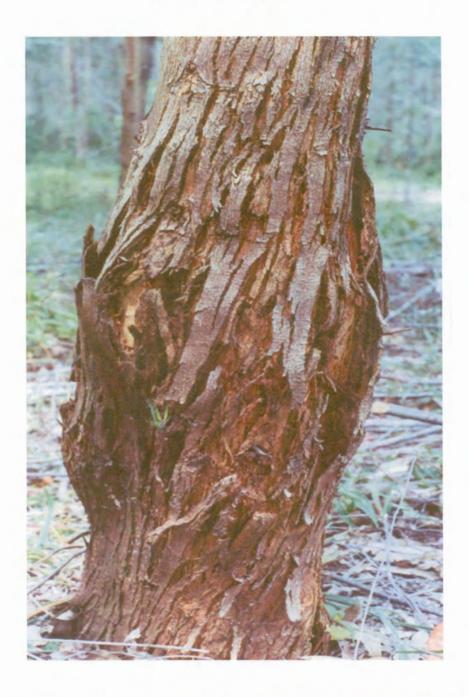


CHAPTER 3



Discovery of the *Eucalyptus* canker pathogen, *Cryphonectria cubensis*, on *Miconia* (Melastomataceae) in Colombia



ABSTRACT

Species in the tropics and subtropics. During recent surveys for native hosts of C. cubensis in Colombia, a fungus with fruiting structures similar to those of C. cubensis was found on native Miconia theaezans and M. rubiginosa, both members of the Melastomataceae. The morphology of this fungus was studied and DNA sequences were obtained for the ITS1/ITS2 region of the rDNA operon and the β-tubulin genes. Pathogenicity of the fungus was also assessed on various Melastomataceae. Isolates from M. theaezans and M. rubiginosa grouped together with other South American C. cubensis isolates from Eucalyptus species and Syzygium aromaticum. Fruiting structures on M. rubiginosa also resembled those of C. cubensis on E. grandis. Cryphonectria cubensis isolates from E. grandis and M. theaezans were mildly pathogenic on the various hosts, although Tibouchina spp. and M. rubiginosa appeared to be more susceptible to C. cubensis than a number of Eucalyptus clones and M. theaezans. The occurrence of C. cubensis on native Miconia spp. supports the view that this pathogen is native to South and Central America.



INTRODUCTION

Cryphonectria cubensis (Bruner) Hodges is one of the most serious pathogens of Eucalyptus spp. (Myrtaceae) in South America (Boerboom & Maas 1970, Hodges et al. 1976, Hodges, Geary & Cordell 1979, Hodges 1980), including Colombia (Van der Merwe et al. 2001). The associated canker disease has also been reported from other parts of the world with tropical, sub-tropical or temperate climates, mostly Africa (Gibson 1981, Roux et al. 2003, Wingfield, Swart & Abear 1989), Southeast Asia (Florence, Sharma & Mohanan 1986, Hodges, Alfenas & Cordell 1986, Sharma, Mohanan & Florence 1985) and Australia (Davison & Coates 1991). In these regions, Cryphonectria canker is most severe in areas with high rainfall and temperature (Boerboom & Maas 1970; Hodges et al. 1976, 1979, Sharma et al. 1985).

Cankers caused by *C. cubensis* are usually found at the base or lower stems of trees, but may also occur higher up on the trunks (Sharma *et al.* 1985, Hodges *et al.* 1976, 1979). The pathogen kills the cambium and in severe cases, can result in tree death (Sharma *et al.* 1985, Hodges *et al.* 1976, 1979). The only practical management option for the disease is planting resistant *Eucalyptus* species and clones (Alfenas, Jeng & Hubbes 1983, Hodges *et al.* 1976, Sharma *et al.* 1985, Van Heerden & Wingfield 2002).

Until recently, *C. cubensis* has been known only to occur on trees belonging to the Myrtaceae. These hosts are predominantly species of *Eucalyptus* but also include clove (*Syzygium aromaticum* (L.) Merr. & Perry) (Hodges *et al.* 1986) and strawberry guava (*Psidium cattleianum* Sabine) (Hodges 1988). The recent discovery of *C. cubensis* on *Tibouchina urvilleana* (DC). Logn. (Fig. 1a) and *T. lepidota* Baill. (Fig. 1b), which are members of the Melastomataceae native to South America, was thus considered intriguing (Wingfield *et al.* 2001). The report of Wingfield *et al.* (2001) has led to subsequent disease surveys and the discovery of the fungus on ornamental *T. granulosa* in South Africa (Myburg *et al.* 2002a).

The possible origin of *C. cubensis* presents an interesting question that is also important in terms of disease management. One hypothesis is that the pathogen originated on clove, also a member of the Myrtaceae, in Indonesia (Hodges *et al.* 1986). The world-wide distribution of this fungus would then have occurred through the establishment of clove



plantations linked to the spice trade (Hodges et al. 1986). The discovery of C. cubensis on native Tibouchina spp. in South America has, however, raised the alternative hypothesis that C. cubensis could have originated in that part of the world (Wingfield et al. 2001).

Results from phylogenetic studies, based on DNA sequence for three gene regions (Myburg, Wingfield & Wingfield 1999, Myburg et al. 2002b), have shown that C cubensis from South America and Southeast Asia resolve into two distinct phylogenetic sub-clades. This suggests that C cubensis in these areas are different from one another and was not introduced into one area from another. Equally intriguing is the recent discovery based on comparisons of β -tubulin and histone H3 gene sequences (Myburg et al. 2002b), that South African isolates of C cubensis are distinct from those of South American and Southeast Asian origin, and probably represent a distinct taxon.

During recent surveys for *C. cubensis* on native Melastomataceae in Colombia, a fungus resembling *C. cubensis* was found on a number of new hosts in the Melastomataceae. The aim of this study was to identify the fungus based on morphology and DNA sequences. Pathogenicity of the isolates originating from the new hosts was also tested on these hosts and on *E. grandis* W. Hill ex Maiden.

MATERIALS AND METHODS

Symptoms and collection of samples

Disease surveys were conducted in various areas of Colombia with different altitudes and precipitation (Fig. 2). Specimens were collected from *Miconia theaezans* (Bonpl.) Cogn. (Fig. 1c) in a natural forest from the La Selva farm of Smurfit Carton de Colombia near the city Pereira in the Risaralda province. Cankers covered in fruiting structures were also found on *M. rubiginosa* (Bonpl.) DC. trees (Fig. 1d) of different ages on the farm Vanessa, near Timba in the Cauca province. These trees occurred within a *Eucalyptus* plantation where *C. cubensis* has previously been collected.

Disease symptoms on the *Miconia* spp. included branch die-back, and cankers on branches, trunks or the tree bases that often resulted in the death of trees or tree parts.



The cankers were generally associated with physical wounds to branches and stems. Fruiting structures were produced abundantly around the edges of the actively growing canker margins.

Specimens collected from cankers were transported to the laboratory for further analysis. Single conidial isolations were made from the fruiting structures by suspending spore masses in sterile water and plating the resulting suspensions on malt extract agar MEA (20 g/l Biolab malt extract agar). Single germinating conidia were then transferred to fresh MEA plates. Representative isolates have been preserved at 5 °C in the culture collection (CMW) of the Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa (Table 1). The original bark specimens from whom isolations were made have been deposited (Table 2) in the herbarium of the National Collection of Fungi, Pretoria, South Africa (PREM).

DNA sequence comparisons

Isolates from *Miconia* spp. and *E. grandis* were included in the DNA sequence comparisons (Table 1). Previously characterised *C. cubensis* isolates from *Eucalyptus* spp. (Myburg *et al.* 2002b) and *S. aromaticum* (Myburg *et al.* 1999, 2003) from different parts of the world were included for comparative purposes. In addition, representative species of *Cryphonectria* and *Endothia*, namely *C. parasitica* (Murr.) Barr, *C. radicalis* (Schw.: Fr.) Barr, *C. nitschkei* (Otth.) Barr, *C. macrospora* (Kobayashi & Ito) Barr and *E. gyrosa* (Schw.: Fr.) Fr. were sequenced by Venter *et al.* (2002). Two *Diaporthe ambigua* Nitschkei isolates were included as outgroup taxa to root the phylogenetic trees.

Isolates for DNA sequence comparisons were grown in Malt Extract Broth (20 g/l Biolab malt extract). DNA was extracted from mycelium as described in Myburg et al. (1999). The internal transcribed spacer (ITS) regions ITS1 and ITS2, as well as the conserved 5.8S gene of the ribosomal RNA (rRNA) operon, were amplified using the primer pair ITS 1 and ITS 4 (White et al. 1990). Two regions within the β-tubulin gene were amplified with primer pairs Bt1a/Bt1b and Bt2a/Bt2b respectively (Glass & Donaldson 1995). The reaction conditions for amplifying these gene regions were the same as those given by Myburg et al. (1999) and Myburg et al. (2002b) respectively. PCR products were visualised on 1% agarose (ethidium bromide stained) gels using a UV light.



Purification of PCR products was done using a QIAquick PCR Purification Kit (Qiagen GmbH, Hilden, Germany).

The purified PCR products were sequenced with the same primers that were used to amplify the respective DNA regions. An ABI PRISMTM Dye Terminator Cycle Sequencing Ready Reaction Kit with AmpliTaq® DNA Polymerase, FS (Perkin-Elmer, Warrington, United Kingdom) was used to sequence the amplification products on an ABI PRISM 3100TM automated DNA sequencer.

The resulting raw nucleotide sequences were edited using Sequence Navigator version 1.0.1 (Perkin-Elmer Applied BioSystems, Inc., Foster City, California) software. Sequences were manually aligned. Phylogenetic trees were inferred using PAUP (Phylogenetic Analysis Using Parsimony) version 4.0b (Swofford 2002). A Templeton Nonparametric Wilcoxon Signed Ranked test (Kellogg, Appels & Mason-Gamer 1996) was applied to the rRNA and β -tubulin gene sequence data sets to determine whether they could be analysed collectively in the parsimony analysis.

A phylogenetic tree was inferred from maximum parsimony (MP) using the heuristic search option with the tree-bisection-reconnection (TBR) branch swapping and MULTREES options (saving all optimal trees) effective. Gaps inserted during manual sequence alignment were treated as fifth character (NEWSTATE) in the heuristic searches. A 1000 replicate bootstrap was executed to assess the confidence levels of the branch nodes of the phylogenetic tree. The sequence data generated in this study have been deposited in GenBank and accession numbers are listed in Table 1.

Morphology

Conidiomata from the bark specimens were rehydrated for one min in boiling water. The structures were then sectioned at -20 °C to a thickness of 12-14 µm with a Leica CM1100 cryostat after embedding them in Leica mountant (Setpoint Premier, Johannesburg, South Africa). Sections were mounted on microscope slides in lactophenol. Structures were also sectioned by hand to observe the morphology of the conidiophores. Twenty measurements, presented as (min-)(mean-SD) – (mean+SD)(-max) µm, of ascospores, asci, conidia and conidiophores suspended in lactophenol and



3% KOH, were taken for the specimens. A measurement range from two structures was obtained for the eustromata and perithecia. Colour notations of Rayner (1970) were used.

Pathogenicity tests

Greenhouse inoculation trials. Three isolates from *E. grandis* in Colombia (CMW 10638, CMW 10639, CMW 10640) and two isolates from *M. theaezans* (CMW 10625, CMW 10626) were screened for pathogenicity on *T. urvilleana* (seven months old) plants in a greenhouse with natural light at ~25 °C. Five trees per isolate were inoculated and an equal number of trees were inoculated with sterile water agar (WA) (20 g/l Biolab agar) plugs as controls. Inoculations were made with a cork borer (9 mm diam). Agar discs of the same size were taken from the edges of actively growing cultures and placed inside the wounds with the mycelium facing downwards. The agar discs were covered with tissue paper moistened with sterile water, and secured with masking tape. The masking tape was removed after ten days.

Trees were inoculated in October 2001 and lesion development was evaluated after four weeks. Lesions were exposed by scraping away the bark and the lengths of the lesions were measured. The most pathogenic isolates from *E. grandis* and *M. theaezans* (CMW 10639 and CMW 10625 respectively) were selected for subsequent field inoculation trials.

In a second greenhouse trial, two isolates from *M. rubiginosa* (CMW 10022 and CMW 10024) were inoculated on *T. urvilleana* and *E. grandis* (clone ZG14), which were 17-24 months old and up to 1.8 m high. A highly pathogenic isolate of *C. cubensis* from South Africa (CMW 2113), used in previous pathogenicity studies (Myburg *et al.* 2002a, Van Heerden & Wingfield 2001, 2002) was included for comparative purposes. Inoculation procedures were the same as those in the first trial and ten trees were inoculated for each of the three isolates and for the negative control using WA discs. Inoculations were done as described above except that a cork borer with a diameter of 6 mm was used. The trial was inoculated in May 2002, and evaluated in June 2002.



Field inoculation trials. The first inoculation trial was conducted at Rancho Grande farm, Restrepo, Valle (76° 30' 49" W and 3° 51' 43" N, 1067 mm/y, 1469 masl). This trial included reciprocal inoculations with isolates from *E. grandis* (CMW 10639) and *M. theaezans* (CMW 10625) selected in the first greenhouse trial. Five tree species were used, namely *T. semidecandra* Cogn. (Fig. 1f), *T. lepidota*, *T. urvilleana*, *M. theaezans* and a clone of *E. grandis* (clone 274). These trees were one year old and were growing in plastic planting containers. Twenty trees of each species were inoculated per isolate, and an equal number of trees were inoculated with WA discs to serve as negative controls. Inoculations were conducted in a similar way to greenhouse inoculations but the diameter of the wound was 4 mm. Trees were inoculated in May 2002 and lesion development was evaluated after twelve weeks. Internal lesion length in the cambium was measured for all field trials.

The second field trial was at the Vanessa farm (Fig. 2), Timba, Cauca province (76° 35' 15" W and 3° 5' 42" N, 3143 mm/y, 2048 msal). Isolate CMW 10022 from *M. rubiginosa*, shown to be pathogenic in the preliminary greenhouse trial, was used. Twenty three-year-old *E. grandis* trees (clone 275), 20 trees from seeds of a cross between *E. grandis* and *E. urophylla* (*E. "urogandis"* clone 212), and 20 *M. rubiginosa* trees were inoculated. The *M. rubiginosa* trees were approximately six years old and formed part of the native vegetation surrounding the commercial plantations. Ten trees of each host were inoculated with MEA to serve as negative controls. The trial was initiated in June 2002 and lesion lengths were measured after 12 weeks in late September 2002. The same inoculation techniques used in greenhouse and other field trials were applied, except that the inoculation wounds were six mm in diameter. The data for the pathogenicity trials were analysed using a one-way Analysis of Variance (ANOVA) with SAS (1990).

RESULTS

DNA sequence comparisons

Amplification of the ITS1, 5.8S and ITS2 rRNA regions as well as the two regions in the β-tubulin gene resulted in PCR products of approximately 600bp and 550bp respectively. The Templeton Nonparametric Wilcoxon Signed Ranked test (Kellogg *et al.* 1996)



showed that the rRNA and the β-tubulin sequence data sets could be combined in the phylogenetic analyses. The combined data set consisted of 32 taxa with the *D. ambigua* isolates as the outgroup (Fig. 3). This data set consisted of 1498 sequence characters of which 886 were constant, 44 were variable parsimony-uninformative and 568 were variable parsimony-informative.

The phylogenetic tree generated from the heuristic search (Fig. 4, tree length = 1198 steps, consistency index/CI = 0.8, retention index/RI = 0.9) resolved the taxa into three clades separately from the outgroup taxa. The largest of the three clades represented C. cubensis, while the other two included representative species of Cryphonectria (C. parasitica, C. radicalis, C. nitschkei and C. macrospora) grouping in the one clade, and E. gyrosa in the other (bootstrap support = 100% respectively).

The *C. cubensis* clade represented this fungus isolated from a variety of hosts originating from South America, Southeast Asia and South Africa. All three geographical areas are represented as three well supported clades in the phylogenetic tree (Fig.4). The Southeast Asian group (bootstrap 98%) included *C. cubensis* isolated from clove and *Eucalyptus* species. The South African group is characterised by *C. cubensis* isolated from *E. grandis* (bootstrap 95%). The South American group (bootstrap 72%) include *C. cubensis* isolated from *Eucalyptus* spp. and *S. aromaticum* as reported previously (Myburg *et al.* 1999, 2002b, 2003). Isolates originating from *M. theaezans* (CMW 9980, CMW 9993, CMW 10626, CMW 10639) and *M. rubiginosa* (CMW 9970, CMW 9996, CMW 10022, CMW 10024, CMW 10025, CMW 10026, CMW 10028), grouped within the South American sub-clade.

Morphology

Specimens from *M. rubiginosa* (PREM 57517) had ascomata similar to those of *C. cubensis* found on *E. grandis* in Colombia (PREM 57294). They could be distinguished from conidiomata since only one to three fuscous-black (13""m), cylindrical necks (380-720 µm long) emerged from the bark (Fig. 5a). Orange (15) stromatic tissue was sometimes visible at the base of the necks (Figs 5a-b). Longitudinal sections revealed umber (15m), *textura porrecta* tissue surrounding the black perithecial necks (Figs 5b-c) and reduced prosenchymatous stromatic tissue present at the base of the neck (Figs 5b,



5d). Asci were fusoid, eight-spored with a refractive apical ring, (19.5-)20.5-24.5(-27.0) μm long and (4.5-)5.0-6.5(-7.0) μm wide (Fig. 5e). Ascopores were fusoid to oval, hyaline with a single septum in the center of the spores, (5.0-)5.5-7.0(-8.5) μm long and 2.0-2.5 μm wide (Figs 5f). The ascomata also resembled those previously described from South America (Bruner 1917, Hodges *et al.* 1979, Hodges 1980) and ascomata previously described from other parts of the world (Heath *et al.* 2003, Myburg *et al.* 2002a, 2003).

Conidiomata of the fungus on *M. rubiginosa* (PREM 57517) were similar in shape to those of *C. cubensis* occurring on *E. grandis* (PREM 57294). Structures were pyriform, superficial and fuscous-black (13****m) with a single attenuated neck and luteous (19) spore drops or tendrils (Figs 5g-h). The tissue of the conidiomatal base was umber (15m), textura globulosa but the neck tissue was textura porrecta (Fig. 5i). Conidiophores were branched, and conidiogenous cells enteroblastic phialidic, cylindrical with inflated bases and attenuated apices (Figs 5j-k). Conidia were hyaline, oblong to oval, aseptate, 3.0-4.0 µm long, 1.5-2.0 µm wide (Fig. 5l). These characteristics were also similar to those described previously (Bruner 1917, Hodges et al. 1979, Hodges 1980, Myburg et al. 2002b, 2003).

A few morphological differences exist between structures on *E. grandis* and *M. rubiginosa*. The stromatic tissues of the ascomata on *E. grandis* were slightly more distinctly erumpent than those on *M. rubiginosa*. Conidiomata on *M. rubiginosa* were much smaller (25-400 μm long in total above surface of bark) than those on *E. grandis* (420-960 μm long in total above surface of bark). Conidiomata on *E. grandis* were also better developed with wide bases (210-420 μm wide above surface of bark) and long, strongly attenuated necks (220-440 μm long), unlike conidiomata on *M. rubiginosa* that had narrow bases (140-260 μm wide above surface of bark) and shorter necks (140-180 μm long).

Pathogenicity tests

Greenhouse inoculations. In the first greenhouse trial (Table 3), inoculation with C. cubensis isolates from E. grandis (CMW 10638, CMW 10639, CMW 10640) and M.



theaezans (CMW 10625, CMW 10626) resulted in lesion formation (Fig. 6). The more pathogenic isolates (CMW 10625, CMW 10638, CMW 10639) were not significantly different from each other (Fig. 6), but differed significantly (P < 0.0014) from the control inoculation (Table 3). Isolates CMW 10639 from *E. grandis* and CMW 10625 from *M. theaezans* were chosen for field inoculations (Fig. 6) because they were most pathogenic for each isolate group from a particular host.

In the second greenhouse trial (Table 4), isolates from *M. rubiginosa* (CMW 10022, CMW 10024) and the South African isolate of *C. cubensis* (CMW 2113) resulted in different size lesions (Fig. 7). The South African isolate was more pathogenic on the *E. grandis* clone than the other isolates tested (Fig. 7). This isolate was also less pathogenic on *T. urvilleana* (Fig. 7) than on the *E. grandis* clone. An isolate from *M. rubiginosa* (CMW 10024) was more pathogenic on *E. grandis* than on *T. urvilleana* (Fig. 7) and it was also more pathogenic on *E. grandis* than the other isolate from *M. rubiginosa* (CMW 10022). Isolate CMW 10022 was equally pathogenic on *E. grandis* and *T. urvilleana* (Fig. 7). All isolates produced lesions significantly larger (P = 0.001) than the control inoculations (Table 4). Only *E. grandis* trees infected by the South African isolate (CMW 2113) produced epicormic shoots below the inoculation points, indicating that the inoculated stems were being girdled.

Field inoculation trials. In the first field trial (Table 5), lesions were produced on all tree species (T. urvilleana, T. lepidota, T. semidecandra, M. theaezans, E. grandis) in response to inoculation with isolates CMW 10693 from E. grandis and CMW 10625 from M. theaezans. The longest lesions were produced on T. urvilleana (Fig. 8a) and T. lepidota (Fig. 8b), while lesions on T. semidecandra (Fig. 8c), although smaller, also differed significantly (P = 0.001) from control inoculations (Fig. 9). Lesions on M. theaezans (Fig. 8d) and the E. grandis clone (Fig. 8e) were only slightly longer than the control inoculations (Fig. 9). Lesions produced by the two isolates (CMW 10639, CMW 10625) were similar in size on each tree species (Fig. 9).

In the second field trial (Table 6), trees of M. rubiginosa (Figs 8f, 10) were more susceptible (P = 0.0001) to the C. cubensis isolate from M. rubiginosa (CMW 10022) than the E. grandis trees tested (Figs 8g-h, 10). Inoculations with isolate CMW 10022 on



the susceptible *E. grandis* clone 275 and the hybrid clone 212 gave rise to lesions that did not differ from those of the control inoculations (Fig. 10).

DISCUSSION

This study reports on the discovery of the serious *Eucalyptus* pathogen *C. cubensis* on native *Miconia* species (Melastomataceae) in Colombia. Isolates of the fungus from *M. theaezans* and *M. rubiginosa* grouped in the sub-clade that characterises *C. cubensis* occurring in South America, as defined in previous studies (Myburg *et al.* 1999, 2002a, 2002b, 2003, Roux *et al.* 2003). Structures on herbarium specimens linked to these isolates had conidiomata and ascomata typical of *C. cubensis* and spores were similar in size to those previously reported for this fungus (Hodges 1980, Myburg *et al.* 2002b, 2003).

Different host bark and environmental conditions have in the past been shown to result in variable morphology of *C. cubensis* structures (Bruner 1917, Hodges *et al.* 1986, Myburg *et al.* 2003). This complicates morphological comparisons between samples from different hosts. For instance, conidiomata on *M. rubiginosa* were much smaller than those on *E. grandis*, but the isolates originating from the specimens of *M. rubiginosa*, were shown to be identical to those from *E. grandis* based on DNA sequences. These differences observed between the conidiomata on *M. rubiginosa* and *E. grandis*, complicates identification. DNA sequences should thus accompany morphological identifications to verify identifications.

Native Melastomataceae in Colombia differed in their susceptibility to *C. cubensis* in the field inoculation trials. In the field trial where five different host species were tested, *T. urvilleana* and *T. lepidota* were highly susceptible to the two isolates of *C. cubensis*. This is in contrast to *M. theaezans* that was highly tolerant to infection. *Tibouchina semidecandra* was less susceptible than the other two species of *Tibouchina*, but more susceptible than *M. theaezans*.

Results of the different pathogenicity trials suggest that in the field, C. cubensis is more pathogenic on M. rubiginosa than on E. grandis. It was previously suggested that C. cubensis could have an origin in South America on native Melastomataceae (Wingfield



et al. 2001). It is generally believed that pathogens are less pathogenic on their native hosts than exotic species (Leppik 1970, Newhouse 1990). Therefore, the *E. grandis* clones used in the trials were expected to be more susceptible to *C. cubensis* than *M. rubiginosa*. However, these commercially grown clones have been subjected to intensive selection for resistance to disease over the past few years. It is thus possible that the clones or seed lots chosen for these trials have high degrees of tolerance to the pathogen. The fact that disease is not commonly seen on native Melastomataceae might also imply that the artificial inoculation techniques used to test pathogenicity, breach barriers that limit infection under natural conditions.

In this study we have shown that *C. cubensis* from South America occurs on *M. theaezans* and *M. rubiginosa*, two species of a genus not previously known as a host of the pathogen. The other recently recognised native hosts of the fungus in this country are *Tibouchina* spp. (Wingfield *et al.* 2001). The first discovery of *C. cubensis* on *M. theaezans*, was in native vegetation far removed from *Eucalyptus* plantations. It thus seems likely that *C. cubensis* occurs naturally on this host. In the case of *M. rubiginosa*, the trees were felled during the establishment of a *Eucalyptus* compartment. The *M. rubiginosa* trees, however, recovered and *C. cubensis* was found on these trees, as well as on the *Eucalyptus* trees in the adjacent compartment. It is unclear in which direction *C. cubensis* spread in this case, although it most likely was already present on *M. rubiginosa*. Further studies will be required to resolve this question.

Members of the Melastomataceae are common in South America, Central America, the Caribbean islands and Hawaii (Everett 1981). The occurrence of *C. cubensis* on species belonging to this family supports the hypothesis that the fungus occurred widely through South and Central America and the Caribbean prior to the commercial planting of *Eucalyptus* species. Detailed population studies will shed more light on the origin or origins of *C. cubensis*, and its movement throughout the world.

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Table 1. Isolates included in this study.

Isolate number ^a	Species identity	Host	Origin	GenBank accession numbers
CMW 2113	Cryphonectria cubensis	Eucalyptus grandis	South Africa	AF 046892, AF 273067, AF 273462
CMW 62	C. cubensis	E. grandis	South Africa	AF 292041, AF 273063, AF 273458
CMW 8755	C. cubensis	E. grandis	South Africa	AF 292040, AF 273064, AF 273459
CMW 8757	C. cubensis	Eucalyptus	Venezuela	AF 046897, AF 273069, AF 273464
CMW 8758	C. cubensis	Eucalyptus	Venezuela	AF 046898, AF 273068, AF 273463
CMW 9970	C. cubensis	Miconia rubiginosa	Colombia	AY 214291, AY 214219, AY 214255
CMW 9996	C. cubensis	M. rubiginosa	Colombia	AY 214292, AY 214220, AY 214256
CMW 10022	C. cubensis	M. rubiginosa	Colombia	AY 262389, AY 262393, AY 262397
CMW 10024	C. cubensis	M. rubiginosa	Colombia	AY 262390, AY 262394, AY 262398
CMW 10025	C. cubensis	M. rubiginosa	Colombia	AY 214293, AY 214221, AY 214257
CMW 10026	C. cubensis	M. rubiginosa	Colombia	AY 214294, AY 214222, AY 214258
CMW 10028	C. cubensis	M. rubiginosa	Colombia	AY 214295, AY 214223, AY 214259
CMW 9980	C. cubensis	M. theaezans	Colombia	AY 214297, AY 214225, AY 214261
CMW 9993	C. cubensis	M. theaezans	Colombia	AY 214298, AY 214226, AY 214262
CMW 10625	C. cubensis	M. theaezans	Colombia	44
CMW 10626	C. cubensis	M. theaezans	Colombia	AY 262392, AY 262396, AY 262400
CMW 10639	C. cubensis	M. theaezans	Colombia	AY 263419, AY 263420, AY 263421
CMW 10775	C. cubensis	Syzygium aromaticum	Brazil	AY 084003, AY 084015, AY 084027



CMW 10776	C. cubensis	S. aromaticum	Brazil	AY 084004, AY 084016, AY 084028
CMW 10777	C. cubensis	S. aromaticum	Brazil	AY 084005, AY 084017, AY 084029
CMW 8756	C. cubensis	E. marginata	Indonesia	AF 046896, AF 273077, AF 375606
CMW 2632	C. cubensis	E. marginata	Australia	AF 046893, AF 273078, AF 375607
CMW 3839	C. cubensis	S. aromaticum	Indonesia	AF 046904, AY 084011, AY 084023
CMW 1651	C. parasitica	Castanea dentata	USA	AF 046901, AF 273074, AF 273467
CMW 1652	C. parasitica	C. dentate	USA	AF 046902, AF 273075, AF 273468
CMW 10455	C. radicalis	C. dentate	Italy	AF 452113, AF 525705, AF 525712
CMW 10477	C. radicalis	C. dentate	Italy	AF 368328, AF 368347, AF 368346
CMW 10463	C. macrospora	Castanopsis cuspidata	Japan	AF 368331, AF 368351, AF 368350
CMW 10518	C. nitschkei	Quercus sp.	Japan	AF 452118, AF 525706, AF 525713
CMW 10435	Endothia gyrosa	Q. palustris	USA	AF 368325, AF 368337, AF 368336
CMW 10442	E. gyrosa	Q. palustris	USA	AF 368326, AF368339, AF368338
CMW 5288	Diaporthe ambigua	Malus domestica	South Africa	AF 543817, AF 543819, AF 543821
CMW 5587	D. ambigua	M. domestica	South Africa	AF 543818,AF 543820,AF 543822

⁸ CMW refers to the culture collection of the Forestry & Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa.



Table 2. Specimens used in morphological comparisons.

Identity	Herbarium no.ª	Linked culture ^b	Host	Origin	Date	Collector
Cryphonectria	PREM 57294	CMW 10639 ^c	Eucalyptus	Vanessa,	2000	M. J. Wingfield
cubensis			grandis	Colombia		
C. cubensis	PREM 57517	CMW 2357	Miconia	Vanessa,	2001	C. A. Rodas
		CMW 9996	rubiginosa	Colombia		
		CMW 10025				
		CMW 10026				
		CMW 10028				
		CMW 10022				
		CMW 10024				

^a PREM, National Collection of Fungi, Pretoria, South Africa.

^b CMW refers to the culture collections of the Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, 0002, South Africa.

^c Isolate CMW 10639 did not originate from PREM 57294, but were collected from the same location.



Table 3. One way ANOVA analysis for lesion length measurements of Colombian *Cryphonectria cubensis* isolates from *Eucalyptus grandis* (CMW 10638, CMW 10639, CMW 10640), *Miconia theaezans* (CMW 10625, CMW 10626) and a negative control inoculated on *Tibouchina urvilleana* seedlings in the greenhouse.

Source	SS	df	MS	F	Pr > F
Isolate	33267.36	5	6653.47	5.66	0.0014
Error	28219.6	24	1175.81		

CV = 55.63578



Table 4. One way ANOVA analysis for lesion length measurements of Colombian *Cryphonectria cubensis* isolates from *Miconia rubiginosa* (CMW 10022 and CMW 10024), a South African *C. cubensis* isolate (CMW 2113) and a negative control inoculated on *Tibouchina urvilleana* and *Eucalyptus grandis* (clone ZG14) seedlings in the greenhouse.

Source	SS	df	MS	F	Pr > F
Host	310624.68	7	44374.95	39.58	0.0001
Error	80714.3	72	1121.03		

CV = 35.99711



Table 5. One way ANOVA analysis for lesion length measurements of Colombian Cryphonectria cubensis isolates from Eucalyptus grandis (CMW 10639), Miconia theaezans (CMW 10625) and a negative control inoculated on one-year-old Tibouchina semidecandra, T. lepidota, T. urvilleana, M. theaezans and E. grandis (clone 274) seedlings in Colombia.

Source	SS	df	MS	F	Pr > F
Isolate	380936.00	2	190468.00	65.59	0.0001
Host	645144.98	4	161286.24	55.54	0.0001
Isolate*Host	349986.03	8	43748.12	15.07	0.0001
Error	792756.03	273	2903.86		

CV = 95.18900



Table 6. One way ANOVA analysis for lesion length measurements of a Colombian *Cryphonectria cubensis* isolate from *Miconia rubiginosa* (CMW 10022) and a negative control inoculated on three-year-old *Eucalyptus grandis* trees (clone 275), trees from a *E. grandis* and *E. urophylla* cross (*E. urogandis* 212) and six-year-old *M. rubiginosa* trees in Colombia.

SS	Df	MS	F	Pr > F
43156.02	2	21578.01	60.43	0.0001
58174.31	2	29087.15	81.50	0.0001
24.37	1	24.37	0.07	0.7945
29622.25	83	356.89		
	43156.02 58174.31 24.37	43156.02 2 58174.31 2 24.37 1	43156.02 2 21578.01 58174.31 2 29087.15 24.37 1 24.37	43156.02 2 21578.01 60.43 58174.31 2 29087.15 81.50 24.37 1 24.37 0.07

CV = 53.02294



Fig. 1. Native Melastomataceae on which Cryphonectria cubensis was found and that were used in pathogenicity trials. (a). Tibouchina urvilleana. (b). T. lepidota. (c). Miconia theaezans. (d). M. rubiginosa. (e). T. semidecandra.



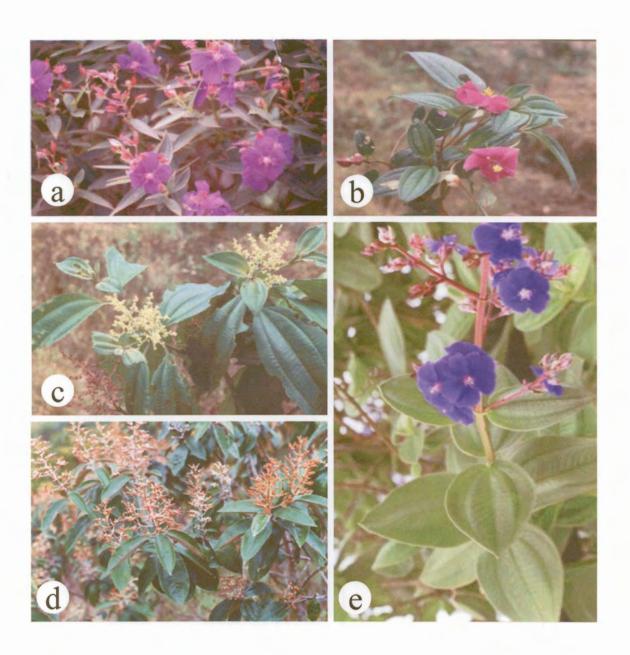


Fig. 2. Map of Colombia showing co-ordinates, altitude and precipitation of the locations where *Cryphonectria cubensis* was discovered on various Melastomataceae, and where field trials were conducted.



Discovery of Miconia theaezans

Selva, Pereira, Risaralda 2048 masl, 3143 mm/y 75° 35' 34" W and 4° 47' 26" N

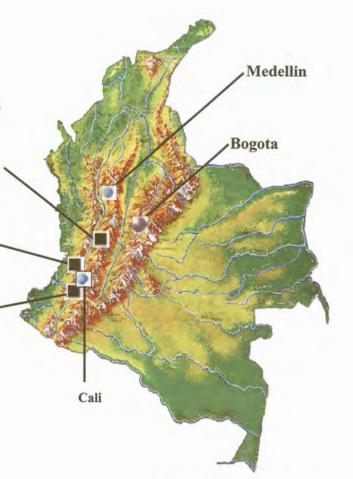
First field inoculation trial

Rancho Grande farm, Restrepo, Valle, 2102 masl, 2414 mm/y 76⁰ 26' 39" W and 4⁰ 1' 51" N

Discovery of Miconia rubiginosa

and second field inoculation trial

Vanessa, Timba, Cauca 1000 masl, 2365 mm/y 76° 35' 15" W and 3° 5' 42" N



Source: Instituto Geografico Agustin Codazzi



Fig. 3. Raw sequence data of the two regions sequenced within the β -tubulin gene (designated as β -tub 1a/1b and β -tub 2a/2b) and the ITS1, conserved 5.8S and ITS2 regions of the rDNA operon. The start of each region is indicated above the alignment. The exon regions of the β -tubulin gene, as well as the conserved 5.8S region of the rDNA operon, are indicated in red. Unknown sequence characters are indicated with a "N", while gaps inserted to achieve sequences alignment are indicated with "-". Bases matching those of **CMW 2113** are indicated with a ".".



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CMW	8755									
CMW	8756							********		
CMW	2632									
CMW	3839									
CMW	8758	GA		A					*********	
CMW	8757									
CMW	9970					TA				
CMW	9996									
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CMW	9980									
CMW	9993									
	10626									
CMW	10022			0.						
CMW	10024									
	10639	***************************************								
CMW	10775									
	10776									
	10777									
CMW	1651					C				
CMW	1652					C				
CMW	10455		T		.ccc					
CMW	10477		T		.CCC					
CMW	10463		T			T				
CMW	10518		T			T				
CMW	10435					C				
CMW	10442					C				C
CMW	5288									C
CMW	5587		C	T.	.CC					C



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CMW	9980						T		A.AA	T.
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CMW	10626						T		A.AA	T.
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CMW	10776									
CMW	10777		T				T	G	A.AA	T.
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CMW	1652			A.	T	T	TT.TTGT.	T = 0.0000000000000000000000000000000000	T	TCGCAAGT
CMW	10455				T	G	GTTTTTTTT.	TT.TTTTC	CC.CTTG.CT	TCGCAAGT
CMW	10477				T	G	GTTTTTTTT.	TT.TTTTC	CC.CTTG.CT	TCGCAAGT
CMW	10463		T	A.	T	T	TT.TATA	T		TCGCAAGC
CMW	10518		T	T.	T	T	TT.T.TGT	TCT		TCGCAGGC
CMW	10435		CT					ACACA.CC		
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CMW	10639	T	T							
CMW	10775	T	T							
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CMW	10777	T	T							
CMW	1651	CT	.GAC-GAA.G	TCTTGG	GCTGTTTGGC	TAACCCTGTC	TTTCTCTCTT	CCCCTTCT.C	$T \dots T$	
CMW	1652	CT	.GAC-GAA.G	TCTTGG	GCTGTTTGGC	TAACCCTGTC	TTTCTCTCTT	CCCCTTCT.C	AT	
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CMW	10477	T	.GAT-AAAGT	CGTCTCTG	GCTTGTTTGC	TAACC. TGTT	TCTCTCCCCC	CCCCCCAAC		
CMW	10463	CT	.GAT-GAA.A	TCTCGG	GCTTCTTGGC	TAACCCCACG	TTTCTCTCTT	TCCTC	T	
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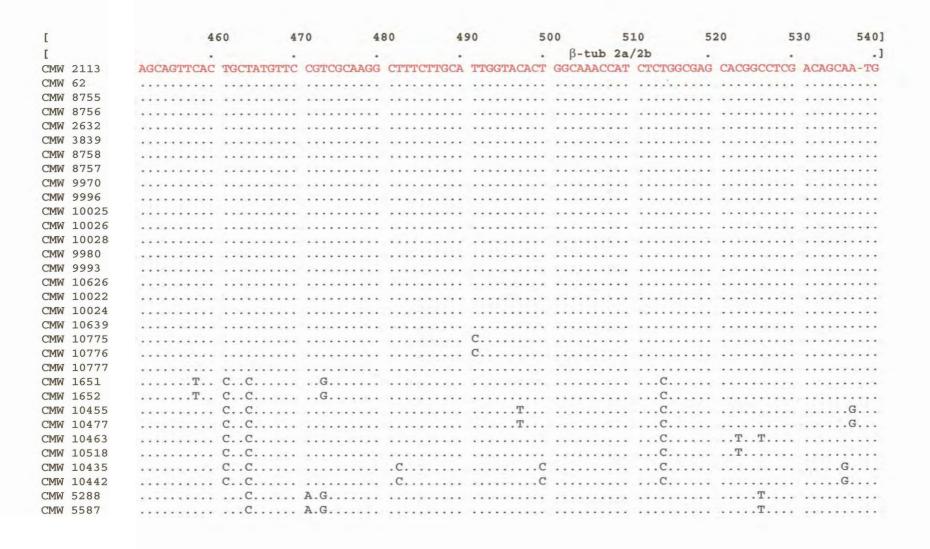


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WIN	62	G	*********		********				*********	
MW	8755	G,	*******	********	STEER COLUMN	********	*******	********	******	*******
MW	8756	G	*******	*******	********				*******	*******
MW	2632	G			, , , , , , , , , , ,					
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WN	9996	G	********							******
MW	10025	G							********	*********
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MW	9980	G								
WIN	9993	G					CALLETTA	*******	*******	
W	10626	G						*********		
W	10022	G								
WIN	10024	G								
WIN	10639	G	********	********		********	********			
W	10775	G								
W	10776	G								
WIN	10777	G								
WIN	1651	CAAC.T-C	ACCTCGGC-A	A.CC.CC	CTTTCCG.	G.CCTT	. TTCTGGTAT	AGGCGAGCTT	CC.TCTT	T
WIN	1652	ACAAGC.TCC	ACCTGGGCCA	A.CC.CC	CTTTCCG.	G.CCTTCT	. TTCTGGTAT	AGGCGAGCAT	CC.TCTT	т
WIN	10455	CAAACA	TCTCGACC.T	GGC.C.		.C	.TTCTGG.AT	AGGCGAAGTT	CCCTCTTT	T
W	10477	CAAACA	TCTCGACC.T	GGC.C.		.C	.TTCTGG.AT	AGGCGAAGTT	CCCTCTTT	T
WIN	10463	C.AACA	TCTCAACCC.	CCTCC	CAAAT.CCG.	GCCCCTC	.TTCTGG.AT	AGGCGAGCTT	CC.TCTT	T
WM	10518	C.AACA	TCTCAGCCCA	C.TGTTCC		, CTC.C.	.TTCTGGTA.	AGGCGAGCTT	CC.TCTT	T
W	10435					CGT				
W	10442	CTG	GCG.G	G.CGC.CG	CGGCTG.	CGT		A		
W	5288	CAAC.TA.GG	CA	-T.GTTT	Libraria	.CCGCCGTCG		- CAAGGCCTT	G	AAT.T
	5587	CAAC TA CC	CA	-u Gunu		CGCCGTCG	120-2003-2	-CAAGGCCTT	G	AAT.T



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CMW	10463	T.A	A	T	A.			T	.T	C
CMW	10518	T.A	A	T	T.			T		C
CMW	10435							T		C
CMW	10442							T		C
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CMW	8755									
CMW	8756									
CMW	2632									
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CMW	8758									
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CMW	1652	TT	T		T				AA	
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CMW 9970								
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CMW 10455	T CGG	AG GGAAAAAAA	AAAAAAAAGG	GGGGAAATTC	TGTTTCCCCT	TTTC.TTTT	CCCCCCTTC	CCCTTCAT
CMW 10477	T CG	.GAG GGAAAAAAA	A AAAAAAAAGG	GGGGAAATTT	GTTTCCCCCT	TTTTTTTTT	CCCCCCTTC	CCCTTTAT
CMW 10463	T CCG	.G.A .T., TGAG	G AGAGTCTC	TCTCTCCTTC	CTTC	-T.GC	CTTCT	ACC
CMW 10518	T CCG	.G.A .TTGAG	G AGAGTCTC	TCTCTCCTTC	CTTC	-T.GC	CTTCT	C
CMW 10435	TTG	.GC	·	,ACTCTC	CTGTGCC.	C	ACCGT	GCAAGCG
CMW 10442	TTG	.GC		ACTCTC	CTGTGCC.	C	ACCGT	GCAAGCG
CMW 5288	AA.GC.G GCC				* * * * * * * * * * * *		ACCGA	GGCCCCTTGG
CMW 5587	AA.GC.G GCC						ACCGA	GGCCCCTTGG



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CMW	10477	.G.AAATC	G.GGGCTG	A		TTT	A.	C	TT-	AA
CMW	10463	.TA.G.	.TGTTG	*******	********		T.	C	AC	A.TA
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CMW	10442	,T,	**					C	C	CA
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CMW	5587	.AA			A .		C.TAG	TA	C	AA



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CMW	62					CG					
CMW	8755					CG					
CMW	8756			,		CG					
CMW	2632										
CMW	3839	*********									
CMW	8758					CG					
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CMW :	10477	T.TTC	TTC	A.	T	T		
CMW :	10463	T	CA			*********		
CMW :	10518	T	CA		T			
	10435				T			
CMW :	10442				T	F		
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Fig. 4. The phylogenetic tree (tree length = 1198 steps, consistency index/CI = 0.8, retention index/RI = 0.9) generated from a combined data set comprising ribosomal and β-tubulin gene sequences. Confidence levels of the tree branch nodes >50% are indicated and were determined by a 1000 replicate bootstrap analysis. Isolates sequenced in this study are bolded. Host species for C. cubensis are indicated in capital letters. The Diaporthe ambigua isolates were used as the outgroup taxa.

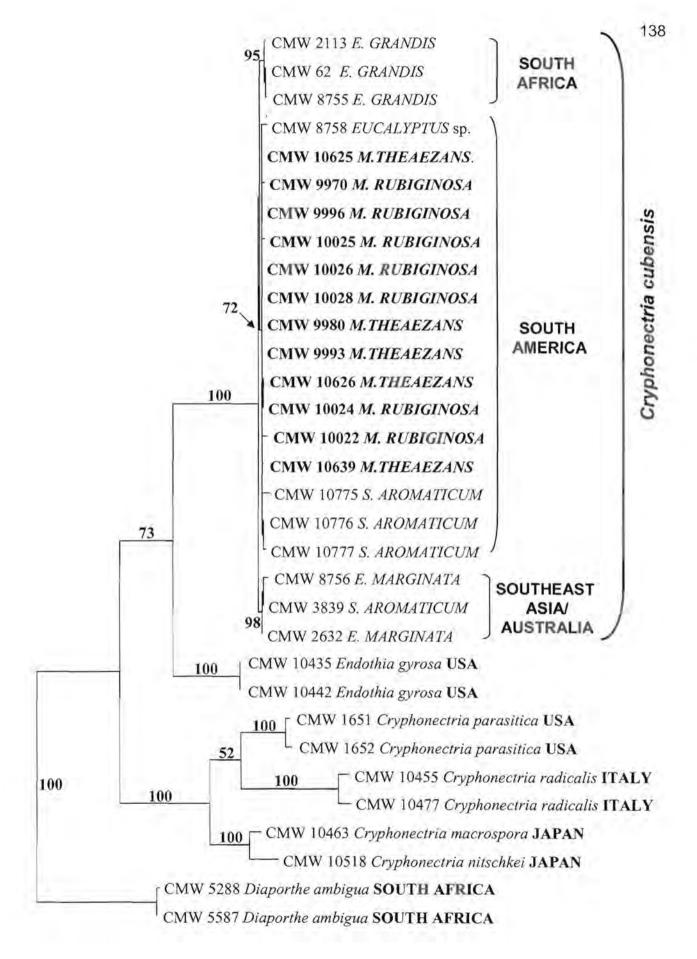


Fig. 5. Light micrographs of Cryphonectria cubensis on Miconia rubiginosa in Colombia. (a). Perithecial neck and orange stromatic tissue (arrow) on bark. (b). Vertical section through ascoma. (c). Perithecial neck and surrounding tissue (arrow).
(d). Stromatic tissue of ascoma. (e). Ascus. (f). Ascospores. (g). Conidioma on bark.
(h). Vertical section through conidioma. (i). Tissue of the conidiomal base and neck (arrow). (j). Conidiophores. (k). Enteroblastic phialidic conidiogenous cell (arrow).
(l). Conidia. Bars a-b, g-h = 100 μm; c-d, i = 20 μm; e-f, j-l = 10 μm.



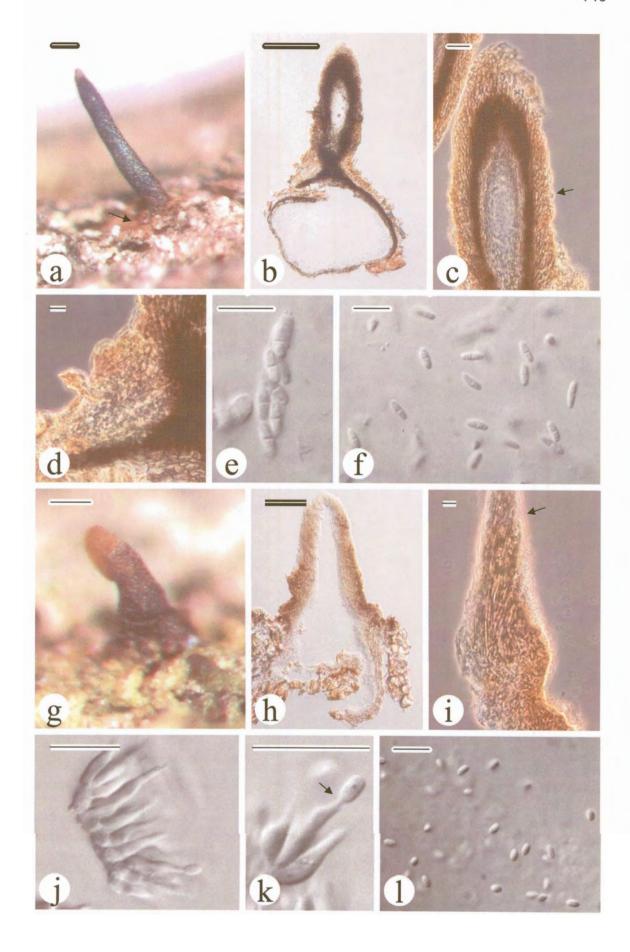




Fig. 6. Results of inoculation trial with isolates of Cryphonectria cubensis from Miconia theaezans (CMW 10625, CMW 10626) and Eucalyptus grandis (CMW 10640, CMW 10638, CMW 10639) from Colombia, and a negative control. Inoculations were done in a greenhouse on seven-month-old Tibouchina urvilleana. Mean length of lesions is shown with 95% confidence limits.

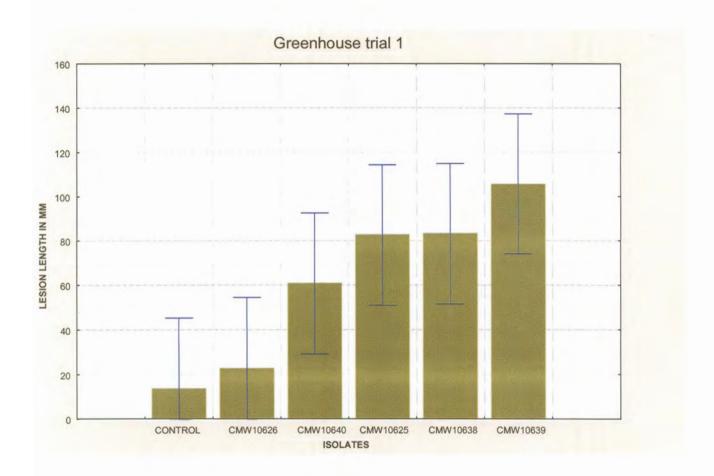




Fig. 7. Results of inoculation trials in the greenhouse with isolates of *Cryphonectria cubensis* from *Miconia rubiginosa* (CMW 10022, CMW 10024) and a negative control. Inoculations were done on one-year-old *Tibouchina urvilleana* and a ZG14 clone of *Eucalyptus grandis*. A *C. cubensis* isolate from *E. grandis* in South Africa (CMW 2113) was also included. Mean length of lesions is shown with 95% confidence limits.



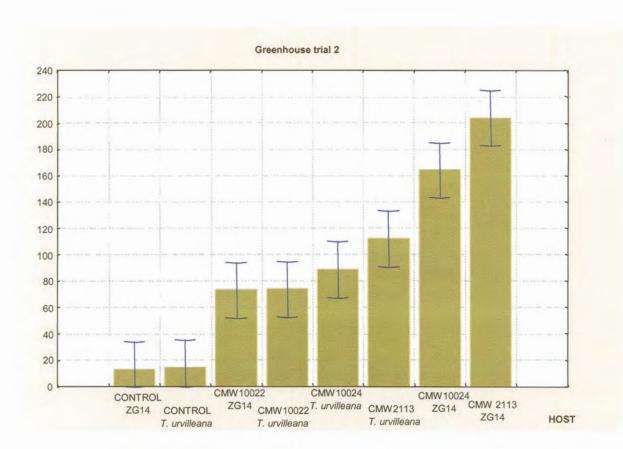




Fig. 8. Lesions produced by isolates of Cryphonectria cubensis from Miconia theaezans (CMW 10625) and M. rubiginosa (CMW 10022) on various hosts inoculated in field trials in Colombia. Control inoculations are indicated with a "c". (a). Lesions on Tibouchina urvilleana inoculated with isolate CMW 10625. (b). Lesions on T. lepidota inoculated with isolate CMW 10625. (c). Lesions on T. semidecandra inoculated with CMW 10625. (d). Lesions on M. theaezans inoculated with CMW 10625. (e). Lesions on an Eucalyptus grandis clone (274) inoculated with CMW 10625. (f). Lesions on M. rubiginosa inoculated with CMW 10022. (g). Lesions on an E. grandis clone (275) inoculated with CMW 10022. (h). Lesions on a cross between E. grandis and E. urophylla ("E. urograndis" 212) inoculated with isolate CMW 10022.



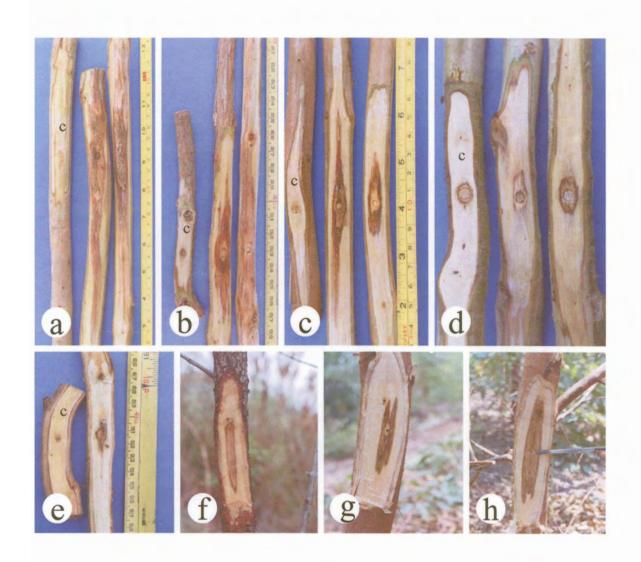




Fig. 9. Results of inoculation trials with isolates of Cryphonectria cubensis from Miconia theaezans (CMW 10625) and Eucalyptus grandis (CMW 10639) from Colombia, and a negative control. The field inoculations were done in Colombia on one-year-old Tibouchina urvilleana, T. lepidota, T. semidecandra, M. theaezans and an E. grandis clone (274). Mean lesion length is shown with 95% confidence limits.

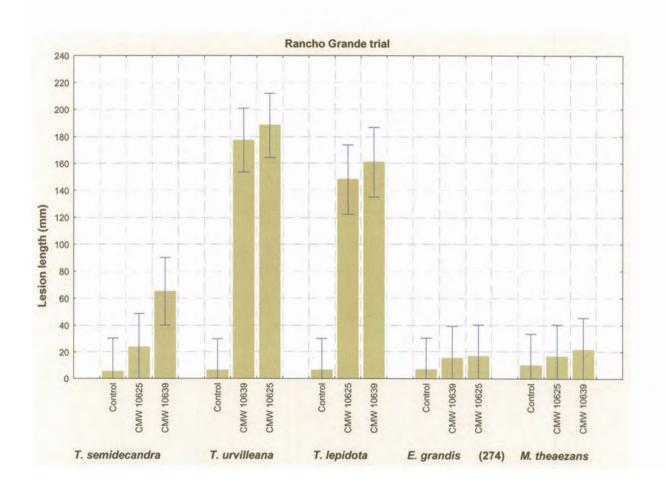




Fig. 10. Results of field inoculation trials with an isolate of *Cryphonectria cubensis* from *Miconia rubiginosa* (CMW 10022) and a negative control. Inoculations were done on six-year-old *M. rubiginosa*, a three-year-old *E. grandis* clone (275) and an *E. urograndis* cross (212). Mean length of lesions is shown with 95% confidence limits.



