

New taxonomic concepts for the important forest pathogen *Cryphonectria parasitica* and related fungi

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Introduction

Species in *Cryphonectria* (*Diaporthales*) are easily recognized on the bark of trees by their large and conspicuous orange stromata (Shear *et al.*, 1917; Barr, 1978). These stromata (Fig. 1a–c) are semi-immersed and erumpent; conidiomata are also orange, pulvinate and stromatic. Species are further identified based on their fusoid to ellipsoid, one-septate ascospores and aseptate, cylindrical conidia (Myburg *et al.*, 2004a). *Cryphonectria* spp. occur on a wide variety of woody hosts and they have a worldwide distribution (Table 1), which included the tropics as well as more temperate areas in the past (Shear *et al.*, 1917; Kobayashi, 1970; Roane, 1986a). Many species in this group are economically significant and include some of the world's most serious tree pathogens.

One of the best known species in *Cryphonectria* is *Cryphonectria parasitica* (Murrill) M. E. Barr (Fig. 2). It was introduced into North America where it devastated the American chestnut (*Castanea dentata*, *Fagaceae*, *Fagales*) throughout its natural range (Anagnostakis, 1987; Heiniger & Rigling, 1994). *Cryphonectria parasitica* was also introduced into Europe, where it resulted in a serious canker

Abstract

Species of *Cryphonectria* include some of the world's most important and devastating tree pathogens. Largely through the application of DNA sequence phylogenies, the taxonomy of these fungi has undergone major changes in recent years. *Cryphonectria*, including the chestnut blight pathogen *Cryphonectria parasitica*, has been restricted to species that have semi-immersed stromata, orange and pulvinate conidiomata, and one-septate ascospores. Other species of *Cryphonectria* with different morphological characteristics have been transferred to new genera that are strongly supported by phylogenetic data. This review represents a summary of the taxonomic changes to species of *Cryphonectria sensu lato*, and we discuss the impact that these changes might have on the understanding of their ecology, pathology and worldwide distribution.

disease on *Castanea sativa* or the European chestnut (Heiniger & Rigling, 1994). Damage caused by this pathogen in Europe has, however, been much less severe than in North America due to reduced virulence imparted by a hypovirus (Heiniger & Rigling, 1994). The fungus and its associated viruses have been widely studied due to the significance of *C. parasitica* and the success of the biocontrol brought about by the hypoviruses (Nuss, 1992; Hillman & Suzuki, 2004; Milgroom & Cortesi, 2004).

Cryphonectria represents a relatively small genus of fungi. Until recently, the genus included only 10 species. Besides *C. parasitica*, these included *C. gyrosa* (Berk. & Broome) Sacc., which was the type species, *C. radicalis* (Schwein.: Fr.) M. E. Barr, *C. nitschkei* (G. H. Otth) M. E. Barr, *C. macrospora* (Tak. Kobay. & Kaz. Itô) M. E. Barr, *C. havanensis* (Bruner) M. E. Barr, *C. longirostris* (Earle) Micales & Stipes, *C. coccolobae* (Vizioli) Micales & Stipes, *C. cubensis* (Bruner) Hodges (Micales & Stipes, 1987) and *C. eucalypti* M. Venter & M. J. Wingf. (Venter *et al.*, 2002). Other than *C. parasitica*, species such as *C. cubensis* (Fig. 3) and *C. eucalypti* are serious canker pathogens of trees (Old *et al.*, 1986; Gryzenhout *et al.*, 2003; Wingfield, 2003), but the majority of the species are saprophytes on wood (Roane, 1986b).



Fig. 1. Fruiting structures of *Cryphonectria* and related genera. (a) Ascostroma of *Cryphonectria*. (b) Longitudinal section through ascostroma of *Cryphonectria*. (c) Conidioma of *Cryphonectria*. (d) Ascostromata of *Chrysosporthe*. (e) Perithecial neck of *Chrysosporthe* (arrow) with brown surrounding tissue. (f) Conidioma of *Chrysosporthe*. (g) Conidioma of *Amphilogia*. (h) Conidioma of *Rostraureum*. (i) Conidiomata of *Aurapex*. Scale bars: a–h = 100 µm, i = 200 µm.

Species of *Endothia* (*Diaporthales*) have commonly been confused with *Cryphonectria*. This is due to their similar orange fruiting structures and a shared anamorph genus, *Endothiella* (Barr, 1978). Members of *Cryphonectria* and *Endothia* have also been recorded to share the same hosts and to occur in the same countries. For example, *E. gyrosa* (Schwein.: Fr.) Fr., *E. singularis* (Syd. & P. Syd.) Shear & N. E. Stevens, *C. parasitica* and *C. radicalis* all occur in North America (Table 1) on members of the *Fagaceae* (Roane, 1986a). *Cryphonectria* has also been treated as a synonym of *Endothia* for a large portion of its taxonomic history (Shear et al., 1917; Kobayashi, 1970; Barr, 1978; Roane, 1986a).

Based on DNA sequence comparisons and phylogenetic analyses, species of *Endothia* can be distinguished (Fig. 4) from those in *Cryphonectria* (Venter et al., 2002; Myburg et al., 2004a). This is strongly supported by morphological differences such as the aseptate ascospores and superficial stromata, which are characteristic in *Endothia* but not in *Cryphonectria* (Myburg et al., 2004a). Currently, *Endothia* includes only two species, *E. gyrosa* (type) and *E. singularis* (Myburg et al., 2004a). A third species with green stromata, *E. viridistroma* Wehm., most likely resides in a genus other than *Endothia* (Myburg et al., 2004a).

Table 1. Hosts, distribution, representative isolates (ex-type isolates in bold) and representative sequences of *Cryphonectria* spp. and related genera

Genus	Species	Distribution	Best known host genera	Representative isolates	Representative sequences*
<i>Cryphonectria</i>	<i>C. parasitica</i>	Japan, China, North America, Europe, Turkey	<i>Castanea</i> , <i>Quercus</i> (<i>Fagaceae</i> , <i>Fagales</i>)	CMW7048 = ATCC48198	AF368330, AF273076, AF273470
				CMW13749 = MAFF410158	AY697927, AY697943, AY697944
	<i>C. nitschkei</i>	Japan, China, Russia	<i>Quercus</i> , <i>Castanea</i> , <i>Castanopsis</i> (<i>Fagaceae</i> , <i>Fagales</i>), <i>Betula</i> , <i>Carpinus</i> (<i>Betulaceae</i> , <i>Fagales</i>), <i>Pyrus</i> , <i>Prunus</i> (<i>Rosaceae</i> , <i>Rosales</i>), <i>Eucalyptus</i> (<i>Myrtaceae</i> , <i>Myrtales</i>), <i>Rhus</i> (<i>Anacardiaceae</i> , <i>Sapindales</i>) and <i>Larix</i> (<i>Pinaceae</i> , <i>Pinales</i>)	CMW13742 = MAFF410570	AY697936, AY697961, AY697962
				CMW13747 = MAFF410569	AY697937, AY697963, AY697964
	<i>C. macrospora</i>	Japan	<i>Castanopsis</i> (<i>Fagaceae</i> , <i>Fagales</i>)	CMW10463 = CBS112920	AF368331, AF368351, AF368350
				CMW10914 = TFM: FPH E55	AY697942, AY697973, AY697974
	<i>C. radicalis sensu lato</i>	Japan, Greece, Italy, Switzerland, France, Portugal	<i>Quercus</i> , <i>Castanea</i> (<i>Fagaceae</i> , <i>Fagales</i>), <i>Carpinus</i> (<i>Betulaceae</i> , <i>Fagales</i>)	CMW10455 = CBS238.54	AF452113, AF525705, AF525712
				CMW10477 = CBS240.54	AF368328, AF368347, AF368346
				CMW10436 = CBS165.30	AF452117, AF525703, AF525710
				CMW10484 = CBS112918	AF368327, AF368349, AF368349
<i>C. havanensis</i>	Cuba	<i>Eucalyptus</i> (<i>Myrtaceae</i> , <i>Myrtales</i>), <i>Spondias</i> , <i>Mangifera indica</i> (<i>Anacardiaceae</i> , <i>Sapindales</i>), <i>Persea gratissima</i> (<i>Lauraceae</i> , <i>Laurales</i>)	n/a	n/a	
<i>C. coccolobae</i>	Bermuda, Florida (USA)	<i>Coccoloba</i> (<i>Polygonaceae</i> , <i>Polygonales</i>)	n/a	n/a	
<i>C. eucalypti</i>	Australia, South Africa	<i>Eucalyptus</i> (<i>Myrtaceae</i> , <i>Myrtales</i>)	CMW7036	AF232878, AF368341, AF368340	
			CMW7037	AF232880, AF368343, AF368342	
<i>Endothia</i>	<i>E. gyrosa</i>	USA	<i>Quercus</i> , <i>Fagus</i> (<i>Fagaceae</i> , <i>Fagales</i>), <i>Liquidambar</i> (<i>Hamamelidaceae</i> , <i>Saxifragales</i>), <i>Acer</i> (<i>Aceraceae</i> , <i>Sapindales</i>), <i>Ilex</i> (<i>Aquifoliaceae</i> , <i>Celastrales</i>), <i>Vitis</i> (<i>Vitaceae</i> , <i>Rhamnales</i>), <i>Prunus</i> (<i>Rosaceae</i> , <i>Rosales</i>)	CMW2091 = ATCC48192	AF046905, AF368337, AF368336
				CMW10442 = CBS118850	AF368326, AF368339, AF368338
<i>Amphilogia</i>	<i>E. singularis</i>	Colorado (USA)	<i>Quercus</i> (<i>Fagaceae</i> , <i>Fagales</i>)	n/a	n/a
	<i>A. gyrosa</i>	Sri Lanka, New Zealand	<i>Elaeocarpus</i> (<i>Elaeocarpaceae</i> , <i>Oxalidales</i>)	CMW10469 = CBS112922 CMW10740 = CBS112923	AF452111, AF525707, AF525714, AF452112, AF525708, AF525715

Table 1. Continued.

Genus	Species	Distribution	Best known host genera	Representative isolates	Representative sequences*
	<i>A. major</i>	New Zealand	<i>Elaeocarpus</i> (Elaeocarpaceae, Oxalidales)	n/a	n/a
<i>Chrysoporthe</i>	<i>Chr. cubensis</i>	South & Central America, Hawaii, Florida (USA), South East Asia, Australia, Central Africa	<i>Eucalyptus</i> , <i>Syzygium</i> (Myrtaceae, Myrtales), <i>Miconia</i> (Melastomataceae, Myrtales)	CMW10639 = CBS115747	AY263419, AY263420, AY263421
				CMW10669 = CBS115751	AF535122, AF535124, AF535126
				CMW8651 = CBS115718	AY084002, AY084014, AY084026
	<i>Chr. austroafricana</i>	South Africa	<i>Eucalyptus</i> , <i>Syzygium</i> (Myrtaceae, Myrtales), <i>Tibouchina</i> (Melastomataceae, Myrtales)	CMW2113 = CBS112916	AF046892, AF273067, AF273462
				CMW9327 = CBS115843	AF273473, AF273060, AF273455
<i>Chr. doradensis</i>	Ecuador	<i>Eucalyptus</i> (Myrtaceae, Myrtales)	CMW11286 = CBS115734	AY214289, AY214217, AY214253	
			CMW11287 = CBS115735	AY214290, AY214218, AY214254	
	<i>Chrysoporthella hodgesiana</i>	Colombia	<i>Tibouchina</i> , <i>Miconia</i> (Melastomataceae, Myrtales)	CMW10625 = CBS115744	AY956970, AY956979, AY956980
				CMW10641 = CBS115854	AY692322, AY692326, AY692325
<i>Rostraureum</i>	<i>R. tropicale</i>	Ecuador	<i>Terminalia</i> (Combretaceae, Myrtales)	CMW9971 = CBS115725	AY167425, AY167430, AY167435
				CMW10796 = CBS115757	AY167428, AY167433, AY167438
	<i>R. longirostris</i>	Puerto Rico, Trinidad & Tabago	Unknown hosts, dead wood	n/a	n/a
<i>Aurapex</i>	<i>A. penicillata</i>	Colombia	<i>Miconia</i> , <i>Tibouchina</i> (Melastomataceae, Myrtales), <i>Eucalyptus</i> (Myrtaceae, Myrtales)	CMW10030 = CBS115740	AY214311, AY214239, AY214275
				CMW10035 = CBS115742	AY214313, AY214241, AY214277

Roane (1986a), Venter et al. (2002), Myburg et al. (2003, 2004a, b), Gryzenhout et al. (2004, 2005a, b, d, 2006), Robin & Heiniger (2001) and Heath et al. (2006).

CMW, Forestry & Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria; ATCC, American Type Culture Collection, Manassas, USA; CBS, Centraalbureau voor Schimmelcultures, Utrecht, the Netherlands; TFM:FPH, Forestry and Forest Products Research Institute, Danchi-Nai, Ibaraki, Japan (E or Ep refers to an isolate); MAFF, Microorganisms Section, MAFF GENE BANK, National Institute of Agrobiological Sciences (NIAS), Ibaraki, Japan; ITS, internal transcribed spacer; n/a, not available.

*Accession numbers given as sequences from the ITS region, and two regions from the β -tubulin genes amplified with primers 1a/1b and 2a/2b, respectively.

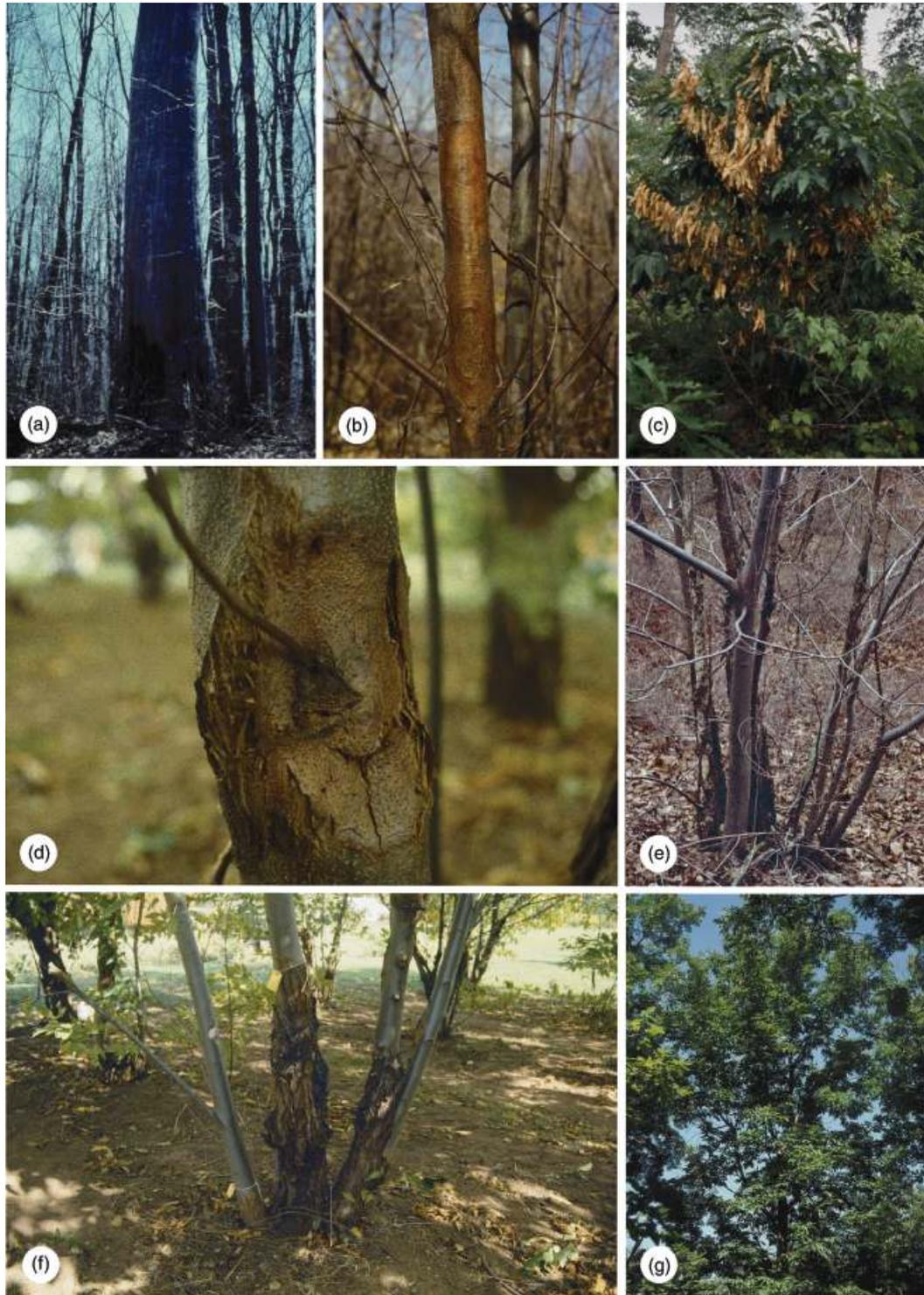


Fig. 2. Disease symptoms of chestnut blight caused by *Cryphonectria parasitica*. (a) A relic *Castanea dentata* tree still standing long after being killed by chestnut blight after its introduction into the USA. (b) Diffuse canker on *Castanea dentata*. (c) Die-back of branches with dead leaves still attached. (d) Sunken canker on *Castanea dentata* with fruiting structures visible. (e) Numerous stump sprouts from *Castanea dentata* roots of tree killed earlier by chestnut blight. (f) Multiple cankers on stump sprouts. (g) One of the few large and surviving specimens of *Castanea dentata* in the USA today.

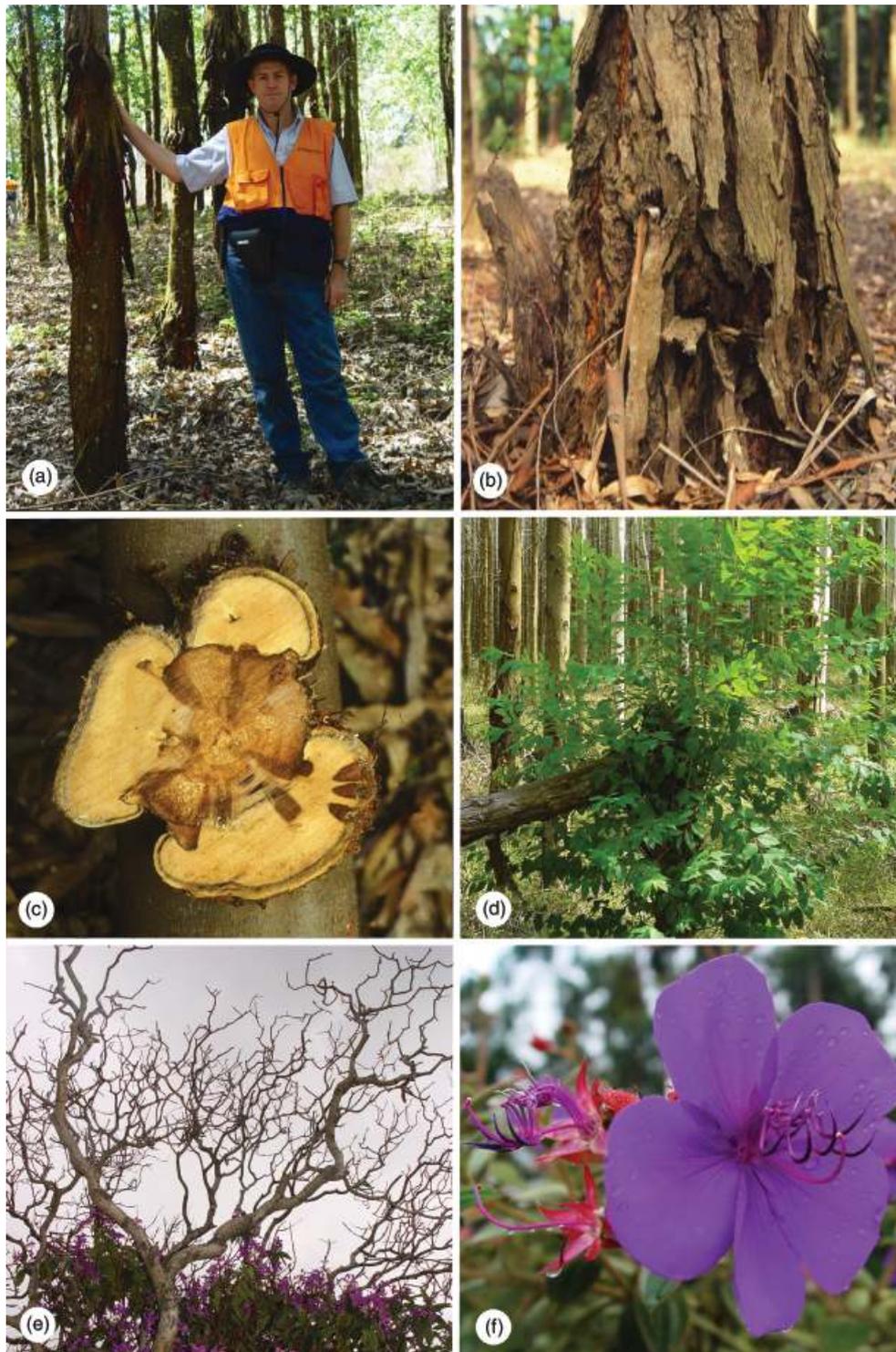


Fig. 3. Disease symptoms of *Chrysosporthe* canker caused by various *Chrysosporthe* species. (a and b) Cankers on the trunks and bases of *Eucalyptus* trees. (c) Cross section of canker showing killed vascular tissue. (d) Stem breakage due to girdling cankers. (e) Die-back of *Tibouchina* spp. (f).

The application of DNA sequence comparisons revealed the fact that the taxonomy of *Cryphonectria* required revision. For example, *Cryphonectria* was shown not to be

monophyletic (Fig. 4), but consisting of many species residing in newly recognized genera (Myburg *et al.*, 2004a; Gryzenhout *et al.*, 2005a). These newly recognized groups

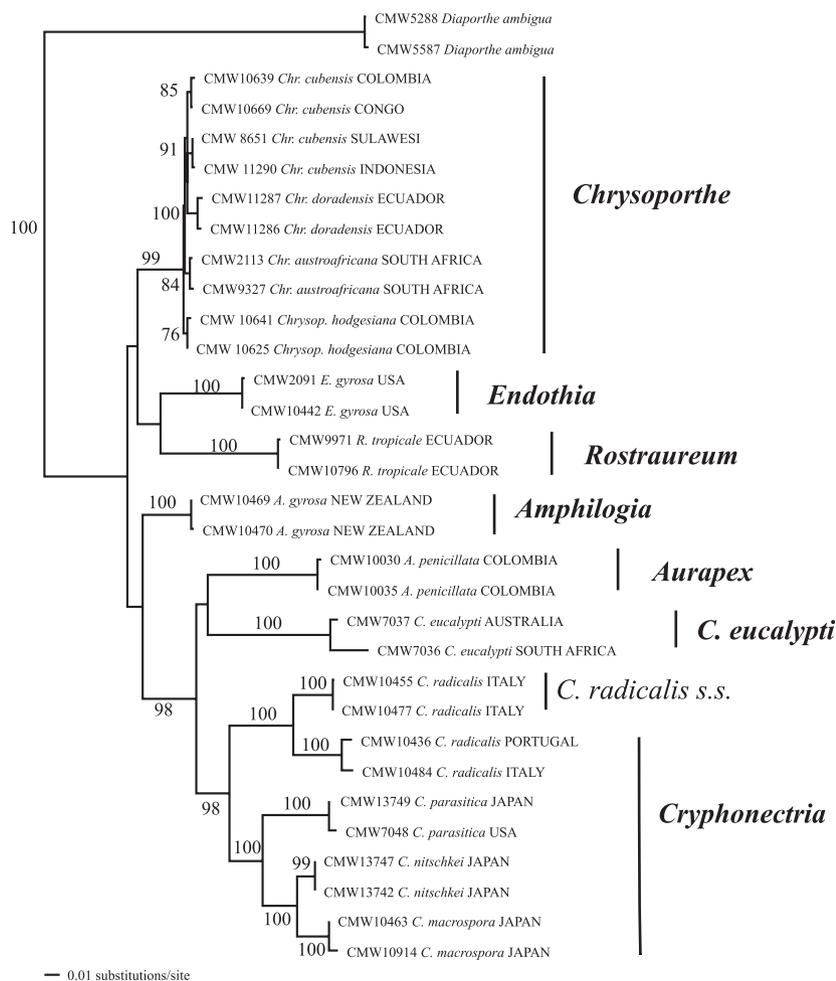


Fig. 4. A phylogenetic tree showing the grouping of *Cryphonectria* and related genera. The tree was obtained from a combined DNA sequence data set of the ITS1, 5.8S rRNA gene and ITS2 regions of the ribosomal operon, and β -tubulin genes, respectively. Alignment was obtained using the web interface (<http://timpani.genome.ad.jp/%7Emafft/server/>) of the alignment program MAFFT ver. 5.667 (Kato *et al.*, 2002). Distance analyses using the Tamura–Nei model, which was shown by Modeltest to be the appropriate model, were employed. The following parameters were used: $G = 0.2301$, $\text{freqA} = 0.1936$, $\text{freqC} = 0.3312$, $\text{freqG} = 0.2287$, $\text{freqT} = 0.2465$; rate matrix 1, 3.1964, 1, 1, 3.8818, 1. Bootstrap confidence levels ($> 70\%$, 1000 replicates) are indicated on the branches. *Diaporthe ambigua*, another species in the *Diaporthales*, was used as an outgroup taxon.

were supported by morphological features that were inordinantly diverse (Fig. 1) to warrant retaining these taxa in a single genus (Myburg *et al.*, 2004a; Gryzenhout *et al.*, 2005a). The primary aim of this review is to provide a summary of the recent changes to the taxonomy of species in *Cryphonectria sensu lato*, and to re-evaluate the host range, ecology and distribution of *Cryphonectria* species.

Revised taxonomy

Cryphonectria

Phylogenetic comparisons have revealed that isolates labeled as *Cryphonectria havanensis* in Japan are identical to those of *C. nitschkei* (Myburg *et al.*, 2004b). It has, furthermore, been

confirmed (Myburg *et al.*, 2004b) that *C. nitschkei* has a wide host range including five plant orders (Table 1). This fungus is restricted to the Far East and is known to occur in Japan, China (Myburg *et al.*, 2004b) and Siberia, Russia (Vasilyeva, 1998).

European isolates originally labeled as *C. radicalis* represent two different species of *Cryphonectria* (Myburg *et al.*, 2004a, b). This was determined independently based on morphology and DNA sequence comparisons (Fig. 4). *Cryphonectria radicalis*, defined by the type specimen from North America, corresponds morphologically to a phylogenetic group containing isolates from Greece, Italy, Switzerland and Japan (Myburg *et al.*, 2004b). This has not been confirmed using phylogenetic analyses, because isolates that can be linked to *C. radicalis* in North America, do not exist.

The other species has ascospores longer than those of *C. radicalis sensu stricto*, but specimens had also previously been labeled as *C. radicalis* (Myburg et al., 2004b). This species could possibly be linked to a second phylogenetic group consisting of isolates labeled as *C. radicalis* from Italy, France and Portugal, but this is also speculative as there are no isolates linked to herbarium specimens for this species. As the results of the DNA sequence-based and morphological comparisons cannot be linked, this species has not yet been described as a unique taxon.

Additional collections of *C. radicalis sensu lato* are clearly needed to resolve questions regarding its taxonomy. The phylogenetic placement of North American *C. radicalis* isolates has yet to be determined. It is also possible that another species of *Cryphonectria*, similar to *C. radicalis sensu lato* and referred to as *E. radicalis mississippiensis* Shear and N. E. Stevens (Shear et al., 1917), occurs in North America (Myburg et al., 2004b). Additional collections from Japan will also be required to determine whether the other, undescribed subclade encompassing isolates labelled as *C. radicalis* coexists with *C. radicalis* in Japan. This question arose because only a single isolate of *C. radicalis* from Japan, which was grouped in the subclade representing *C. radicalis sensu stricto*, has been available for study (Myburg et al., 2004b). Isolates of *C. radicalis sensu lato* will, however, be difficult to detect in nature because they are possibly displaced by or their occurrence is masked by *C. parasitica*, especially in Europe and North America (Hoegger et al., 2002).

One of the fungi associated with cankers on *Eucalyptus* that has come into consideration during taxonomic studies of *Cryphonectria* is *C. eucalypti*. This fungus was previously known as *Endothia gyrosa*, which is a well-known associate of stem and branch cankers on native tree species in the United States (Stipes & Phipps, 1971; Roane et al., 1974). Rather unusually, it is also a name that was applied to the causal agent of stem cankers on *Eucalyptus* in Australia (Walker et al., 1985; Old et al., 1986) and South Africa (Van der Westhuizen et al., 1993). One of the reasons that the fungus on *Eucalyptus* was treated as *E. gyrosa* is that it has orange stromata and aseptate ascospores, which made it similar to *Endothia* spp. (Walker et al., 1985). Phylogenetic and morphological studies of isolates from *Eucalyptus* and those of *E. gyrosa* from the USA (Venter et al., 2001, 2002) showed that these fungi are not the same, and that the fungi from *Eucalyptus* are more closely related to *Cryphonectria*. This led to a name being provided for the fungus on *Eucalyptus* in *Cryphonectria* as *C. eucalypti* (Venter et al., 2002).

Although phylogenetic studies have grouped *C. eucalypti* closely with *Cryphonectria*, the fungus is unlike other species of *Cryphonectria*, which all have single septate ascospores (Venter et al., 2002; Myburg et al., 2004a). *Cryphonectria*

eucalypti has aseptate ascospores, and, thus, based on morphological characteristics, has been suspected to represent a distinct genus (Myburg et al., 2004a). This hypothesis is confirmed in the new phylogenetic tree presented in the present study (Fig. 4), showing that *C. eucalypti* groups separately from species in *Cryphonectria sensu stricto*, and a new genus should thus be erected for this species.

New type for *Cryphonectria*

A group of isolates from *Elaeocarpus* spp. in New Zealand, labeled as *C. gyrosa* and *C. radicalis*, was shown in DNA sequence-based phylogenetic analyses (Fig. 4) to group separately from other *Cryphonectria* spp. (Myburg et al., 2004a). Their distinct grouping was defined morphologically by the one- to three-septate ascospores, conical and superficial conidiomata (Fig. 1g), and conidia of variable size (Myburg et al., 2004a; Gryzenhout et al., 2005b). These isolates are also unique in being associated with root cankers on *Elaeocarpus* spp. in New Zealand (Pennycook, 1989).

In resolving the identity of the fungus defined by the isolates from New Zealand, it was realized that the fungus shared the same morphology as specimens of *C. gyrosa* from Sri Lanka (Myburg et al., 2004a; Gryzenhout et al., 2005b, c). Because *C. gyrosa* was commonly recognized as the type of *Cryphonectria* (Barr, 1978), this implied that isolates residing in the new clade from New Zealand should have had the name *Cryphonectria*, rather than those of the clade defining currently known *Cryphonectria* spp., including *C. parasitica* (ICBN, Art. 7.2, Greuter et al., 2000).

Studies on the type status of *C. gyrosa* showed that *C. gyrosa* was erroneously cited as the type of *Cryphonectria* (Gryzenhout et al., 2005c). The error arose because *C. gyrosa* was mechanically selected as type at the time, while the species included in the original sub-genus *Cryphonectria*, namely *C. abscondita* Sacc. and *C. variicolor* Fuckel, were ignored as choice for type (Gryzenhout et al., 2005c). This erroneous lectotypification of *C. gyrosa* and the separate grouping of the isolates similar to *C. gyrosa* from *Cryphonectria* spp. prompted a proposal to conserve the name *Cryphonectria* against a new type (Gryzenhout et al., 2005c). The proposal was accepted by the International Association of Plant Taxonomists (IAPT) Nomenclature Committee for Fungi (Gams, 2005). The original species *C. variicolor* and *C. abscondita* were not suitable as new types and *C. parasitica* was chosen as the type for the genus. This was justified largely because of its importance as a pathogen and the viruses that have been characterized from it (Gryzenhout et al., 2005c).

The clade containing *C. gyrosa* and the isolates from New Zealand could thus be described as a distinct genus with the new name *Amphilogia* (Gryzenhout et al., 2005b). *Amphilogia gyrosa* (Berk. & Broome) Gryzenh. & M. J. Wingf. occurs

on *Elaeocarpus* spp. in both New Zealand and Sri Lanka. This genus includes a second species, *A. major* Gryzenh. & M. J. Wingf., which also occurs on *Elaeocarpus* spp., but is currently known only from the South Island of New Zealand (Gryzenhout *et al.*, 2005b).

New genera for *Cryphonectria* spp.

Only *C. parasitica*, *C. radicalis sensu lato*, *C. nitschkei* and *C. macrospora* group in the well-supported clade that represents *Cryphonectria* (Fig. 4), and they all have the morphological characteristics that define *Cryphonectria* (Myburg *et al.*, 2004a, b). The taxonomic position of *C. havanensis* and *C. coccolobae* remains confused because no isolates exist for these species that can be used in phylogenetic studies based on DNA sequence comparisons (Myburg *et al.*, 2004a). The remaining species described in *Cryphonectria* have, however, now been transferred to newly described genera, or will be transferred soon. These new genera have largely been recognized based on DNA sequence data (Fig. 4). Robust morphological characters also support the phylogenetic grouping of these new genera (Fig. 1).

Chrysoporthe is a new genus that has been described to house isolates of *C. cubensis* from various parts of the world (Gryzenhout *et al.*, 2004). The fungi previously collectively known as *C. cubensis* are some of the most serious canker pathogens (Wingfield, 2003) of commercially grown *Eucalyptus* (*Myrtaceae*, *Myrtales*), and they are also pathogenic to other plant genera in the *Myrtales* (Fig. 3; Table 1). Species in *Chrysoporthe* are all characterized by limited ascostromatic tissue covering the perithecial bases, long perithecial necks covered in black stromatic tissue, and superficial, generally pyriform and fuscous black conidiomata (Fig. 1d–f; Gryzenhout *et al.*, 2004; Myburg *et al.*, 2004a). The anamorph genus *Chrysoporthella* has been described for asexual structures of *Chrysoporthe* (Gryzenhout *et al.*, 2004).

Analyses of DNA sequence data have shown that isolates labeled as *Chr. cubensis* from different parts of the world group in five distinct subclades (Fig. 4) of *Chrysoporthe* (Gryzenhout *et al.*, 2004, 2005d). These taxa are all pathogens of trees (Fig. 3). Four species (Table 1) could be described based on obvious morphological and ecological characteristics. These species include *Chr. cubensis* (Bruner) Gryzenh. & M. J. Wingf. for the *Eucalyptus* pathogen in South America, South East Asia, Australia and Central Africa (Gryzenhout *et al.*, 2004). This species is also able to infect *Syzygium aromaticum* or clove (Hodges *et al.*, 1986; Myburg *et al.*, 2003) and *Miconia* spp. (Rodas *et al.*, 2005). *Chr. austroafricana* Gryzenh. & M. J. Wingf. (Gryzenhout *et al.*, 2004) causes cankers on *Eucalyptus* (Wingfield *et al.*, 1989), *Tibouchina* (Fig. 3e, f, Myburg *et al.*, 2002) and *Syzygium* spp. (Heath *et al.*, 2006) in South Africa. *Chr. doradensis* Gryzenh. & M. J. Wingf. is a newly described

species (Gryzenhout *et al.*, 2005d) that is pathogenic to *Eucalyptus* spp. in Ecuador. *Chrysoporthella hodgesiana* Gryzenh. & M. J. Wingf., for which the teleomorph has not yet been found (Gryzenhout *et al.*, 2004), infects native *Tibouchina* spp. (Wingfield *et al.*, 2001; Gryzenhout *et al.*, 2004) and *Miconia* spp. (Rodas *et al.*, 2005) in Colombia.

Chrysoporthella cubensis isolates reside in two distinct phylogenetic subclades (Fig. 4, Gryzenhout *et al.*, 2004). One subclade consists of isolates from South and Central America, and Eastern Africa (Gryzenhout *et al.*, 2004), while the other subclade includes isolates from South East Asian countries, Australia, Tanzania and Hawaii (Myburg *et al.*, 2003). Fungi in these two subclades are indistinguishable from each other morphologically, although they represent two geographically distinct groups (Gryzenhout *et al.*, 2004). Population-level techniques will most likely be required to determine whether fungi in these two subclades represent distinct species.

A fungus pathogenic to *Terminalia ivorensis* and *Terminalia superba* (*Combretaceae*, *Myrtales*) in Ecuador has recently been discovered and characterized (Fig. 4). This fungus has been described in the new genus *Rostraureum* and it is referred to as *R. tropicale* Gryzenh. & M. J. Wingf. (Gryzenhout *et al.*, 2005a). *Rostraureum* (Fig. 1h) is characterized by superficial, orange, rostrate conidiomata with long necks, and semi-immersed ascostromata with little stromatic tissue, except for a white sheath of tissue around the perithecial necks. *Cryphonectria longirostris* also has these characteristics, but can be distinguished from *R. tropicale* based on conidial size (Gryzenhout *et al.*, 2005a). For these reasons, *C. longirostris* has been transferred to *Rostraureum* (Gryzenhout *et al.*, 2005a). In contrast to *R. tropicale*, there is no evidence to suggest that *R. longirostris* (Earle) Gryzenh. & M. J. Wingf. is pathogenic (Earle, 1901).

A newly discovered genus related to *Cryphonectria* and *Chrysoporthe*

Extensive sampling of fungi similar to *Chrysoporthe* and *Cryphonectria* has led to the discovery of a new fungus, *Aurapex penicillata* Gryzenh. & M. J. Wingf. nom. prov., from Colombia. This fungus is associated with canker and die-back symptoms on native *Melastomataceae* (*Tibouchina*, *Miconia*) and *Eucalyptus* trees (Gryzenhout *et al.*, 2006). Morphologically, this fungus is similar to *Chrysoporthella*, with black, superficial and pyriform conidiomata (Fig. 1i). It can, however, be distinguished from *Chrysoporthella* based on the different tissue organizations in the two fungi and because the tips of the conidiomatal necks are orange as opposed to necks that are uniformly black in *Chrysoporthella* (Fig. 1f). Phylogenetically, the fungus groups alone but close to *Cryphonectria* and allied genera (Fig. 4). No teleomorph has been found for *A. penicillata*, and it was thus described

as the mitotic genus *Aurapex* nom. prov. residing in the *Diaporthales*.

Position of *Cryphonectria* and allied genera in the *Diaporthales*

Large subunit DNA sequence comparisons of an extensive collection of genera in the *Diaporthales* have revealed that species of *Cryphonectria*, *Endothia* and *Chrysosporthe* form a well-supported and distinct clade in the order (Castlebury *et al.*, 2002). This clade has been referred to as the *Cryphonectria–Endothia* complex. Castlebury *et al.* (2002) proposed that the unique grouping of these isolates in the *Diaporthales* is supported by morphological features such as stromatic tissue that is orange at some stage in the life cycle of the fungus, and the tissue that turns purple in 3% KOH and yellow in lactic acid. The unique grouping and morphological characteristics of these genera suggest that *Cryphonectria* and related genera most likely represent a new family in the *Diaporthales*.

Conclusions

Recent taxonomic revisions have restricted the name *Cryphonectria* to only seven species. Other species related to *Cryphonectria* now reside in the three genera *Chrysosporthe*, *Rostraureum* and *Amphilogia*. The species conclusively shown to belong in *Cryphonectria* include *C. parasitica*, which is now also recognized as the type of the genus, *C. nitschkei*, *C. radicalis sensu lato* and *C. macrospora*. In DNA sequence comparisons, these species reside in a distinct clade representing *Cryphonectria sensu stricto*. Of these *Cryphonectria* species, only *C. parasitica* is a serious and primary plant pathogen (Anagnostakis, 1987).

Cryphonectria havanensis, *C. coccolobae* and *C. eucalypti* currently retain their position in *Cryphonectria*. However, the taxonomic relationship of *C. havanensis* and *C. coccolobae* with species in the *Cryphonectria* clade must still be clarified. Likewise, *C. eucalypti* should reside in a taxon apart from *Cryphonectria* because of its distinct ascospore morphology (Myburg *et al.*, 2004a) and phylogenetic data presented for the first time in this study.

Cryphonectria spp., as they are now recognized, occur in temperate areas of Asia, Europe and North America (Table 1). Only *C. havanensis* and *C. coccolobae* occur in the Caribbean area, while *C. eucalypti* is known from Australia and South Africa (Table 1). *C. parasitica*, *C. radicalis sensu lato*, *C. nitschkei* and *C. macrospora* occur on a wide range of woody plants residing in five plant orders (Table 1). These species are all known from Japan, and it seems probable that this part of the world represents a centre of origin for these fungi. Only *C. radicalis sensu lato* occurs naturally in Europe (Myburg *et al.*, 2004b), and additional species remain to be described in this group. *Cryphonectria radicalis* is also

known in the USA, based on herbarium specimens from 1828 (Myburg *et al.*, 2004b), although its presence in that country needs to be confirmed based on fresh specimens and DNA sequence comparisons.

During the course of the last decade, wide-ranging changes have been made to the taxonomy of *Cryphonectria* and related genera. These have emerged largely from studies on species such as *Chr. cubensis* that causes a serious canker disease on *Eucalyptus* and related plants (Wingfield, 2003). These studies commenced during the time when DNA sequence comparisons and the phylogenetic species concept was emerging as a dominant taxonomic approach, and they would not have been possible without them. Taxonomic studies described in this review provide a framework that should lead to a better understanding of the important tree pathogens residing in this group. They are also likely to lead to the discovery of additional species and to promote a more lucid understanding of the global distribution of invasive or potentially invasive tree pathogens.

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