 | | | | | N |
| PREM 51 | 1644 | .T | CG | .G | TATAT | CC.G |
| PREM 51 | 1831 | .T | CG | .G | TATAT | CC.G |
| PREM 51 | 1830 | .T | CG | .G | TATAT | CC.G |
| PREM 51 | 1643 | .TT | C | | T.TAT.A. | CT.GA |
| IFO 866 | 57 | GAGGTA | CG | | .GT.T.TA.A | .AA.G |
| N. cras | ssa. | T.GC.G | GCG. | CGG.GTG | .GAA.CTAAA | C.CTTGA. |
| | | 160 | 1.70 | 100 | 100 | |
| PREM 51 | 639 | TTAAAATT | | / 180 //////////////////////////////////// | 23220000222 | 200 |
| PREM 51 | 829 | ************************************** | CIGUGIOGCH | INACIAIAAA | ANAAGTTAAAA | ACTITCAACA |
| PREM 51 | 645 | N. | | NINTRO I | •••••••••• | * * * * * * * * * * |
| PREM 51 | 644 | TC | * * * * * * * * * * | · · · · · · · WINININ | N | * * * * * * * * * * |
| PREM 51 | 831 | TC | • • • • • • • • • • • | * * * * * * * * * * | | ******* |
| PREM 51 | 830 | TC | • • • • • • • • • • • | | . N | ***** |
| PREM 51 | 643 | TC | | ******** | | ********* |
| IFO 866 | 7 | A TTC | | m mam | | ******* |
| N. Cras | 1928 | CT | CTVC ACM | 3 m m | . 101A | |
| the second | | • • • • • • • • • • • • • • • • • • • | a to be a tor a statute. | *** * * * * * * * * * | | |

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| | 210 | 220 | 230 | 240 | 250 |
|--|---|---|---|--|--|
| DREM 51639 | ACCCATCTCT | TOCOTOTAGO | ATCGATGAAG | AACGCAGC | GAAATGCGAT |
| DDEM 51020 | | 10001011100 | in com cime | | |
| TREM SIGAS | ********* | ******** | | | M |
| DDDW E1644 | | * * * * * * * * * * * | • • • • • • • • • • • | | |
| PREM SIG44 | | | | | |
| PREM 51831 | * * * * * * * * * * | | | | ******** |
| PREM 51830 | | ******** | . N | | ******** |
| PREM 51643 | ******** | ******** | | | |
| IFO 8667 | N | * * * * * * * * * * | ******** | AGN. | NN.N |
| N. crassa | | TG | * * * * * * * * * * | * * * * = = * * * * | * * * * * * * * * * |
| | | | | | |
| | 260 | 270 | 1 28 | 29 | 0.00 |
| DDFM 51539 | AACTAATCTC | aammonacaa | TTCAC_TCAA | TNATYTCAATN | mmmca accca |
| DDEM 51929 | 11101101010 | nni i dendrin | 11000-1000 | C | ***0000000 |
| TOPM SIGAS | | | | 0 0 | |
| DDDM E1CAA | | | | | |
| PREM DI044 | * * * * * * * * * * * | ********* | | | . 14 |
| PREM 51831 | | · · · · · · · · · · · · · · · | | | |
| PREM 51830 | ******* | * * * * * * * * * * * | | .CNN.C | .1 |
| PREM 51643 | ********* | ******** | ***** | .c | ·N · · · · · · · · |
| IFO 8667 | | ********* | * * * * * * * * * * * | .CC | .N |
| N. crassa | .G | | | .CC | |
| | | | | | |
| | - <u>1</u> 472-13 | 10 | | | |
| | 31(| 320 | 330 | 341 | 350 |
| PREM 51639 | CATTGNNCCT | GGTAGTATTC | TGCCAGGCAT | GCCTGTNCGA | GCGTCATTTC |
| PREM 51829 | NN | N | | N | ******** |
| PREM 51645 | CN | N | | N | ********* |
| PREM 51644 | CC | N | | C | |
| PREM 51831 | CN | N | | N | |
| PREM 51830 | CG | C | | C | |
| PREM 51643 | NN | N | | N | N |
| IFO 8667 | CNC | A.CC | TG | C | G |
| N. crassa | NCG | C.CC | GC.A | N.T. | G |
| | | | | | |
| | | | | | |
| | | | | | |
| | 360 | 370 | 380 | 391 | 400 |
| PREM 51639 | 360 ACCACTCAAG |) 370 ACTTGCTTTA |) 380 GTTTTGGTGT |) 390 TGGAGGTCCT | 0 400 GTTCTTACCC |
| PREM 51639 PREM 51829 | 360 ACCACTCAAG |) 37(ACTTGCTTTA |) 380 GTTTTGGTGT |) 39 TGGAGGTCCT | 400 GTTCTTACCC |
| PREM 51639 PREM 51829 PREM 51645 | 360 ACCACTCAAG |) 37(ACTTGCTTTA |) 380 GTTTTGGTGT |) 391 TGGAGGTCCT | GTTCTTACCC |
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| | 510 | 520 | 530 | 540 | 550 |
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| PREM 51639 | GTAACATGCC | GTTAAAGGTT | ACAGAAGGGC | TTATAGTGGG | TGGTGATAGA |
| PREM 51829 | G. | | | | |
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| PREM 51831 | C.G. | .C | | | |
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Fig. 10. Alignment of bases of the ITS1 and ITS2 regions and 5.8r RNA gene for three isolates of *Ceratocystis* sp. from black wattle in S.A., four authentic isolates of *C. fimbriata* from various other areas, one isolate of *C. moniliformis* and *Neurospora crassa* which was used as an outgroup. N indicates unknown bases; a dot indicates bases identical to the corresponding base in the *Ceratocystis* sp. from South Africa (PREM 51639); dashes represent deletions in the sequence.



Fig. 11. Dendrogram obtained with PAUP analysis from ITS1 and ITS2 regions and the 5.8S gene of the rRNA operon, showing the phylogenetic relationships between the *Ceratocystis* sp. from black wattle in South Africa, *C. fimbriata* isolates from other areas and *C. moniliformis.* The bootstrap values are expressed as % confidence intervals.

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culture on 2% MEA plates. Perithecial bases 104-200 (158) µm in diameter, yellowish brown, globose, unornamented; perithecial necks, 208-840 (510) µm long, 20-32 (27) µm wide at base, 16-24 (17) µm wide just below ostiolar hyphae, black at base becoming lighter near tip, smooth-walled, extending into perithecial base with a "collar". Ostiolar hyphae 40-60 (49) um, hyaline, divergent arrangement (Figs. 2, 9). Asci evanescent. Ascospores (Figs. 2, 4, 5d, 6) one-celled, hyaline, elliptical in face view, hat-shaped in side view, 4-6 (5.2) µm long, 3.5-5 (4) µm wide, accumulating in slimy droplet at tip of neck, double brim (Fig. 6) present at opposite ends of ascospores above continuous brim, without gelatinous sheath. Conidia produced on both host and 2% MEA. Two conidial forms on superficial mycelium, cylindrical 8-24 (15) um long, 3-4 (3.5) µm wide (Figs. 2, 5c); barrel-shaped 6-10 (7.4) µm long, 4-8 (6.2) um wide (Figs. 3, 5b), hvaline, truncated ends, produced by ring wall building, 1-celled, produced in chains, sometimes forming aggregated slimy masses. Conidiophores 24-104 (54) um long, 3-5 (3.8) um wide, septate, mononematous, hyaline, smooth walled. Hyphae 2-5 (3.2) µm, hyaline, septate.

Specimens examined: On branches from A. mearnsii with die-back symptoms, Mkomasi River Valley, Natal Province, South Africa, 1992, M. Morris, PREM 51641 HOLOTYPE. Paratypes from A. mearnsii, Mkomasi River Valley, Natal Province, South Africa, 1992, M. Morris, PREM 51637, PREM 51639. Paratypes from A. mearnsii, East London, Cape Province, South Africa, 1992, M. Morris, PREM 51645.

The most obvious morphological characters distinguishing C. albofundus occurring on black wattle in South Africa from C. fimbriata, are the perithecial base colour and arrangement of ostiolar hyphae. The former isolates are characterized by light bases and dark, black necks as opposed to dark bases in C. fimbriata. Isolates of C. albofundus have divergent ostiolar hyphae in contrast to the convergent arrangement of the ostiolar hyphae of C. fimbriata.

The herbarium material of *C. fimbriata* from *Protea* in South Africa shares the characteristic light perithecial bases and dark necks with the *C. albofundus* isolates from *A. mearnsii* in South Africa. Significant differences in sizes of various structures were observed between isolates from black wattle and those from *Protea* sp. However, differences were also observed amongst the isolates from *A. mearnsii*. We believe that perithecial colour is the most stable and reliable morphological character. It is thus likely that the collections from *Protea* in South Africa represent *C. albofundus* and are thus distinct from *C. fimbriata*.

Comparisons of rRNA gene DNA sequence in this study supported morphological observations that *C. albofundus* from black wattle in South Africa represents a distinct taxon. Analysis of sequence data from ITS1 and ITS2 regions has shown variability for the different isolates while sequences of the 5.8S gene correlate well for the different isolates. Based on the variability of the ITS regions it is possible to distinguish between the isolates from *A. mearnsii* in South Africa and authentic *C. fimbriata* isolates in phylogenetic trees. If the sequences of the different isolates were too conserved, no distinction could have been made.

Sequencing of ribosomal DNA holds the advantages that the rRNA operon is repeated and easily detectable (*Metzenberg*, 1991). The rRNA operon includes both conserved and variable regions (*Hillis* and *Dixon*, 1991; *Metzenberg*, 1991) and depending on the level of comparison, different regions can be used for analysis. The 5.8S rRNA gene is very small and well conserved (*Blanz* and *Unseld*, 1988) while intergenic transcribed spacers (ITS) on either side of the 5.8S gene are highly variable (*Chambers* et al., 1986; *Nazar* et al., 1988). This region has proved useful in previous taxonomic studies (*Otsuka* et al., 1983; *Viljoen* et al., 1993; *Seifert* et al., 1995).

Ceratocystis fimbriata is the type species of Ceratocystis s.s. and has been known to science for more than 100 years (Halsted, 1890). It has a worldwide distribution and a wide range of hosts to which the fungus has developed considerable specificity (De Vay et al., 1963; De Vay et al., 1968; Kile, 1993; Kojima, 1993). It is possible that C. fimbriata represents a species complex representing numerous distinct species that are morphologically and ecologically similar. C. albofundus might then represent one of these genetic entities and studies on allied species are necessary to resolve this question.

At this stage, very little is known concerning the distribution or losses associated with *C. albofundus* in South Africa. Acacia mearnsii is, however, a commercially important forest tree and the appearance of this virulent pathogen in recent years is of understandable concern. The distinct differences between *C. albofundus* and *C. fimbriata* shown in this study suggest that the fungus might have been present in the country for a considerable time. Indeed, the occurrence of this fungus associated with native *Protea* spp. adds further credence to the hypothesis that the fungus is native to South Africa. If this is the case, we must assume that the fungus has adapted to pathogenicity on the exotic *A. mearnsii*.

In addition to being an important commercial forest species in South Africa, *A. mearnsii* is also a serious invader weed that particularly contaminates river courses (*Boucher*, 1978). Any pathogen with the potential to reduce the negative impact of the tree but without resulting in losses to commercial operations would be of interest. If *C. albofundus* is native to South Africa, as results of the present study suggest, it would be more acceptable to use the fungus for biological control of weed *A. mearnsii*. Additional studies, particularly on the infection biology and host range of *C. albofundus* are required before decisions can be taken on this issue.

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