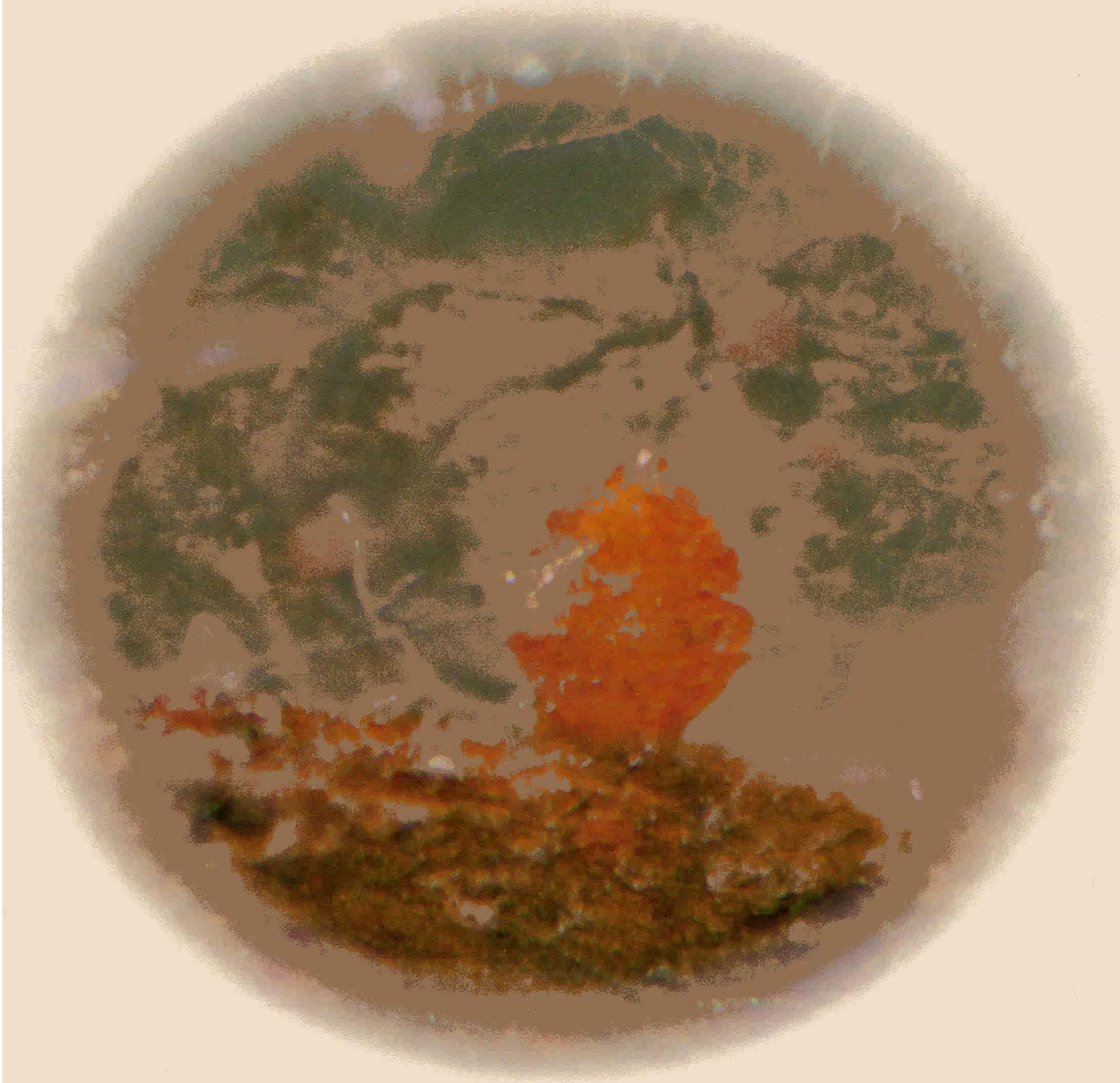

Phylogenetic relationships and population dynamics of *Calonectria*

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Declaration

I the undersigned hereby declare that the work contained in this dissertation is my own original work and has not previously in its entirety or in part been submitted at any university for a degree.

7/12/99
Date

Summary

This dissertation is presented as a collection of separate publications and an amount of redundancy has thus been unavoidable. Although several species are newly described they are not effectively published and will thus be formally published in scientific journals. There were two main objectives:

I. To investigate the variability and mating compatibility of species and populations, in order to contribute to the systematics of *Calonectria*.

II. To identify loci that would be useful for DNA sequence comparisons in this genus and to present a reliable phylogeny of *Calonectria* and other closely related hypocrealean taxa.

In the introductory review a synopsis of the current knowledge regarding the taxonomy and life cycle of *Calonectria* and *Cylindrocladium* spp. is presented. The importance of these pathogens are noted, as well as the problems related to identifying them. Aspects regarding specific species complexes and topics are discussed in more detail in the following chapters.

The morphological and phylogenetic variation was investigated for the *Cy. candelabrum* species complex in Part 2. DNA sequence comparisons of the ribosomal 5.8S gene and flanking ITS1 and ITS2 spacers were employed in order to determine whether mating incompatibility and general morphology was supported by molecular evidence. Although only small differences were found these proved to be consistent and resulted in the recognition of *Calonectria scoparia* (anamorph *Cylindrocladium candelabrum*), and the description of three new species, namely *Calonectria pauciramosa* (anamorph *Cylindrocladium pauciramosum*), *Calonectria insularis* (anamorph *Cylindrocladium insulare*) and *Calonectria mexicana* (anamorph *Cylindrocladium mexicanum*).

The *Cylindrocladium scoparium* cultures studied in Part 3 were isolated from several hosts in the U.S.A. Isolates were mated in all combinations, and one successful mating was selected to establish whether recombination occurred. RAPD and mating type data of parental isolates and progeny confirmed *Cy. scoparium* to have a heterothallic mating system. Furthermore, to determine the phylogeny of *Cy. scoparium* with several morphologically similar *Cylindrocladium* spp., DNA

sequences of the ribosomal 5.8S gene and the flanking internal transcribed spacers (ITS), as well as part of the high mobility group (HMG) box (forming part of the *MAT-2* mating type gene) and the β-tubulin gene, were analysed. Maximum parsimony yielded concordant trees for all three data sets. These data supported the morphological and biological species concepts proposed for *Cy. scoparium* and other, similar, small-spored *Cylindrocladium* spp.

Part 4 represented an investigation into the mating compatibility and mating type distribution of populations of *Cy. pauciramosum*. This enabled the determination of the effective population for the different areas studied. A sample collected over a period of six years, reflecting a number of locations in South Africa were found have 1:1 mating type ratio, as expected in a random mating population. However, the mating type ratio was found to be significantly different in single nursery populations. In the South African nursery, the *MAT-1* mating type was dominant, while the *MAT-2* was more common in other samples obtained from nurseries in Italy and the U.S.A. This was consistent with one or more founder effects. The high percentage of hermaphrodites also suggested that recent introductions had occurred in nurseries in Italy and the U.S.A. In addition to this, DNA sequence comparisons of the β-tubulin gene was used to investigate variation below species level in *Cy. pauciramosum*. All isolates from South Africa, Australia, U.S.A. and a group from Italy had identical sequences. A second group with identical sequences were found in the Italian sample. In addition to this, variation was found between all isolates from Brazil, Colombia and Mexico. Some of these base pairs were shared between the South and Central American isolates as well as isolates of *Cy. candelabrum*. This points towards a speciation event in South or Central America.

After investigating variation below species level, this study was also expanded to generic level. In Part 5 information obtained in the preceding chapters culminated in a phylogeny of all known species in *Calonectria* and *Cylindrocladium* based on DNA sequence comparisons of the β-tubulin gene. Many clades, containing small numbers of isolates were strongly supported by bootstrap. However, relationships between these clades were often ambiguous. A number of phylogenetic placements based on DNA data did not always agree with preconceived morphological relationships. Two large groupings were evident and both contained small-spored, one-septate species. The only morphological character that correlated with DNA based phylogenies was vesicle shape of the anamorph.

Finally, in Part 6, the generic phylogeny was investigated. In order to obtain a generic phylogeny a subset of *Calonectria* species was selected, as well as isolates from other genera, closely related to *Calonectria*. All of these genera were originally described under the broad concept of *Nectria* sensu lato. A gene tree phylogeny, based on β-tubulin was presented for selected nectriaceous genera with anamorphs bearing cylindrical macroconidia. Based on molecular data and the distinct anamorph genera, new teleomorph genera were proposed for *Cylindrocladiella* (*Nectricladiella*), *Gliocladiopsis* (*Glionectria*) and *Xenocylindrocladium* (*Xenocalonectria*). *Calonectria* was also found to form a monophyletic lineage. Eight species of *Cylindrocladiella* were recognised, with two having teleomorphs in *Nectricladiella*, namely *N. camelliae* (*Ce. microcylindrica*) and *N. infestans* (*Ce. infestans*).

This study concluded that the current morphological species concepts in *Cylindrocladium* and its *Calonectria* teleomorphs can comprise several biological as well as phylogenetic species. The use of mating testers in this study was shown to provide a powerful tool to separate morphologically similar, but genetically isolated species. The biological and morphological species also agreed with the phylogenetic concepts used, but only vesicle shape were found to define phylogenetic clades. However, phylogenetic species concepts based on DNA sequences data obtained from genomic regions such as the β-tubulin and *MAT-2* genes and additional areas will become increasingly important for further taxonomic studies in *Calonectria* and related genera.

Opsomming

Hierdie studie word aangebied as 'n samevoeging van 'n aantal onafhanklike publikasies en 'n sekere mate van oorvleueling sal dus voorkom. Alhoewel 'n aantal spesies nuut beskryf word in hierdie tesis, is hulle nie effektief gepubliseer nie, en sal dergelike publikasie in toepaslike wetenskaplike joernale plaasvind. Die hoofdoel van hierdie studie was tweërlei:

I. Om die varieerbaarheid en paringsvermoëns van spesies en bevolkings te ondersoek en by te dra tot die sistematiek van *Calonectria.*

II. Om die lokusse te identifiseer wat bruikbaar kan wees vir DNA volgorde vergelykings in hierdie genus en om 'n betroubare filogenie van *Calonectria* en naby verwante spesies in die Hyporeales te genereer.

In die inleidende oorsig is die huidige kennis aangaande die taksonomie en lewensiklus van *Calonectria* en *Cylindrocladium* spp. bespreek. Die belang van hierdie spesies is aangedui, sowel as die probleme waarmee hulle geassosieer word. Punte wat van toepassing is op spesifieke spesie komplekse word later in meer detail bespreek.

Die morfologiese en filogenetiese variasie op spesie vlak word ondersoek in Deel 2. DNA volgorde vergelykings van die ribosomale 5.8S geen en die naasliggende ITS1 en ITS2 intergeniese areas was gebruik om die paringsonvermoë en morfologiese karakters te onderskryf. Dit het die herbeskrywing van 'n bestaande spesie, *Calonectria scoparia* (anamorf *Cylindrocladium candelabrum*), en die beskrywing van drie nuwe spesies, *Calonectria pauciramosa* (anamorf *Cylindrocladium pauciramosum*), *Calonectria insularis* (anamorf *Cylindrocladium insulare*) and *Calonectria mexicana* (anamorf *Cylindrocladium mexicanum*) tot gevolg gehad.

In die daaropvolgende deel was die herkombinering van *Cy. scoparium* beskou met behulp van RAPD merkers. Parings is uitgevoer en die RAPD en paringstipe data het bevestig dat hierdie spesie heterotallies is. In die tweede deel van hierdie hoofstuk was DNA volgorde vergelykings gedoen op fragmente wat verkry is van drie verskillende lokusse, die 5.8S ribosomale geen en ITS areas en dele van die *MAT-2* geen se HMG kas asook die β-tubulien geen. Hierdie data was aangewend om die filogenie van *Cy. scoparium* en ander kleinspoorvormende heterotalliese

Cylindrocladium spesies te ondersoek. Dit het die drie nuut beskryfde spesies van die vorige hoofstuk ingesluit en morfologies en biologies spesie konsepte bevestig.

Deel 4 bevat 'n ondersoek na die paringsvermoëns van *Cy. pauciramosum* op bevolkingsvlak. As gevolg hiervan kon die effektiewe bevolking in verskillende areas bepaal word. A monster wat oor 'n tydperk van ses jaar en 'n verskeidenheid van geografies gebiede versamel is het 'n paringstipe verhouding van 1:1 gehad. Dit is volgens verwagting in 'n bevolking wat vrylik paar. In spesifieke kwekerye was die geval egter anders. In die Suid-Afrikaanse kwekery was die *MAT-1* paringstipe oorheersend, terwyl *MAT-2* meer voorgekom het in Italië en V.S.A. Die hoë aantal hermafrodiete dui ook daarop dat die spesie onlangs ingebring is. DNA volgorde vergelykings was ook gebruik om variasie onder spesievlak te ondersoek. Alle isolate van Suid-Afrika, Australië, V.S.A. en 'n groep van Italië het indentiese volgordes gehad. 'n Tweede groep in die Italiaanse bevolking is ook gevind met identiese DNA volgordes. In die Suid en Sentraal Amerikaanse bevolkings is die meeste variasie gevind en sommige van die basis paar verskille is gedeel met *Cy. candelabrum*. Dit dui op 'n spesiasie in Suid Amerika.

In Deel 5 is die inligting wat verkry is vantevore uitgebrei na generiese vlak toe. Dit het 'n filogenie van alle bestaande *Calonectria* en *Cylindrocladium* spesies tot gevolg gehad, gebaseer op DNA volgordes van 'n deel van die β-tubulien geen. Verskeie klades is deur statisties analise ondersteun. Verhoudinge tussen hierdie groepe was egter minder duidelik. Twee groot groepe was ook onderskei en die engiste morfologiese karakter was met die geen filogenie ooreengestem het is die vorm van die "vesicle" op die kondiofore van die anamorf.

Tot slotsom, in Deel 6 is die verteenwoordigende groepe spesies van *Calonectria* en naby verwante genera vergelyk. Hierdie genera is alreeds voorheen bespreek onder die wye taksonomiese konsep *Nectria* sensu lato. 'n Geen boom gebaseer op β-tubulien was aangedui. Aan die hand van hierdie data en unieke anamorf verwantskappe is nuwe teleomorf genera voorgestel vir *Cylindrocladiella* (*Nectricladiella*), *Gliocladiopsis* (*Glionectria*) en *Xenocylindrocladium* (*Xenocalonectria*). Dit is ook bevind dat *Calonectria* monofileties is. Ag spesies van *Cylindrocladiella* is aangedui, waarvan twee teleomorwe het in *Nectricladiella*, naamlik *N. camelliae* (*Ce. microcylindrica*) en *N. infestans* (*Ce. infestans*).

Hierdie studie het dus bevind dat die huidige morfologies spesie konsepte in *Cylindrocladium* ook biologiese en filogeneties spesies omskryf. Die gebruik van paringstoetsers is aangedui as 'n goeie metode om morfologies eenderse spesies te onderskei. Dit wil egter voorkom asof filogenetiese spesie konspte gebaseer op DNA gebiede soos die β-tubulien en *MAT-2* geen, asook ander areas meer belangrik sal word vir verder taksonomies studies in hierdie swam.

"An acquaintance with fungi is in the highest degree necessary to man."
Linneaus C (1707-1778)

"Nothing in the whole world is coarse or despicable, but everything that the Divine Power has created and preserves is most worthy of contemplation...since in our judgement the very smallest of created things, equally as the greatest, have their miracles."
Holmskjold T (1732-1794)

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The Creator of us all.

"The classification of the Pyrenomycetes will never be either natural or philosophical, until the species become known in the most minute details of their frutification."

De Notaris G (1805-1877)

Table of contents

1. An introduction to *Calonectria* and *Cylindrocladium* systematics

Background

The Hypocreales constitutes one of the 46 ascomycetous orders recognised in the current Dictionary of Fungi (Hawksworth et al 1995). Several members of this order have been studied extensively because they fill ecological niches that make them important in many fields of human endeavour. Hypocrealean species range from agents of biological control and producers of antibiotics to elicitors of potent mycotoxins (reviewed by Rossman 1996). The genus *Calonectria* De Not. is especially important and its members are pathogenic to a wide variety of plants in warm and humid conditions world-wide.

Descriptive accounts on the Hypocreales have centred primarily on species of the genera *Hypocrea* Fr., *Hypomyces* (Fr.) Tul. and *Nectria* (Fr.) Fr. (Rossman 1996). The genus *Nectria* sensu lato has been a repository for all species having fleshy, uniloculate ascocarps with a hypocrealean centrum with hyaline, non-apiculate, bicellular ascospores, and phialidic anamorphs (Rossman 1993). Recently several informal groupings of *Nectria* were re-described as genera within the family *Nectriaceae* (Rossman et al 1999). Genera were segregated from *Nectria* on the basis of single characters, including ascospore septation and conidiomatal morphology. *Calonectria,* relevant to this study, were already seperately circumscribed previously by Rossman (1979b) and were one of these genera.

Teleomorph

The genus *Calonectria* (*Ca.*) was erected by De Notaris (1867) based on the type species *Ca. daldiniana* De Not. which has since proved to be a later synonym of *Ca. pyrochroa* (Desm.) Sacc. (Rossman 1979a). In Saccardo's description *Calonectria* was delimited for *Nectria*-like species with multiseptate ascospores (Saccardo 1883). Although Rossman (1979a, b, 1983) accepted differences in ascospore septation to exist at generic level, the concept of distinguishing genera on the basis of a single character was not supported. This viewpoint was in agreement with the work of Booth (1959) and subsequent authors who used a combination of characters that included anatomy of the perithecial wall, as well as ecology and presence of specific anamorphs for generic delimitation. Therefore, members of *Calonectria* were defined

as species with brightly coloured ascocarps that change colour when placed in 3% KOH solution (KOH+), have a warty to scaly wall structure, darkened stromatic base, and *Cylindrocladium* Morgan anamorphs (Rossman 1993, Rossman et al 1999).

A number of *Calonectria* species have been described in the previous two decades. Five species of *Calonectria* were accepted and monographed by Rossman (1983). A subsequent review included 10 species of *Calonectria* with *Cylindrocladium* anamorphs as well as an additional six *Cylindrocladium* species for which no *Calonectria* state was known (Peerally 1991). The most recent monograph was that by Crous and Wingfield (1994). These authors circumscribed sixteen *Calonectria* species with *Cylindrocladium* anamorphs, and seven *Cylindrocladium* species without known teleomorphs.

The emphasis of the last two monographs was firmly placed on features of the *Cylindrocladium* anamorph. The reasons for this are twofold. Firstly, the anamorph state is the form most frequently encountered in the field and secondly, nearly all species can be distinguished only on their asexual characters. This is due to the fact that ascospore size, as well as ascus and perithecial morphology can only place taxa into one of three species complexes. Furthermore, in many cases, species are heterothallic, and the *Calonectria* state is rarely observed. In line with the arguments presented above, preference in this document will be given to the terminology and morphological characters of the *Cylindrocladium* state in the rest of this study.

Anamorph

The asexual genus, *Cylindrocladium* (*Cy.*), was first erected by Morgan (1892) for a species found growing on an old pod of *Gleditsia triacanthos* L. in Ohio, U.S.A. This genus was delimited by the author as follows "Sterile hyphae, creeping, branched forked or trichotomously branched the sporophores in pairs or threes at the extremities of the branchlets and cymosely arranged; spores solitary, cylindrical, 1-septate, hyaline". The type species was described as *Cy. scoparium* Morgan. Most notably, no mention was made of the appendage on the conidiophores. However, subsequent descriptions by Massey (1917) and Anderson (1918) clearly indicated this feature, which later authors found to be so characteristic for *Cylindrocladium* (Boedijn & Reitsma 1950, Sobers & Seymour 1967, Peerally 1991, Crous & Wingfield 1994). Presently four conidial types are known for *Cylindrocladium*, namely chlamydospores, microconidia, macroconidia and megaconidia (Crous & Seifert 1998). *Cy. scoparium*, however, forms macroconidia and chlamydospores only. As

no cultures were obtained by Morgan (1892), nor any mention made of chlamydospores, it is clear that the generic name represents the macroconidial form.

Several authors described species under different generic names that were eventually synonomised under *Cylindrocladium*. *Diplocladium cylindrosporum* Ellis & Everh. was described with a sterile appendage, swollen at the tip, but was subsequently redisposed to *Cylindrocladium* by Boedijn and Reitsma (1950). A similar fate was in store for the genera, *Candelospora* Hawley apud Rea & Hawley (Boedijn & Reitsma 1950), *Tetracytium* Vanderwalle (Subramanian 1971) and *Cylindrocladiopsis* J.M. Yen (Crous & Seifert 1998).

Species of *Cylindrocladium* have been defined based on various features of the conidiophores and the conidia (Crous & Wingfield 1994). The use of one such character, the stipe eminating from the conidiophores and the shape of its apical vesicle has elicited much difference of opinion. Before the important review done by Boedijn and Reitsma (1950), taxonomists concentrated mainly on conidial morphology. The importance of the presence of a vesicle and its shape as a species defining character was only emphasised several years later (Bell & Sobers 1966, Sobers & Seymour 1967). However, subsequent authors rejected this species concept due to the variability of this feature (Hunter & Barnett 1978, Rossman 1983). Peerally (1991) argued that vesicle shape can be a reliable taxonomic character in fresh cultures and that this must be used in combination with conidial characters for identification of *Cylindrocladium* species. This view was also supported by subsequent authors (Crous et al 1992, Uchida & Aragaki 1992b). Crous et al (1992) showed that the osmotic potential of the medium influences vesicle shape and that vesicle morphology can be a reliable character when standardised media and growth conditions are applied. Consequently, this approach was combined with other morphological characters in order to delimit several *Cylindrocladium* species (Crous & Wingfield 1994).

Closely related genera

The anamorph genus *Cylindrocladiella* Boesew. was erected by Boesewinkel (1982) to accommodate several small-spored species that were previously placed in *Cylindrocladium*. *Cylindrocladiella* (*Ce.*) was reported to have different conidiophore branching patterns, conidial shapes, dimensions, as well as cultural characteristics. The recognition of *Nectria camelliae* Shipton as the teleomorph for one of these species made a strong case for the seperation of *Cylindrocladiella*. More recent

studies have confirmed the genera *Cylindrocladium* and *Cylindrocladiella* to be distinct (Crous & Wingfield 1993, Crous et al 1994, Victor et al 1998). Samuels (1991) allocated *N. camelliae* (anamorph: *Ce. infestans*) to *Nectria* subg. *Dialonectria,* while (Rossman et al 1999), in a re-evaluation of the group, placed it in *Cosmospora* (*Cs.*) as *Cs. camelliae* (Shipton) Rossman & Samuels, based on its teleomorph morphology. In comparison to *Calonectria*, the perithecial walls of *Cs. camelliae* are smooth and narrow, while the ascospores are 1-septate and much smaller.

Several genera with characters morphologically similar to those of *Calonectria* have previously been described under the generic concept of *Nectria* sensu lato in the *Nectriaceae* (Rossman et al 1999). Molecular character based phylogenies in this group have largely confirmed morphological groupings. Sequence comparisons of the nuclear large-subunit (28S) ribosomal DNA obtained from several genera in the Hypocreales indicated that some clustered closely to *Calonectria* (Rehner & Samuels 1994). *Leuconectria clusiae* Rossman et al (anamorph: *Gliocephalotrichum bulbilium* J.J. Ellis & Hesselt.), as well as *Nectria radicicola* Gerlach & Nilsson (anamorph: *Cylindrocarpon destructans* (Zinnsm.) Scholten) showed the closest similarity, with two typical species of *Nectria*, *N. pseudotrichia* Berk. & Kurt. [anamorph: *Tubercularia lateritia* (Berk.) Seifert] and *N. cinnabarina*, forming part of this subclade, but grouping more distantly.

In morphological studies, several similarities were found between the *Gliocephalotrichum* and *Cylindrocladium* anamorphs of *Leuconectria* and *Calonectria* (Rossman & Samuels 1993). The most notable was the formation of cylindrical conidia, penicillate conidiophores, and a brown pigment diffusing in agar media. Perithecial anatomy in *N. radicicola* and its relatives was also observed to be similar to that of *Calonectria* (Samuels & Brayford 1990). Samuels and Seifert (1987) also recognised similarity between *Cylindrocladium* and the *Cylindrocarpon* Wollenw. (*Co.*) anamorphs of *N. radicicola.*

In addition to these genera, several other anamorph form genera are similar to *Cylindrocladium,* having cylindrical macroconidia and phialidic conidiogenous cells. Among these are *Gliocladiopsis* S.B. Saksena, *Xenocylindrocladium* Decock et al and *Curvicladium* Decock & Crous. Of these genera, only *Xenocylindrocladium* (Decock et al 1997) has been linked to a teleomorph, forming part of the *Nectria* sensu lato clade.

Characterisation of *Cylindrocladium* and *Calonectria* species

Morphology and cultural characteristics

As mentioned previously, the most recent taxonomic concept for *Calonectria* places emphasis on the features of its *Cylindrocladium* anamorph. The standardisation of growth conditions (Peerally 1991, Crous et al 1992, Crous & Wingfield 1994) enabled the use of characters previously described as variable and unreliable (Hunter & Barnett 1978, Rossman 1983). Besides the shape and size of the apical vesicles, species are differentiated on the dimensions and septation of conidia, phialide shape, stipe length, conidiophore branching pattern and cultural characteristics. Teleomorph characteristics evaluated for interspecies differentiation include ascospore size and septation, perithecial colour and morphology.

In addition to these characters, the taxonomic value of the occurrence of micro- and megaconidial states has also been evaluated. Sobers (1968) discussed the presence of a small-spored form of *Cy. pteridis* Wolf that was observed in cultures growing on water agar and on plant material. This microconidial form has also been reported in at least eight of the *Cylindrocladium* species treated in the monograph of Crous and Wingfield (1994). Microconidia are generally cylindrical, straight or curved and 1-septate, although 3-septate conidia have been reported for *Cy. multiseptatum* and *Cy. rumohrae* (El-Gholl et al 1997, Crous et al 1998b). Crous and Wingfield (1994) questioned the usefulness of this character for taxonomic studies however, as the microconidia are not produced by all strains of a species.

The term "megaconidia" was only recently defined as a fourth conidial type for *Cylindrocladium* (Crous & Seifert 1998). This conidial state has been infrequently reported before (Sobers 1971, Alfieri et al 1972, Uchida & Aragaki 1992a). In agreement with the terminology used for *Fusarium* conidia, "normal" conidia are referred to as macroconidia, while the larger conidial type has been termed as megaconidia (Crous & Seifert 1998). Megaconidia were reported for four species of *Cylindrocladium* and were described as multiseptate, widest in the middle, straight to curved or bent at right angles, and significantly larger than macroconidia. As in the case of microconidia the value of this as a taxonomic character is limited, but can be important in cases where some strains form only these conidia (Crous & Seifert 1998).

The functions and roles of the mega- and microconidial states in the *Calonectria* life cycle are still uncertain and open to speculation. The occurrence of microconidial states is not unique in the *Nectriaceae* and it is regularly found in *Cylindrocarpon* and *Fusarium* Link:Fr. species (Booth 1971). Another conidial state intermediate between micro- and macroconidia was termed mesoconidia for species of *Fusarium* (Pascoe 1990a). Mesoconidia are thought to be produced under dry conditions in order to allow air dispersal (Pascoe 1990b). A similar relationship with regard to specific environmental conditions and functions of micro- and megaconidia may occur in *Cylindrocladium.*

Cardinal temperature requirements for growth, as well as the production of chlamydospores and microsclerotia were evaluated by Crous & Wingfield (1994). Several species were found to grow at either high or low temperatures, and to produce sparse or extensive amounts of chlamydospores on malt extract agar. Although chlamydospore formation influences colony colour, these characters were found to be of much less taxonomic value than in related hypocrealean genera (Crous & Wingfield 1994).

Physiological and biochemical characteristics

The response of a number of *Cylindrocladium* species to various nutritional and environmental conditions has been studied by Hunter and Barnett (1978). No major variations were observed in utilisation of different C and N sources, although species differed in sporulation. However, different C sources had an effect on microsclerotial production (Weaver 1974), while the ratio of C to N also influenced this character (Hunter & Barnett 1975). Long term storage and excessive subculturing resulted in sterility in older cultures, which could only be observed as white mycelium (Hunter & Barnett 1978). Variations were found in thiamine sufficiency, and effects of light on sporulation. Optimum temperatures for growth were found to vary between 25-30°C for all species studied (Hunter & Barnett 1978). Other biochemical studies included aminopeptidase substrate specificities used by Stevens et al (1990) to distinguish *Cylindrocladium* pathogens found in Wisconsin, U.S.A. Recent work was also done to determine the structures of acidic fungal polysaccharides isolated from cell-walls of *Cylindrocladium* species by means of ^{13}C NMR spectroscopy (Ahrazem et al 1997). This study revealed the usefulness of using these markers for chemotaxonomy and emphasised the possiblities of finding new polysaccharidic structures in fungal cell walls.

Molecular characteristics

Protein characterisation

Because of the similarity and variability in several morphological characters used for *Calonectria* and *Cylindrocladium* taxonomy, the use of molecular characters has become increasingly important. Several molecular characters have been applied in attempts to solve problems relating to phylogeny and the identification of species. Total proteins and isozyme analysis have been used extensively to distinguish species in numerous fungal genera (Alfenas 1998). In *Cylindrocladium* taxonomy, total protein and isozyme profiles have been used to aid in the delimitation of species (Crous et al 1993a, b, c, El-Gholl et al 1993, El-Gholl et al 1997), and to investigate variation below species level (Crous et al 1998a). However, environmental conditions can influence protein expression and thus invalidate some results (Michelmore & Hulbert 1987).

DNA characterisation

Restriction fragment length polymorphisms (RFLPs) have been used for several years for fungal population studies and taxonomy for several years (McDonald & McDermott 1993). In *Cylindrocladium* RFLPs from nuclear DNA has been applied, together with morphological observations to support proposals for several new species (Crous et al 1995, Crous et al 1997a, Crous et al 1997b) and has also indicated variation within existing species (Overmeyer et al 1996, Jeng et al 1997). Based on these data, some species were shown to be conspecific (Crous et al 1995). Other DNA based molecular characters were obtained through random amplified polymorpisms (RAPDs) (Overmeyer et al 1996, El-Gholl et al 1997, Victor et al 1997) and AT-DNA profiles (Victor et al 1997).

DNA sequence comparisons are being used increasingly frequently in fungal systematics. In the Hypocreales, numerous phylogenies using DNA sequence comparisons from a wide variety of loci have already been made at several levels (e.g. O'Donnell 1993, Spatafora & Blackwell 1993, Rehner & Samuels 1994, Rehner & Samuels 1995, Glenn et al 1996, O'Donnell et al 1998). In most cases this has led to a better understanding of the underlying morphological phylogeny. The first sequence data for *Calonectria* spp. were obtained by O'Donnell (1993) and subsequently by Rehner and Samuels (1994). In this study (O'Donnell 1993) the DNA sequence of the 5' end of the 28S ribosomal RNA gene from an isolate identified as *Ca. pyrochroa* was included in a comparison of various other hypocrealean species with *Fusarium* anamorphs. The second study (Rehner &

Samuels 1995) compared a wider array of hypocrealean species. Subsequent sequencing data was obtained from the 5.8S ribosomal RNA gene and the two flanking internally transcribed spacers (ITS1 and ITS2) of several isolates by Hamelin (1996) in order to devise primers for detection of *Cy. floridanum* Sobers & C. P. Seym. and *Co. destructans* in nursery seedlings. DNA sequence comparisons between *Cylindrocladium* species were made by Jeng et al (1996) when isolates of *Cy. floridanum* were compared with *Cy. scoparium* using the DNA sequences obtained from the same genomic area. Although the authors did not do a phylogenetic analysis, differences could be ascertained between these two species. Besides larger molecular based studies done on hypocrealean and other species that included 28S rRNA sequences from *Cy. floridanum* and *Cy. scoparium* (O'Donnell 1993, Rehner & Samuels 1995, Ogawa et al 1997), no DNA sequence based phylogeny of *Cylindrocladium* at species and generic level has yet been published.

Calonectria and *Cylindrocladium* as plant pathogens

Since the first description of *Cylindrocladium scoparium* (Morgan 1892) was made from material collected on dead pods of honey locust, it created the impression that this species may be saprophytic. However, the first reports of a plant disease caused by this fungus were by Massey (1917) and subsequently by Anderson (1918). These authors described the fungus as the causal agent of crown cankers on roses. Since then *Cy. scoparium* has been associated with a wide range of disease problems in over 30 plant families throughout the world (Booth & Gibson 1973, French & Menge 1978, Peerally 1991, Waipara et al 1996). This is also true for other species in *Cylindrocladium* (e.g. Bell & Sobers 1966, Cordell & Rowan 1975, French & Menge 1978, Mohanan & Sharma 1985, Chase & Poole 1988, Peerally 1991, Koike et al 1999). Prominent diseases caused by *Cylindrocladium* spp. include Cylindrocladium black rot (CBR), a devastating pod and root necrosis disease of peanuts caused by *Cy. parasitica* Crous et al (Porter et al 1984), Cylindrocladium cutting rot of *Eucalyptus* cased by several *Cylindrocladium* spp. (Ferreira 1989) and Cylindrocladium root and petiole rot of *Spathiphyllum* by *Cy. spathiphylli* (Chase & Poole 1988), to name but a few. Symptoms caused by other *Cylindrocladium* spp. include damping-off, root rot, crown canker, leaf spot, seedling and shoot blight, needle blight, wilt, fruit rot, tuber rot, cutting rot, die-back and stem lesions.

Samuels 1995) compared a wider array of hypocrealean species. Subsequent sequencing data was obtained from the 5.8S ribosomal RNA gene and the two flanking internally transcribed spacers (ITS1 and ITS2) of several isolates by Hamelin (1996) in order to devise primers for detection of *Cy. floridanum* Sobers & C. P. Seym. and *Co. destructans* in nursery seedlings. DNA sequence comparisons between *Cylindrocladium* species were made by Jeng et al (1996) when isolates of *Cy. floridanum* were compared with *Cy. scoparium* using the DNA sequences obtained from the same genomic area. Although the authors did not do a phylogenetic analysis, differences could be ascertained between these two species. Besides larger molecular based studies done on hypocrealean and other species that included 28S rRNA sequences from *Cy. floridanum* and *Cy. scoparium* (O'Donnell 1993, Rehner & Samuels 1995, Ogawa et al 1997), no DNA sequence based phylogeny of *Cylindrocladium* at species and generic level has yet been published.

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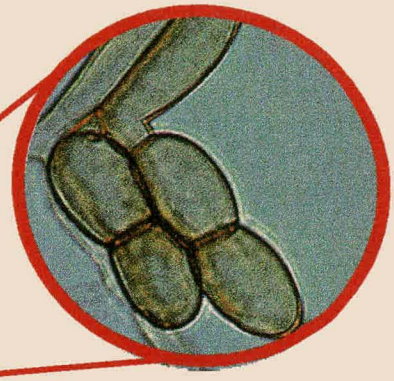
Research on the pathology of *Cylindrocladium* and *Calonectria* species has concentrated mainly on the identification of the pathogens, tests for pathogenicity, the role of microsclerotia in disease aetiology and control through chemical means (Peerally 1991). In addition to this, several comparative studies have shown differences between pathogenicity and *in vitro* fungicide resistance of various species (Sobers & Litrell 1974, Sharma & Mohanan 1991a, Blum et al 1992, Sharma & Mohanan 1992). Less is known of variation below species level. Studies by Rowe and Beute (1975) done on the pathogenicity of various *Cy. parasitica* (as *Cy. crotalariae*) isolates showed no variation for isolates from different geographic origins, although recent observations (B. Shrew, pers. comm.) suggest that such variation may well occur in the U.S.A. Furthermore, results by Sharma (1991b) provided evidence that physiological strains exist in *Cy. quinqueseptatum*.

The infection process of *Cylindrocladium* spp. appears to be similar on a range of hosts. This is summarised in Fig. 1. Usually infection of plants in nurseries and plantations comes from diseased plant material or soil originating from adjacently infected areas, or by transportation (Anderson 1918, Thies & Patton 1970, Crous et al 1991). The primary propagule for nursery infections has been determined to be microsclerotia, consisting of chains or clusters of chlamydospores (Thies & Patton 1970). Additional infection of plants within nurseries and plantations can occur through splash dispersal of conidia (Mohanan & Sharma 1986), or wind-born ascospores. Perithecia can also develop on infected material and act as a source of inoculum (Crous et al 1991). To date no research has been conducted at the population level to establish what role the sexual and asexual propagules play in establishing genetic variation in the disease life cycle of *Calonectria*.

Usually the presence of free water is essential for germination of the infectious propagule to occur (Anderson 1918, Anderson et al 1962). Colonisation of plant leaves and stems has been observed after inoculation with conidia and appressorium formation occurs 4 h after inoculation for *Cy. quinqueseptatum* (Sharma & Mohanan 1990). Chlamydospores and microsclerotia were described developing in several plant tissues (Anderson 1918, Bugbee & Anderson 1963). This infected plant material can release the microsclerotia into the soil when infected plant remains fall on the ground where they can survive without a host for periods of up to 15 years or more (Sobers & Litrell 1974, Crous et al 1991).

Fig. 1. Disease cycle of a *Cylindrocladium* sp. in a nursery

1. Fungus enters nursery in diseased plants or as microsclerotia in soil



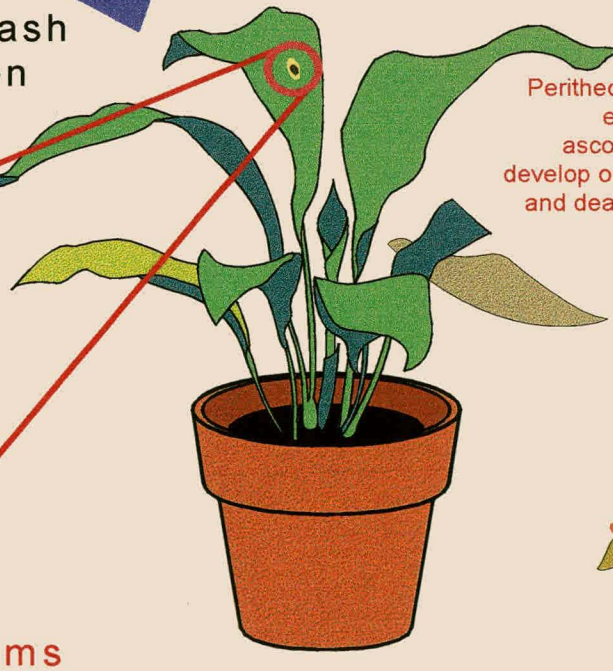
Conidia develop on living and dead plant tissue

2. Microsclerotia re-enter soil from diseased plant remains

Microsclerotia can survive for extensive periods

3. Conidia are splash dispersed between plants, initiating new infections

Leaf spot symptoms



Perithecia with exuding ascospores develop on living and dead plant tissue

4. Ascospores can act as secondary inoculum (or primary inoclum for new infections)

Conclusions

Although the phylogenetic placement of *Calonectria* within the Hypocreales has been studied previously, the interspecies phylogeny of *Calonectria* has only been determined through morphological comparisons and molecular markers such as RFLPs and RAPDs. Sequence determinations have been made, but no DNA based phylogenetic study has yet been carried out on species in this genus. Because *Calonectria* species are common as the causal organisms of economically important plant diseases (mainly as *Cylindrocladium* spp.) world-wide, accurate identification of different species is essential. A phylogenetic assessment of the various species in the genus would therefore aid species identification. It would also facilitate a re-evaluation of the significance of the various morphological characters previously used for species identification. This information would aid studies into the diversification and mating isolation of species in *Calonectria.*

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2. The *Cylindrocladium candelabrum* species complex includes four distinct mating populations*

Abstract

Cylindrocladium candelabrum-like isolates were collected from a wide variety of geographic locations and compared based on their morphology, sexual compatibility and the nucleotide sequences of their rDNA ITS regions. All isolates included in this study mated to produce *Calonectria* teleomorphs with viable progeny. Four distinct mating populations were identified, each representing a genetically isolated, biallelic, heterothallic population. Several representative isolates of each mating population, reflecting geographic diversity, were chosen for sequence comparisons. The internal transcribed spacer (ITS) regions 1 and 2 that flank the 5.8S rDNA gene, as well as the gene itself, were sequenced and compared. All isolates representing the same group yielded similar sequences, but small, consistent differences were found between the groups. Based on these results we recognise *Calonectria scoparia* (anamorph *Cylindrocladium candelabrum*), and describe three new species, namely *Calonectria pauciramosa* (anamorph *Cylindrocladium pauciramosum*), *Calonectria insularis* (anamorph *Cylindrocladium insulare*) and *Calonectria mexicana* (anamorph *Cylindrocladium mexicanum*).

Introduction

Cylindrocladium scoparium Morgan, the type species of *Cylindrocladium* Morgan (*Cy.*) (Morgan 1892), has been associated with a wide range of plant disease problems in over 30 families throughout the world (Booth & Gibson 1973, French & Menge 1978, Peerally 1991, Waipara et al 1996). This species is, however, the most commonly incorrectly identified taxon in the genus. *Cy. scoparium* sensu stricto has been confirmed from only North America, but has possibly also been introduced into Europe (Overmeyer et al 1996).

Cylindrocladium scoparium, still incorrectly treated by many researchers as synonymous with *Cy. floridanum* Sobers & C. P. Seym., has been the subject of

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much controversy. Victor et al (1997) used morphology, sexual compatibility, RAPD markers and A+T-rich total DNA polymorphisms to compare *Cy. scoparium* (teleomorph *Calonectria morganii* Crous et al), *Cy. candelabrum* Viégas (teleomorph *Ca. scoparia* Peerally), *Cy. ovatum* El-Gholl et al (teleomorph *Ca. ovata* D. Victor & Crous) and *Cy. floridanum* (teleomorph *Ca. kyotensis* Terash.). This study showed that these species represent distinct taxa. Furthermore, evidence was presented to show that more than one species possibly exists in the *Cy. floridanum* complex. Additionally, based on DNA fingerprinting with human minisatellite DNA as a probe, Jeng et al (1997) showed the presence of three groups of isolates in collections of *Cy. floridanum* from Canada and the U.S.A.

Among the small-spored species of *Cylindrocladium, Cy. scoparium* has also commonly been confused with taxa such as *Cy. ovatum* and *Cy. candelabrum*. All three of the latter species are heterothallic. In a recent study Crous et al (1998) confirmed the biallelic, heterothallic nature of *Cy. ovatum*. In earlier studies, however, very low mating percentages were obtained for *Cy. candelabrum* and *Cy. scoparium* (Crous et al 1993a, Overmeyer et al 1996), suggesting that further research was required to elucidate their mating systems.

Cylindrocladium candelabrum, which was originally described from leaves of a *Luma* sp. in Brazil, was characterised by Viégas (1946) as having narrowly ellipsoidal vesicles and 1-septate conidia, 40-88 x 5-6 µm. Crous et al (1993a) re-examined the type specimen (IACM 440), and found it to be almost completely devoid of material, but the few conidia that were observed were 46-70 x 3.5-5 µm, and the vesicles were ellipsoidal to narrowly obpyriform. A neotype (PREM 51045) was subsequently designated, and two isolates PPRI 4153 and 4163 identified as the two mating tester strains.

The species concept of *Cy. candelabrum* was complicated by Peerally (1991) who considered it synonymous with *Cy. ellipticum* Alfieri et al. The latter species was later shown to be a synonym of *Cy. scoparium* (Crous et al 1993a). To readily distinguish these species, *Cy. scoparium* was circumscribed as having ellipsoidal to pyriform vesicles (widest above the middle), while those of *Cy. candelabrum* were ellipsoidal to obpyriform (widest below the middle). However, a high degree of plasticity was observed amongst *Cy. candelabrum*-like isolates. This was particularly true in their vesicle shape, conidiophore branching pattern and conidial dimensions. Due to the low mating type frequency of isolates in previous studies, no clear

indication was obtained on the nature and relevance of this variation amongst *Cy. candelabrum* isolates, and the species was accepted as being highly variable.

Molecular tools have become increasingly useful in providing additional evidence that has supported the interpretation of morphological variation. Several techniques including protein profiles (Crous et al 1993a), RAPDs (Victor et al 1997) and RFLPs (Crous et al 1997b), have been applied to the taxonomy of *Cylindrocladium* spp. The nucleotide sequences of the ribosomal DNA (rDNA) region contain intermittent functional and non-functional regions (Furlong et al 1983). The more conserved rDNA genes allow for comparisons between higher taxa. For example, Rehner and Samuels (1995) compared the nucleotide sequences of the 28S rDNA gene from a wide range of hypocrealean taxa, including *Cy. scoparium* and *Cy. floridanum*. More variable areas are provided by intergenic regions such as the internal transcribed spacers (ITS1 and ITS2) that flank the 5.8S rDNA gene. Various researchers have used these sequences to resolve intra- and interspecies phylogenies (Nazar et al 1991, Sreenivasprasad et al 1994, Bryan et al 1995, Jeng et al 1996, Witthuhn et al 1998).

Recently Jeng et al (1997) published ITS1, ITS2 and 5.8S rDNA sequences of *Cy. scoparium* and *Cy. floridanum*. In these comparisons, one six base pair nucleotide deletion and three point mutations were found in the ITS2 region. This indicated the potential of this region to be used as a tool to differentiate between morphologically similar *Cy. candelabrum*-like species. Accordingly, the present study was undertaken to investigate the application of a biological species concept as well as a phylogenetic species concept to isolates provisionally accommodated in the *Cy. candelabrum* species complex. Using these data, it was possible to evaluate the value of morphological characters in *Cylindrocladium*.

Materials and Methods

Isolates

Cylindrocladium candelabrum isolates were either obtained from symptomatic material, or they were baited from soil samples. Soil samples were collected and treated as explained in Crous et al (1997a). Type specimens were lodged at the National Collection of Fungi in Pretoria (PREM), and ex-type cultures maintained in the culture collection of the Department of Plant Pathology, University of Stellenbosch, South Africa (STE-U).

Table I. Isolates selected for sequencing.

Species	STE-U no.	Origin
Cy. pauciramosum	951	Mexico
(Group 1)	971	South Africa
	1160	Colombia
	1691	Australia
Cy. candelabrum	1674	Brazil
(Group 2)	1675	Brazil
	1676	Brazil
	1678	Brazil
Cy. insulare	766	Madagascar
(Group 3)	768	Madagascar
	616	Brazil
	954	Mexico
Cy. mexicanum	927	Mexico
(Group 4)	928	Mexico
	941	Mexico
	966	Mexico

Sexual compatibility

One hundred single conidial *Cy. candelabrum*-like isolates (listed under the results), originating from various geographic locations were mated in all possible combinations. This was achieved by removing 3 mm diam agar plugs from the periphery of actively growing cultures and placing them on CLA plates as described by Crous et al (1993a). Two different isolates were placed in a Petri dish with carnation leaves between them. Following this, plates were packed in stacks of 10, sealed in plastic bags and incubated on the laboratory bench at 22°C. Protoperithecia appeared after 2 wk and successful matings were determined after 2 mo of incubation. Successful matings were regarded as those isolate combinations that produced perithecia with fertile, extruding ascospores.

Mating groups were subsequently distinguished and strains that resulted in prolific matings were selected from each group. For each mating group identified, ascospores were obtained from two matings, involving four separate isolates. Seven single ascospores were sub-cultured for each mating group, and these were crossed in all possible combinations in order to reconfirm the biallelic, heterothallic nature of each mating population. Two isolates of opposing mating type were selected as tester strains from these isolates, and these were subsequently mated with the tester strains of the other groups to reconfirm that no mating was occurring between groups.

Both strands of the ITS1 and ITS2 intergenic spacers as well as the 5.8S ribosomal gene were sequenced and compared. Sequences were deposited at GenBank (AF059280-AF059283). DNA was amplified using the primers ITS1 (5'-dTCCGTAGGTGAACCTGCGG) and ITS4 (5'-dTCCTCCGCTTATTGATATGC) (White et al 1990). The region amplified was the 5.8S ribosomal gene and the two internal transcribed spacers (ITS1 and ITS2) flanking the gene. PCR amplifications were performed on a Hybaid Omnigene Temperature Cycler (Hybaid, Middlesex, U.K.). Reactions comprised of 1 µl Expand High Fidelity DNA polymerase (Boehringer Mannheim, Mannheim, Germany) and 1 µl reaction buffer containing 1.5 mM $MgCl_2$ (Boehringer Mannheim), with $MgCl_2$ added to make up the final buffer concentration to 5.5 mM. Liquid paraffin oil was overlaid to prevent evaporation. Other reagents added to the final volume of 100 µl were 250 µM of each NTP, 0.5 µM of each primer and 25 ng DNA. PCR conditions were a denaturing step at 94°C for 1 min followed by 10 cycles of 56°C for 30 s, 72°C for 2 min and 94°C for 15 s. This was followed by a further 20 cycles at the same settings except for a 20 s time increase at 72°C.

PCR products were purified using Wizard PCR Preps (Promega Corporation, Madison, Wisconsin). Both strands of the PCR product were sequenced using the ABI Prism 377 DNA Sequencer (Perkin-Elmer, Norwalk, Connecticut). A Dye Terminator Cycle Sequencing Ready Reaction Kit containing AmpliTaq DNA Polymerase (Perkin-Elmer) was used for the sequencing reactions. The reactions were carried out with a concentration of 20 to 40 ng of DNA template and 3.2 pmol primer in a total volume of 10 µl. The cycle sequencing reaction was done by PCR under conditions of 96°C for 30 s, 50°C for 15 s, and 60°C for 4 min. This was repeated for 25 cycles. DNA was finally purified using Centri-Sep Spin columns (Princeton Separations, Adelphia, New Jersey) and loaded onto the sequencing gel.

Phylogenetic analysis of the ITS1 and ITS2 DNA sequences was performed by using the PAUP (Phylogenetic Analysis Using Parsimony) 3.1.1 program (Swofford 1993). The branch and bound algorithm, with gaps treated as a fifth character was used. Confidence intervals were determined using a 1000 bootstrap replications. All uninformative characters were ignored. Sequences of *Cy. scoparium* and *Cy. floridanum,* previously published by Jeng et al (1997), were used for comparison. In addition to this, a sequence of *Fusarium subglutinans*, deposited by Waalwijk et al (1996), was obtained (EMBL accession number X94167) and used as outgroup.

Morphological comparisons

Isolates were cultured on 2% malt extract agar (MEA) (Biolab, Midrand, South Africa), plated onto carnation-leaf agar (CLA) (Crous et al 1992), incubated at 25°C under near-ultraviolet light, and examined after 7 d. Only material occurring on carnation leaves was examined. Mounts were prepared in lactophenol, examined under Nomarski and phase contrast, and measurements made at x 1000 magnification. Wherever possible, each measurement represents at least 30 observations, and extremes are given in parentheses. Cardinal temperature requirements for growth and cultural characteristics were determined after 6 d on MEA, using procedures described by Crous and Wingfield (1994), and colony colours coded according to Rayner (1970). Cultures of *Cy. candelabrum* were identified using the keys of Crous and Wingfield (1994).

Results

Sexual compatibility

All matings between the selected isolates resulted in perithecia containing fertile ascospores, except where STE-U 216 was concerned (Fig. 1). Whether this isolate constitutes another mating population, or has lost the ability to mate, remains unresolved. Control inoculations indicated that all isolates used were self sterile. Isolates of the same mating type yielded no perithecia when mated, confirming the biallelic, heterothallic mating system commonly found in ascomycetes (Yoder et al 1986). Four distinct mating populations (Groups 1-4) were observed. No successful matings were observed between the different mating groups, and subsequent crossings between ascospore progeny of prolific mating strains confirmed the distinctiveness of the mating groups (results not shown).

Sequence analysis

No differences were detected between isolates for their 5.8S sequences. The four isolates selected per mating group (Table 1), revealed ITS sequences that were 100 % similar within each group, irrespective of geographic location. For the purpose of comparison a single sequence, representing the four isolates from one species, was subsequently used to compare isolates of the four mating populations. A number of single and double base pair substitutions and deletions were found between all the species in the ITS1 and ITS2 regions (Fig. 2).

Fig1

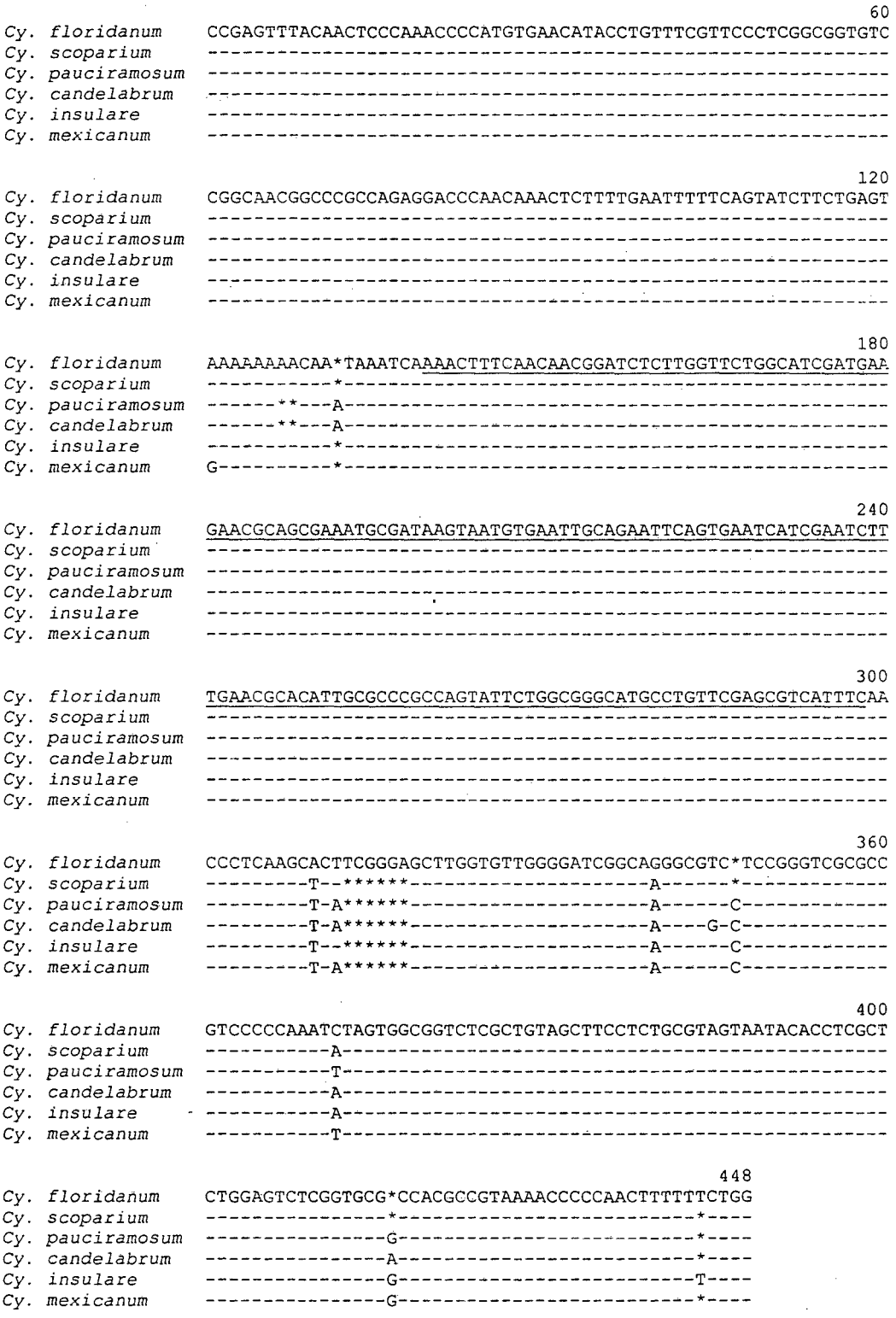


Fig. 2. Nucleotide comparison of the rDNA ITS region of *Cylindrocladium* isolates. *Cylindrocladium scoparium* and *Cy. floridanum* are included for comparison with the consensus sequences of each mating population (biological species) shown as indicated. The sequence of *Cy. floridanum* is shown in full. Asterisks indicate sites of nucleotide deletion. Sequences are shown beginning with the 5' end of ITS1, followed by the 5.8 S gene shown underlined and the 3' end of ITS2.

Previous work done by Jeng et al (1997) showed one six base pair deletion and 3 single base substitutions when the sequences of *Cy. floridanum* and *Cy. scoparium* were compared. None of the other species sequenced contained a six base pair deletion found in the *Cy. floridanum* ITS2 region.

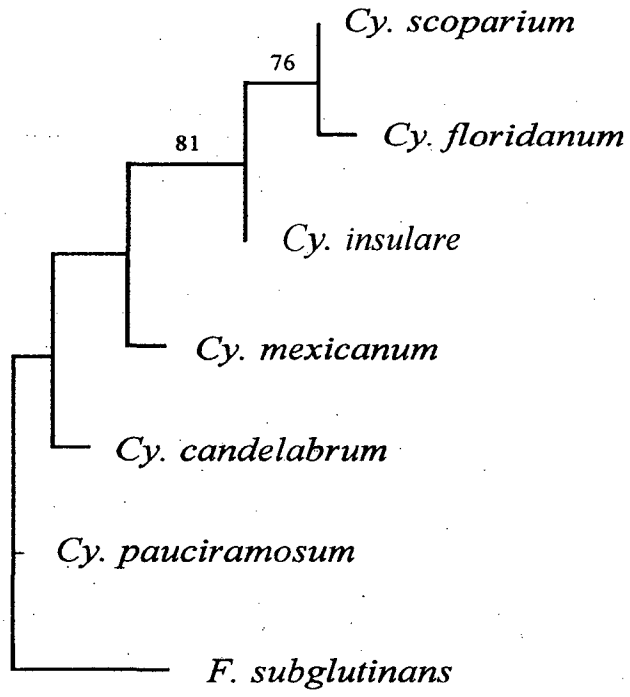


Fig. 3. Phylogeny of the species in the *Cylindrocladium candelabrum* complex. One of four most parsimonious trees generated with a branch and bound algorithm in PAUP 3.1.1. Trees were obtained from aligned sequences of the 5.8S gene and flanking ITS1 and ITS2 regions (15 steps, CI =0.8, RI = 0.786). Bootstrap values above 50 % are shown. A *Fusarium subglutinans* sequence (EMBL accession number X94167) was used as outgroup.

Additional differences were observed in the ITS1 region of the four species in the *Cy. candelabrum* complex. Single base pair substitutions in the ITS2 region at base pairs could distinguish *Cy. floridanum* from the other species' sequences, while a similar single base difference could differentiate the four species in the *Cy. candelabrum* complex from *Cy. scoparium* and *Cy. floridanum*. Further single base deletions and substitutions distinguished all species on the basis of sequence dissimilarity. Accordingly, a phylogenetic tree was produced using PAUP analysis (Swofford 1993). Figure 3 shows one of the four most parsimonious trees obtained by branch and bound analysis of the informative sites of the 5.8S and flanking ITS1 and ITS2 DNA regions for the six species mentioned above. All four most parsimonious trees indicated a closer relationship between the sequences of *Cy. insulare* and those of *Cy. scoparium* and *Cy. floridanum*. The exact relationships between the other species were ambiguous.

Morphological comparisons

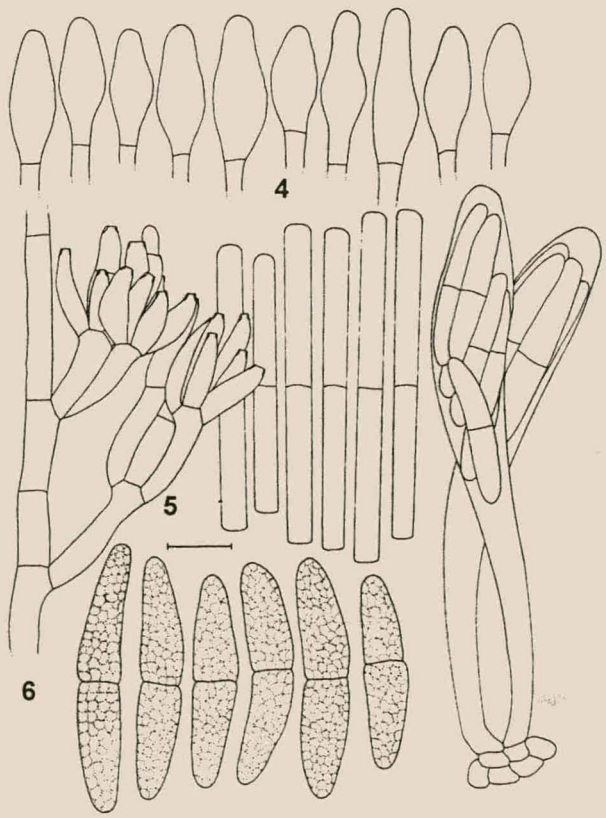
Several morphological characters were studied. This included the shape and diameter of the terminal vesicles extending from the conidiophore stipes, conidial size, conidiophore branching pattern, ascospore shape, size, perithecial colour, anatomy, morphology, and cultural characteristics.

The morphological similarities of the anamorph and teleomorph states corresponded well with the results obtained in the mating studies, and grouped isolates into four distinct groups. The four groups identified based on these features were further supported by their distinct DNA sequences, which led us to conclude that they represent four biological species, which are subsequently described below.

Species descriptions

Calonectria pauciramosa, C.L. Schoch & Crous sp. nov. Figs. 4-11

Anamorph. *Cylindrocladium pauciramosum* C.L. Schoch & Crous sp. nov.

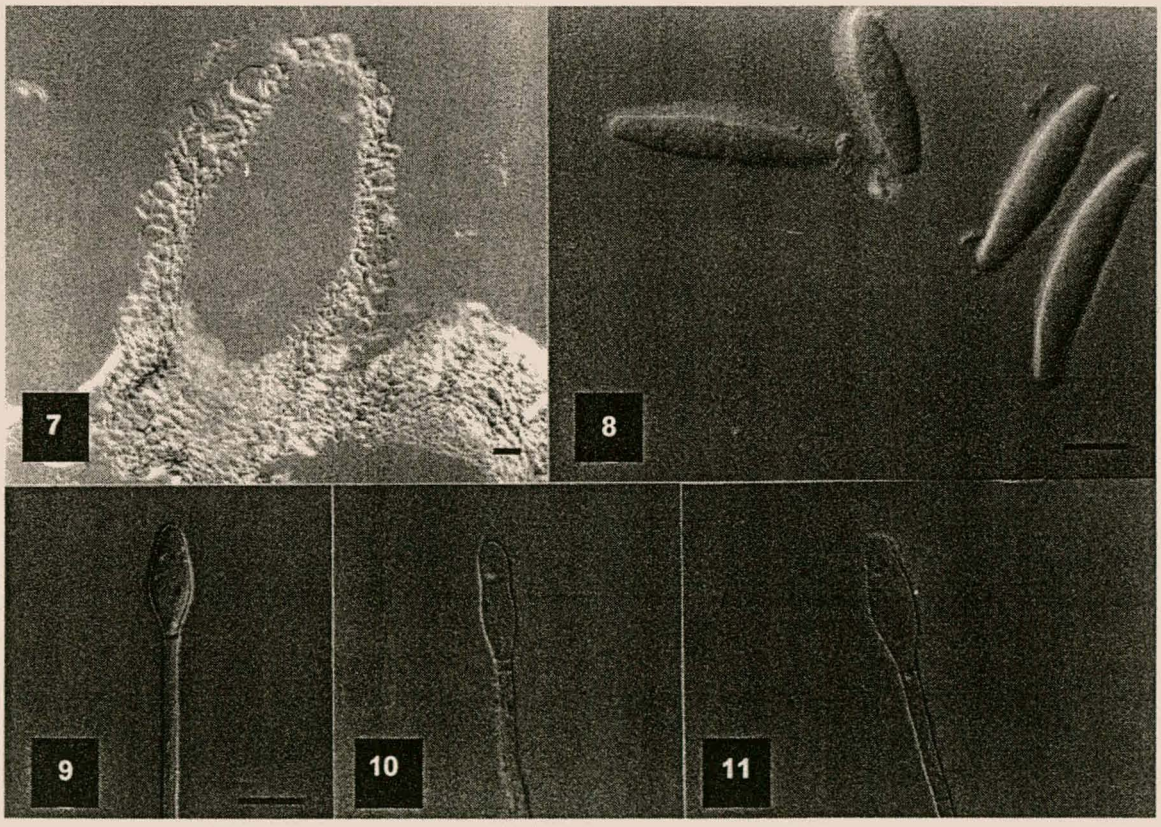


Figs. 4-6. *Calonectria pauciramosa* and its anamorph *Cylindrocladium pauciramosum*. 4. Terminal vesicles on stipe extensions. 5. Conidiophore and conidia. 6. Asci and ascospores. Bar = 10 µm.

Etymology. Refers to the relatively low number of conidiophore branches in the species.

Holotypes. BRAZIL × SOUTH AFRICA. BRAZIL. BAHIA: Nursery, *Eucalyptus* sp., Jul. 1990, *A. C Alfenas*; Knysna, soil, Nov. 1994, *P. W. Crous*, heterothallic mating of STE-U 1670 (PREM 55753 anamorph) × STE-U 971 (PREM 55752 anamorph holotype), Apr. 1997 *C. L. Schoch* (PREM 55754 teleomorph holotype).

Description. Perithecia subglobosa ad ovoidea, 250-400 µm alta, 170-300 µm lata, crocea ad rubro-brunnea, pariete exteriore verrucosa, ostiolo papillato. Asci clavati, in stipitem longum tenuem gradatim angustatae, 70-140 x 8-25 µm, 8-spori. Ascosporae hyalinae, fusiformes, 1-septatae, nihil vel leviter ad septum constrictae, (30-)33-38(-40) x 6-7(-8) µm. Filum septatum, hyalinum (120-)180(-230) µm, in vesiculam obpyriformam ad late ellipsoidam (5-)7-9(-11) µm diam terminans. Conidia cylindrica, hyalina, 1-septata, apicibus obtusis, (30-)45-55(-60) x (3.5-)4-5 µm. Microconidiophora ignota.



Figs. 7-11. *Calonectria pauciramosa* and its anamorph *Cylindrocladium pauciramosum*. 7. Vertical section through a perithecium. 8. Ascospores. 9-11. Terminal vesicles. Bars = 10 µm.

Perithecia orange to red-brown, subglobose to ovoid, 250-400 µm high, 170-300 µm wide, turning dark red in 3% KOH; ostiole papillate. Perithecia rough-walled, wall consisting of two layers: outside layer of *textura globulosa*, 20-50 µm wide; inner

layer of *textura angularis*, 5-10 µm wide, outer cells 40-55 x 15-35 µm; hymenial layer of *textura prismatica*, hyaline, 5-10 µm wide; perithecial base up to 100 µm wide, consisting of dark red, angular cells. *Asci* 8-spored, clavate, 70-140 x 8-25 µm, tapering to a long thin stalk. *Ascospores* aggregated in the upper third of the ascus, hyaline, fusoid with rounded ends, straight to slightly curved, 1-septate, not or slightly constricted at the septum, (30-)33-38(-40) x 6-7(-8) µm. *Macroconidiophores* comprised of a stipe, a sterile elongation and a penicillate arrangement of fertile branches. Stipe septate, (120-)180(-230) µm long, terminating in an obpyriform to broadly ellipsoidal vesicle, (5-)7-9(-11) µm diam; primary branches aseptate or 1-septate, 12-45 x 5-6 µm; secondary branches aseptate, 15-20 x 5 µm, and tertiary branches aseptate, 12-15 x 5 µm, each terminal branch producing 2-6 phialides; phialides doliiform to reniform, hyaline, aseptate, 10-13 x 2.5-4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight, (30-)45-55(-60) x (3.5-)4-5 µm, 1-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Microconidiophores* not observed. *Chlamydospores* dark brown, thickened, formed in extensive numbers throughout the medium, and aggregated to form microsclerotia.

Cultures. Colony colour (underneath) 13i fulvous, (surface) 13i sienna with abundant white aerial mycelia. Colony margin irregular, with extensive chlamydospores and sparse sporulation on aerial mycelia. Colonies obtaining a radius of 17-20 mm diam on MEA after 6 d in dark at 25°C.

Cardinal temperatures for growth. Minimum above 5°C, maximum below 35°C, optimum 25°C. This is both a high and low temperature species, growing below 5°C, and above 30°C.

Substrate. *Acacia cyclops*, *Azalea* sp., *Eucalyptus* spp., *Fragraria* sp., *Protea* sp., *Rhododendron* sp., soil.

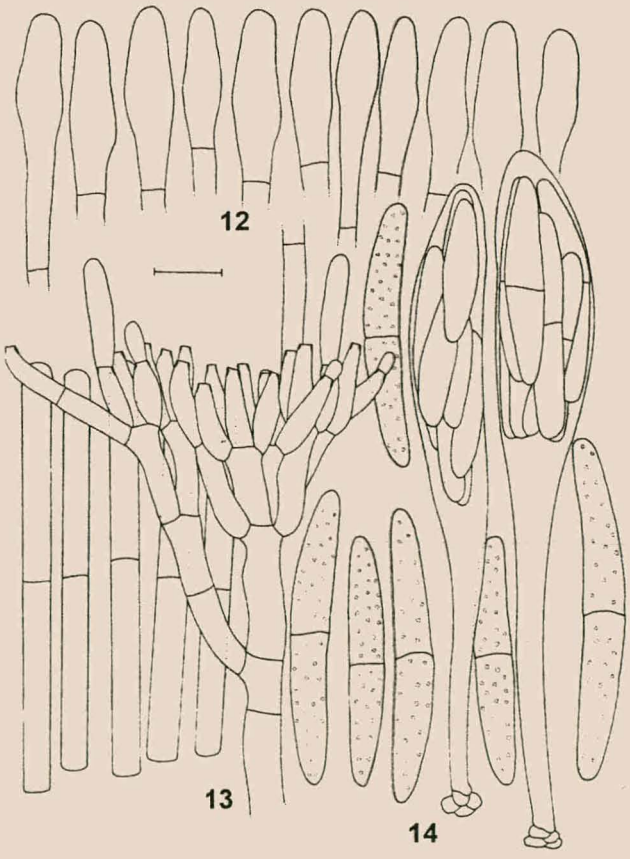
Distribution. Australia, Brazil, Colombia, Mexico, South Africa.

Additional cultures examined. AUSTRALIA. QUEENSLAND: Locality unknown, strawberry, 1991, *D. Hutton* (N167/91 = STE-U 1691; N335/91 = STE-U 1692). BRAZIL. BAHIA: Vivieros, *Eucalyptus* sp., Jul. 1990, *A. C. Alfenas* (UFV 25 = STE-U 1670; UFV 27 = STE-U 1671). SANTA CATARINA: Florianópolis, soil, Apr. 1994, *M. J. Wingfield* (STE-U 911-913, 923-925). COLOMBIA. CÓRDOBA: La Selva, Jun. 1995, *M. J. Wingfield* (STE-U 1160-1163). MEXICO. VERACRUZ: Catemaco,

Laguna Encantada, soil, Apr. 1994 *M. J. Wingfield* (STE-U 951). SOUTH AFRICA. KWAZULU-NATAL: Kwambonambi, *Eucalyptus grandis* seedlings, Feb. 1990, *P. W. Crous* (STE-U 247, 249, 256, 257, 271, 274, 344, 346); *Eucalyptus grandis,* Oct. 1995, *P. W. Crous* (STE-U 1239); Pietermaritzburg, *Eucalyptus nitens*, Mar. 1990, *P. W. Crous* (STE-U 391); WESTERN CAPE: *Acacia cyclops*, Jul. 1990, *M. Morris* (CMM 953 = STE-U 1693); George, *Azalea* bushes, Feb. 1993, *S. Lamprecht* (STE-U 575); Knysna, soil, Nov. 1994, *P. W. Crous* (STE-U 971, 972); MPUMALANGA: Kruisfontein, *Eucalyptus grandis* trunk, Sept. 1989, *P. W. Crous* (STE-U 138, 143); Sabie, soil, Feb. 1990, *P. W. Crous* (STE-U 356, 358); Klipkraal, *Eucalyptus grandis* seedlings, Feb. 1990, *P. W. Crous* (STE-U 286-288); Witrivier, *Azalea* sp., May 1990, *S. Lamprecht* (STE-U 379, 380); NORTHERN PROVINCE: Piet Retief, pine cuttings, Nov. 1994, *P. W. Crous* (STE-U 958, 959); Tzaneen, *Eucalyptus grandis* seedlings, Feb. 1990, *P. W. Crous* (STE-U 282-284), *Eucalyptus grandis* cuttings, Jun. 1990, *S. de Buisson* (STE-U 416, 417).

Calonectria scoparia Peerally, Mycotaxon 40: 341 (1991). Figs. 12-18

Anamorph. *Cylindrocladium candelabrum* Viégas, Bragantia 6: 370 (1946).



Figs. 12-14. *Calonectria scoparia* and its anamorph *Cylindrocladium candelabrum*. 12. Terminal vesicles on stipe extensions. 13. Conidiophore and conidia. 14. Asci and ascospores. Bar = 10 µm.

Holotypes. BRAZIL. BAHIA. Picadao, Conceicao de Barra, *Eucalyptus grandis*, Apr. 1992, *A. C. Alfenas* & *F. A. Ferreira* (PREM 51045 neotype of teleomorph; Crous et al 1993a); Copener, *Eucalyptus* sp., *A. C. Alfenas,* PREM 51044 (neotype of anamorph; Crous et al 1993a), culture ex-type PPRI 4135.

Description. *Perithecia* red-brown, subglobose to ovoid, 350-450 µm high, 300-350 µm wide, turning dark red in 3% KOH, frequently in clusters of 3-4; ostiole papillate. Perithecia rough-walled, wall consisting of two layers: outside layer of *textura globulosa*, 50-100 µm wide; inner layer of *textura angularis*, 5-10 µm wide, outer cells 35-45 x 18-30 µm; hymenial layer of *textura prismatica*, hyaline, 5-10 µm wide; perithecial base up to 150 µm wide, consisting of dark red, angular cells. *Asci* 8-spored, clavate, 70-130 x 7-15 µm, tapering to a long thin stalk. *Ascospores* aggregated in the upper third of the ascus, hyaline, fusoid with rounded ends, straight to slightly curved, 1-septate, not to slightly constricted at the septum, (40-)45-50(-60) x 5-6 µm; becoming 3-septate once discharged. *Macroconidiophores* comprised of a stipe, a sterile ongation and a penicillate arrangement of fertile branches. Stipe septate, (100-)170(-220) µm long, terminating in an ellipsoidal to narrowly obpyriform vesicle, (5-)6-7(-8) µm diam; primary branches aseptate or 1-septate, 20-45 x 4-5 µm; secondary branches aseptate, 15-25 x 4-5 µm, tertiary branches aseptate, 15-20 x 4-5 µm, and quaternary branches aseptate, 10-15 x 4-5 µm, each terminal branch producing 2-6 phialides; phialides doliiform to reniform, hyaline, aseptate, 10-20 x 3-4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight, (45-)58-68(-80) x 4-5(-6) µm, 1-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Microconidiophores* not observed. *Chlamydospores* dark brown, thickened, formed in extensive numbers throughout the medium, and aggregated to form microsclerotia.

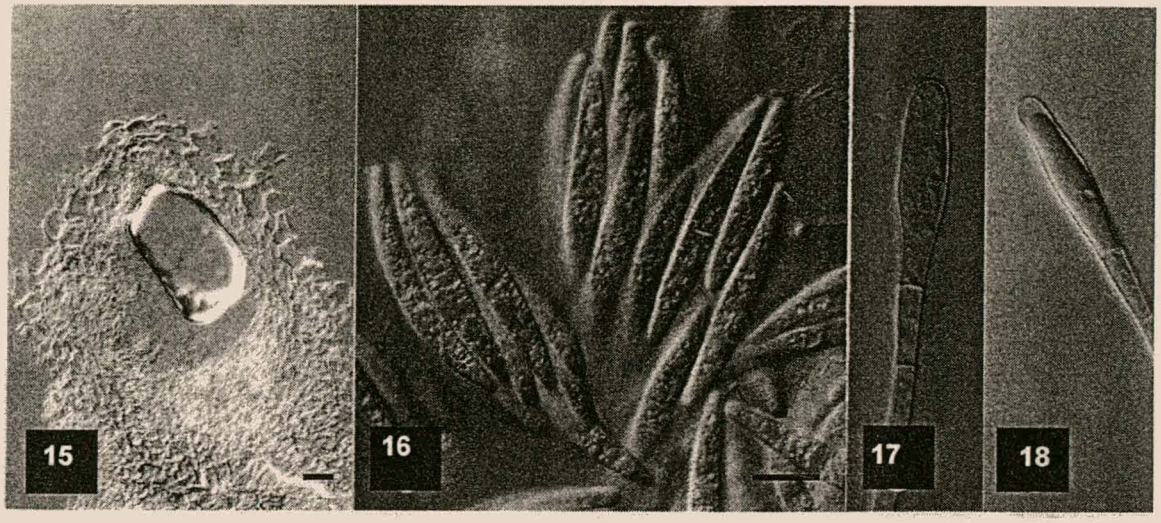
Cultures. Colony colour (underneath) 13i fulvous, (surface) 13i sienna. Colony margin irregular with sparse to moderate aerial mycelia, and extensive chlamydospores. Colonies obtaining a radius of 12-17 mm diam on MEA after 6 d in the dark at 25°C.

Cardinal temperatures for growth. Minimum above 5°C, maximum below 35°C, optimum 25°C. This is both a high and low temperature species, with medium sporulation on aerial mycelium.

Substrate. *Eucalyptus* spp., *Luma* sp., soil.

Distribution. Brazil, Venezuela.

Additional specimens deposited. BRAZIL. BAHIA: Vivieros, soil, heterotallic mating of STE-U 1675 (PREM 55755 anamorph) × STE-U 1677 (PREM 55756 anamorph), Apr. 1997, *C. L. Schoch,* (PREM 55757 teleomorph).



Figs. 15-18. *Calonectria scoparia* and its anamorph *Cylindrocladium candelabrum.* 15. Vertical section through a perithecium. 16. Ascospores. 17, 18. Terminal vesicles. Bars = 10 µm.

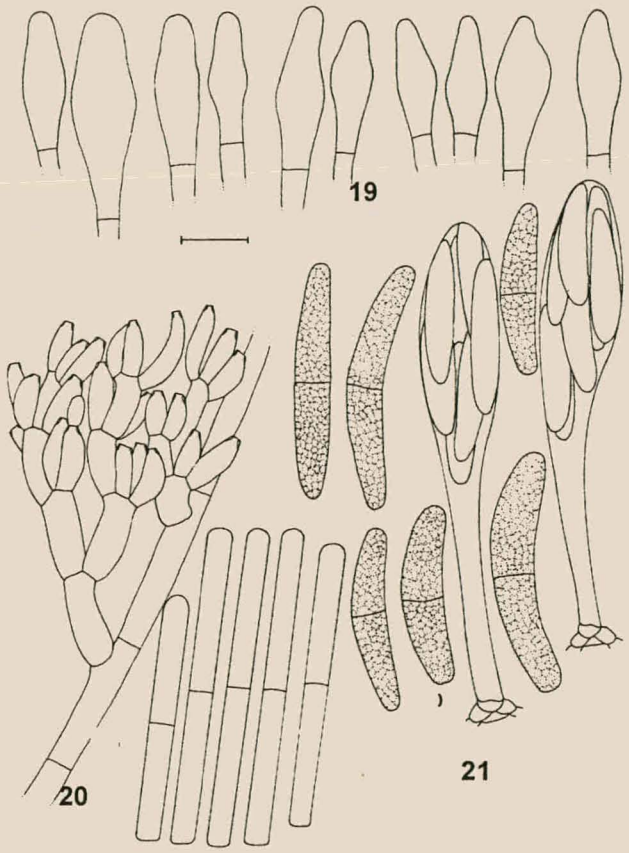
Additional cultures examined. BRAZIL. AMAZONAS: Locality unknown, *Eucalyptus* sp., 1991, *A. C. Alfenas* (UFV 117 = STE-U 1675; UFV 118 = STE-U 1676; UFV 121 = STE-U 1677; UFV 122 = STE-U 1678; UFV 126 = STE-U 1679; UFV 128 = STE-U 1680; UFV 129 = STE-U 1681; UFV 130 = STE-U 1682; UFV 132 = STE-U 1683); *Eucalyptus* sp., 1991, *J. C. Dianese* (D1038 = STE-U 1684); Belém, *Eucalyptus* sp., Feb. 1990, *M. J. Wingfield* (STE-U 313); BAHIA: Copener, *Eucalyptus* sp., Jul. 1990, *A. C. Alfenas* (UFV 63 = STE-U 1674); Vivieros, *Eucalyptus* sp., Jul. 1990, *ACA*: (UFV 29 = STE-U 1672); MINAS GERAIS: Ipatinga, *Eucalyptus* sp., Jul. 1990, *A. C. Alfenas* (UFV 45 = STE-U 1673); Bocaiúva, *Eucalyptus* sp., Jul. 1990, *A. C. Alfenas* (UFV 170 = STE-U 1685); Bom Despacho, *Eucalyptus* sp., Jul. 1990, *A. C. Alfenas* (UFV 172 = STE-U 1686); SÃO PAULO: São Paulo, *Eucalyptus* cuttings, Mar. 1993, *P. W. Crous* (STE-U 586, 594, 597, 600-602, 604, 605). VENEZUELA. Locality unknown, soil, Jun. 1995, *M. J. Wingfield*, (STE-U 1183).

Calonectria insularis, C.L. Schoch & Crous sp. nov. Figs. 19- 25

Anamorph. Cylindrocladium insulare, sp. nov.

Etymology. In reference to its geographic distribution.

Holotypes. MADAGASCAR: Tamatave, soil, Apr. 1997, *P. W. Crous*, heterothallic mating of STE-U 766 (PREM 55758 anamorph holotype) × STE-U 768 (PREM 55759 anamorph), Apr. 1997, *C. L. Schoch,* (PREM 55760 teleomorph holotype).



Figs. 19-21. *Calonectria insularis* and its anamorph *Cylindrocladium insulare.* 19. Terminal vesicles on stipe extensions. 20. Conidiophore and conidia. 21. Asci and ascospores. Bar = 10 µm.

Discriptions. Perithecia subglobosa ad ovoidea, 350-450 µm alta, 300-350 µm lata, crocea ad rubra, pariete exteriore verrucosa, ostiolo papillato. Asci clavati, in stipitem longum tenuem gradatim angustatae, 70-120 x 7-18 µm, 8-spori. Ascosporae hyalinae, fusiformes, 1-septatae, ad septum nihil constrictae, (27-)30-36(-42) x 5-6(-7) µm. Ascosporae evolentes usque ad constrictae dismissae ab asco. Filum septatum, hyalinum (110-)160(-250) µm, in vesiculam obpyriformam ad late ellipsoidam (4-)7-10(-13) µm diam terminans. Conidia cylindrica, hyalina, 1-septata, apicibus obtusis, (33-)40-50(-60) x 3.5-4 µm. Microconidiophora ignota.

Perithecia orange to red, subglobose to ovoid, 350-450 µm high, 300-350 µm wide, turning dark red in 3% KOH; ostiole papillate. Perithecia rough-walled, wall consisting of two layers: outside layer of *textura globulosa*, 40-80 µm wide; inner layer of *textura angularis*, 5-10 µm wide, outer cells 25-45 x 20-35 µm; hymenial layer of *textura prismatica*, hyaline, 5-10 µm wide; perithecial base up to 100 µm wide, consisting of dark red, angular cells. *Asci* 8-spored, clavate, 70-120 x 7-18 µm, tapering to a long thin stalk. *Ascospores* aggregated in the upper third of the ascus, hyaline, fusoid with rounded ends, straight to slightly curved, 1-septate, not constricted at the septum, becoming constricted once discharged, (27-)30-36(-42) x 5-6(-7) µm. *Macroconidiophores* comprised of a stipe, a sterile elongation and a penicillate arrangement of fertile branches. Stipe septate, (110-)160(-250) µm long, terminating in an obpyriform to broadly ellipsoidal vesicle, (4-)7-10(-13) µm diam; primary branches aseptate or 1-septate, 10-45 x 4-5 µm; secondary branches aseptate, 10-25 x 4-5 µm, tertiary branches aseptate, 10-17 x 4-5 µm, and quaternary branches aseptate, 10-12 x 4-5 µm, each terminal branch producing 2-6 phialides; phialides doliiform to reniform, hyaline, aseptate, 9-14 x 3-5 µm, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight, (33-)40-50(-60) x 3.5-4 µm, 1-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Microconidiophores* not observed. Dark brown, thickened *chlamydospores* formed in extensive numbers throughout the medium, and aggregated to form microsclerotia.

Cultures. Same characteristics as *Cy. pauciramosum* with colonies obtaining a radius of 18-23 mm diam on MEA after 6 d in the dark at 25°C.

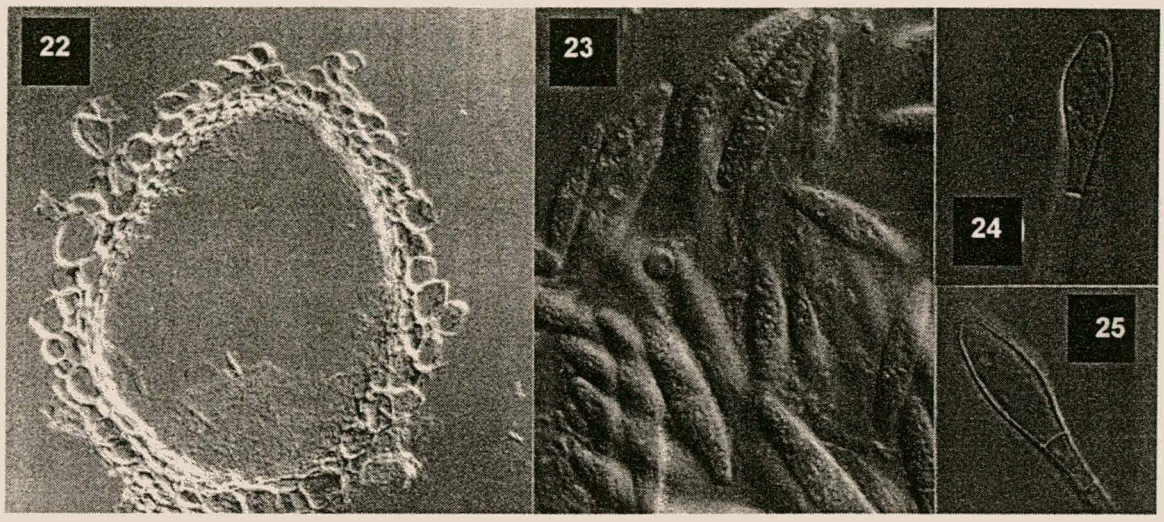
Cardinal temperatures for growth. Minimum above 15°C, maximum above 35°C, optimum 25-30°C. This is a high temperature species.

Substrate. *Acacia sp., Auracaria heterophylla, Medicago sativa, Persea americana,* Pisum sativum, *Eucalyptus* sp., soil.

Distribution. Brazil, Hawaii, Indonesia, Madagascar, Malaysia, Mauritius, Mexico.

Additional cultures examined. BRAZIL. AMAZONAS: Belém, soil, Apr. 1993, *M. J. Wingfield* (STE-U 616, 620, 625, 626). INDONESIA. SUMATRA: Sei Kobaro, *Acacia mangium* rhizosphere, Jan. 1994, *A. C. Alfenas* (STE-U 722). MADAGASCAR. Tamatave, soil, Apr. 1994, *P. W. Crous* (STE-U 766, 768). MALAYSIA. MALAY

PENINSULA: Kemasik, *Acacia* sp., Dec. 1995, *M. J. Wingfield* (STE-U 1281, 1282). MAURITIUS. Rivière Noire, soil, Apr. 1996, H. Smith (STE-U 1473, 1474). Pampalmousses, soil, Apr. 1996, H. Smith (STE-U 1475). MEXICO. VERACRUZ: Conejos, Puente Nacional, soil, Apr. 1994, *M. J. Wingfield* (STE-U 952, 954). U.S.A. HAWAII: Locality unknown, *Medicago sativa,* 1981, *M. Aragaki* (A 890 = STE-U 1687); *Auracaria heterophylla,* 1987, *M. Aragaki* (A 1570 = STE-U 1688); *Pisum sativum,* 1988, *M. Aragaki* (A 1823 = STE-U 1689); *Persea americana*, 1988, *M. Aragaki* (A 1853 = STE-U 1690).



Figs. 22-25. *Calonectria insularis* and its anamorph *Cylindrocladium insulare.* 22. Vertical section through a perithecium. 23. Ascospores. 24, 25

Calonectria mexicana, C.L. Schoch & Crous sp. nov. Figs. 26-35

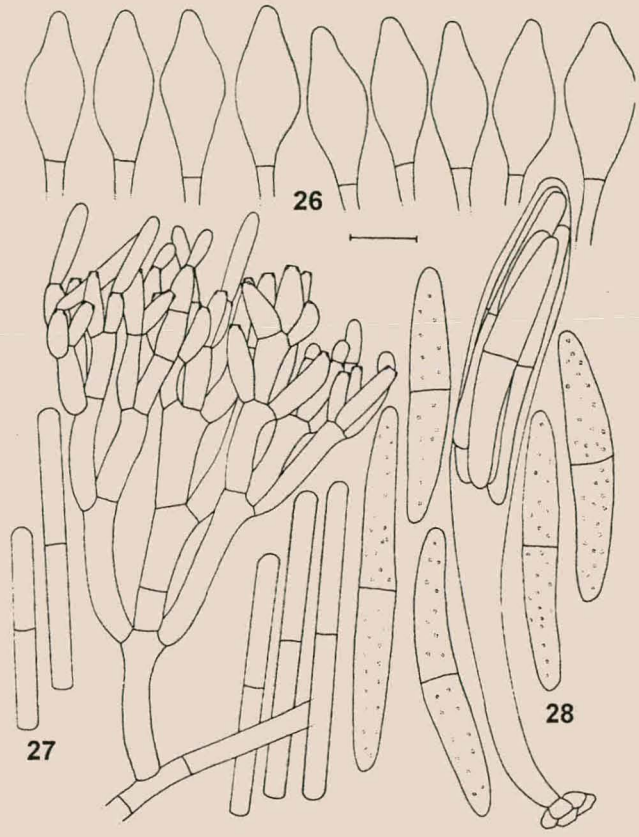
Anamorph. Cylindrocladium mexicanum, sp. nov.

Etymology. In reference to its country of origin.

Holotypes. MEXICO. YUCATAN: Uxmal, soil., Apr. 1994 *M. J. Wingfield*; HOLPECHÉN: Campeche, soil., Apr. 1994, *M. J. Wingfield*, heterothallic mating of STE-U 927 (PREM 55761 anamorph holotype) × STE-U 941 (PREM 55762 anamorph), Apr. 1997, *C. L. Schoch* (PREM 55763 teleomorph holotype).

Decriptions. Perithecia subglobosa ad ovoidea, 400-450 µm alta, 350-450 µm lata, crocea ad rubra, pariete exteriore verrucosa, ostiolo papillato. Asci clavati, in stipitem longum tenuem gradatim angustatae, 70-120 x 10-20 µm, 8-spori. Ascosporae hyalinae, fusiformes, 1-septatae, nihil vel leviter constrictae ad septum,

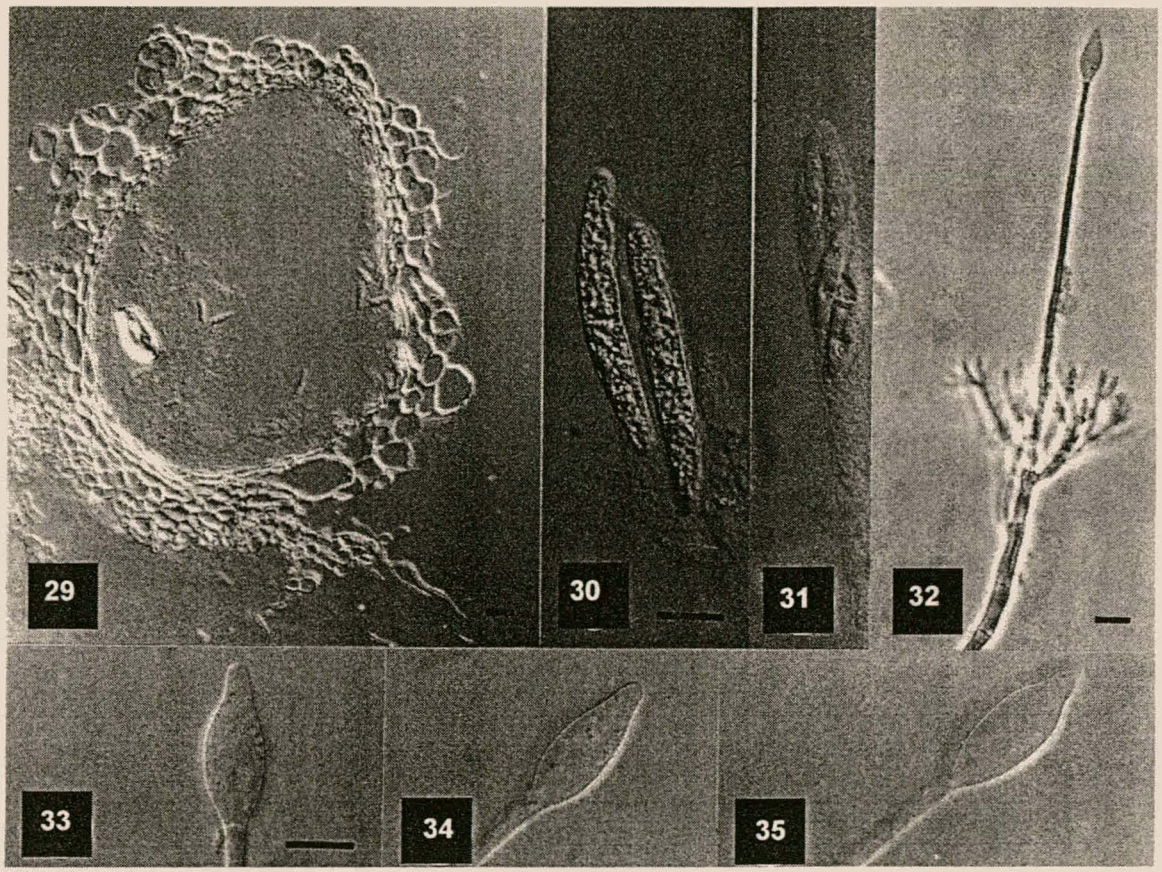
(35-)40-55(-65) x 5-6(-7) µm. Ascoporae evolentes usque ad tres septa dismissae ab asco. Filum septatum, hyalinum (160-)180(-250) µm, in vesiculam late ellipsoidam apicibus papillatis (7-)8-10(-12) µm diam terminans. *Conidia* cylindrica, hyalina, 1-septata, apicibus obtusis, (35-)40-48(-52) x 3-4(-4.5)µm. Microconidiophora ignota.



Figs. 26-28. *Calonectria mexicana* and its anamorph *Cylindrocladium mexicanum*. 26. Terminal vesicles on stipe extensions. 27. Conidiophore and conidia. 28. Asci and ascospores. Bar = 10 µm.

Perithecia orange to red, subglobose to ovoid, 400-450 µm high, 350-450 µm wide, turning dark red in 3% KOH; ostiole papillate. Perithecia rough-walled, wall consisting of two layers: outside layer of *textura globulosa*, 35-90 µm wide; inner layer of *textura angularis*, 5-15 µm wide, outer cells 20-35 x 20-30 µm; hymenial layer of *textura prismatica*, hyaline, 5-10 µm wide; perithecial base up to 100 µm wide, consisting of dark red, angular cells. *Asci* 8-spored, clavate, 70-120 x 10-20 µm, tapering to a long thin stalk. *Ascospores* aggregated in the upper third of the ascus, hyaline, fusoid with rounded ends, straight to slightly curved, 1-septate, not or slightly constricted at the septum, (35-)40-55(-65) x 5-6(-7) µm; becoming 3-septate once discharged. *Macroconidiophores* comprised of a stipe, a sterile elongation and a penicillate arrangement of fertile branches. Stipe septate, (160-)180(-250) µm long, terminating in a broadly ellipsoidal vesicle with a papillate apex, (7-)8-10(-12) µm diam; primary branches aseptate or 1-septate, 17-45 x 4-6 µm; secondary

branches aseptate, 15-25 x 4-5 µm, tertiary branches aseptate, 11-17 x 3-5 µm, and quaternary branches aseptate, 10-15 x 2.5-4 µm, each terminal branch producing 2-6 phialides; phialides doliiform to reniform, hyaline, aseptate, 7-16 x 3-4 µm, apex with minute periclinal thickening and inconspicuous collarette. *Conidia* cylindrical, rounded at both ends, straight, (35-)40-48(-52) x 3-4(-4.5) µm, 1-septate, lacking a visible abscission scar, held in cylindrical clusters by colourless slime. *Microconidiophores* not observed. *Chlamydospores* dark brown, thickened, formed in extensive numbers throughout the medium, and aggregated to form microsclerotia.



Figs. 29-35. *Calonectria mexicana* and its anamorph *Cylindrocladium mexicanum*. 29. Vertical section through a perithecium. 30. Ascospores. 31. Asci. 32. Conidiophore with extending stipe and terminal vesicle. 33-35. Terminal vesicles. Bars = 10 µm.

Cultures. Colony colour (underneath) 13b – 13i (orange to sienna), (surface) similar as underneath with moderate white aerial mycelia. Colony margin irregular with extensive chlamydospores and sparse sporulation on aerial mycelium. Colonies obtaining a radius of 17-20 mm diam on MEA after 6 d in the dark at 25°C.

Cardinal temperatures for growth. Minimum above 10°C, maximum above 35°C, optimum 25-30°C. This is both a high and low temperature species.

Substrate. soil.

Distribution. Mexico.

Additional cultures examined. MEXICO. CAMPECHE: Holpechén, soil, Apr. 1994, *M. J. Wingfield* (STE-U 941-943, 966, 967); YUCATAN: Uxmal, soil, Apr. 1994, *M. J. Wingfield* (STE-U 926-928, 944-946).

Discussion

This study was initiated in order to investigate the morphological variability observed within the *Cy. candelabrum* species complex. Mating studies revealed the existence of four distinct mating populations in this complex. These findings were further supported by differences in morphology, and sequence data. In accordance with the biological species concept, different species were therefore proposed for each mating population.

Previous mating studies between isolates of *Cy. scoparium* and *Cy. candelabrum* showed these species to be genetically isolated (Crous et al 1993a). Within the *Cy. candelabrum*-complex, however, prominent differences were observed when perithecia of South African x South African, or South African x Brazilian matings were compared with some Brazilian x Brazilian matings. In light of the distribution data of some of these species (*Cy. pauciramosum* and *Cy. candelabrum*) as circumscribed in the present study, it is obvious that the variation observed by Crous et al (1993a) can now be ascribed to different biological species. In light of the results presented here, previous mating groups observed in *Cy. candelabrum* (as *Cy. scoparium*; Ribeiro 1978), suggest that yet other, undescribed biological species could exist in this complex. Recent molecular work done in another homothallic species complex, *Cy. floridanum* (Victor et al 1997), suggests that this aggregation of distinct biological taxa in species complexes is much more common in *Cylindrocladium* than expected earlier.

The high proportion of successful matings obtained in the present study, and recently by Crous et al (1998) in *Cy. ovatum*, can possibly be ascribed to the fact that these matings were conducted at 22°C, compared to previous studies that used 15 and 25°C as optimum temperature. Within each species, however, isolates showed

varying degrees of success in mating with opposing mating types. For example, in *Cy. pauciramosum* STE-U 138 mated only with two other opposing mating type strains, while in *Cy. candelabrum* STE-U 1678 mated successfully in all instances. Age of isolates as well as differences in their female fertility could account for this variation. It appears that *Cy. pauciramosum* and *Cy. insulare* are largely allopatric in character, with isolates available from various localities.

Sequence data can quantify relatedness among taxa, and is commonly used to clarify different taxonomic questions (Viljoen et al 1993, Rehner & Samuels 1995). The sequences of the ITS1 and ITS2 flanking regions of the 5.8S ribosomal gene indicated small, but consistent differences between the species proposed in this study. Although a high degree of sequence variation in this region has been reported before (Chambers et al 1986), a low amount of variation was observed between the *Cylindrocladium* species examined in the present study. Within a biological species no variation could be observed at all. Even in the case of *Cy. insulare*, identical sequences were observed for isolates from disparate geographic areas like Madagascar, Mexico and Brazil. When compared to a similar situation in *Gibberella fujikuroi,* where several mating populations exist between isolates with similar morphological features (Leslie 1995), the high relatedness in the *Cy. candelabrum* complex becomes more evident. However, sequences of the 5.8S gene and ITS1 and ITS2 flanking regions proved problematic in differentiating the different mating populations in the *Gibberella fujikuroi* complex (Waalwijk et al 1996). Although the species in this study could be differentiated using sequence results, further consideration will have to be given to other, more variable DNA regions. Studies conducted in the hypocrealean genus *Fusarium* (O'Donnell 1996), could prove useful in this regard.

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3. Recombination in *Cylindrocladium scoparium* and phylogeny with other heterothallic small-spored *Cylindrocladium* species*

Abstract

The *Cylindrocladium scoparium* cultures studied were isolated from several hosts in the U.S.A. Isolates were mated in all combinations, and one successful mating was selected to establish whether recombination occurred. RAPD and mating type data of parental isolates and progeny confirmed *Cy. scoparium* to have a biallelic heterothallic mating system. Furthermore, to determine the phylogeny of *Cy. scoparium* with several morphologically similar *Cylindrocladium* spp., DNA sequences of the ribosomal 5.8S gene and the flanking internal transcribed spacers (ITS), as well as part of the high mobility group (HMG) box (forming part of the *MAT-2* mating type gene) and the β-tubulin gene, were analysed. Maximum parsimony yielded concordant trees for all three data sets. These data supported the morphological and biological species concepts proposed for *Cy. scoparium* and other, similar, small-spored *Cylindrocladium* spp.

Introduction

Cylindrocladium scoparium Morgan is the type species of the anamorph genus *Cylindrocladium* Morgan (Morgan 1892). Members of this genus have *Calonectria* De Not. teleomorphs, are ubiquitous plant pathogens and have been isolated mainly in tropical and subtropical regions of the world. *Cylindrocladium scoparium* (teleomorph *Calonectria morganii* Crous et al) has reportedly been associated with a wide range of disease symptoms, including damping off, root rot, cutting rot, stem cankers, leaf-spot and seedling blight (Cordell & Rowan 1975). Although this species has been reported from over 30 plant families (Booth & Gibson 1973, French & Menge 1978, Peerally 1991, Waipara et al 1996), recent data (Part 2) suggest that many of these records were incorrectly ascribed to *Cy. scoparium*.

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* Submitted: Schoch CL, Crous PW, Cronwright G, Witthuhn RC, El-Gholl NE, Wingfield B. 1999. Recombination in *Cylindrocladium scoparium* and phylogeny with other heterothallic small-spored *Cylindrocladium* species. Mycologia.

The main taxonomic criteria used for the identification of *Cylindrocladium* species are conidial and ascospore size and septation, vesicle shape and diameter, and perithecial morphology. Although the reliability of the terminal vesicle as criterion for species identification has been questioned by some workers (Hunter & Barnett 1978, Rossman 1983), Crous et al (1992) showed that this is useful when studied under controlled conditions on carnation-leaf agar (CLA) (Fisher et al 1982).

However, uncertainty still exists regarding the identification of *Cy. scoparium*, and it has frequently been confused with other species with 1-septate, small conidia. These include *Cy. ovatum* El-Gholl et al (ovoid vesicles), *Cy. floridanum* Sobers & C.P. Seym. (sphaeropedunculate vesicles) and *Cy. candelabrum* Viégas (obpyriform vesicles). Victor et al (1997) compared isolates of these taxa and showed that they represent different species. The latter study also confirmed the existence of genetically distinct groups among isolates of *Cy. floridanum*, which was initially reported by Jeng et al (1997). A similar situation has also been found to exist in other species complexes such as *Cy. gracile* (Crous et al 1995, 1997a, b) and *Cy. candelabrum* (Part 2).

Cylindrocladium scoparium has been reported from various areas worldwide, including Africa (Doidge 1950, Darvas et al 1978, Botha & Crous 1992), South America (Palmucci et al 1996, Tozetto & Ribeiro 1996), Europe (Overmeyer et al 1996, Polizzi & Azzaro 1996), Asia (Mohanan & Sharma 1985, Srinivasan & Gunasekaran 1995) and New Zealand (Waipara et al 1996). However, the presence of *Cy. scoparium* has only been confirmed from North America and Brazil (Crous et al 1993a), and many of the isolates discussed in the previously mentioned reports have proven to be the newly described *Cy. pauciramosum* C.L. Schoch & Crous, which forms part of the *C. candelabrum* species complex (Part 2).

The low mating frequency reported in previous studies of *Cy. scoparium* (Crous et al 1993a) and related species (Victor et al 1997) have complicated studies in these fungi by limiting the use of mating testers for species identification. Overmeyer et al (1996) reported only a single mating between mating type tester strains obtained from the American Type Culture Collection (ATCC). Furthermore, no successful matings were obtained with any of the additional thirty-two strains isolated from various hosts in Germany. High success rates were, however, recently obtained for matings done with *Cy. ovatum* (Crous et al 1998) and species in the *Cy.*

candelabrum species complex (Part 2). These results confirmed that these species have biallelic, heterothallic mating systems.

A similar mating system was originally described for *Cy. scoparium* (Crous et al 1993a). Results obtained by Overmeyer et al (1996) indicated a different scenario, because only one parent was reported to contribute to the genetic makeup of progeny. However, as so few matings with *Cy. scoparium* have proven successful in the past (Crous et al 1993a, Overmeyer et al 1996, Victor et al 1997), it was decided to also employ molecular techniques to provide more information on whether recombination occurred or not.

Random amplified polymorphic DNA (RAPD) is a technique that has been applied to answer various genetically oriented questions. Previous studies have applied RAPD data in order to show recombination among agricultural crops (Echt et al 1992) and fungal pathogens (Nicholson et al 1995, Campbell et al 1999) This technique was therefore chosen to verify whether recombination occurred during matings of *Cy. scoparium*.

The phylogenetic relatedness of various *Cylindrocladium* species as suggested by morphological features is still largely uncertain. Several molecular characters have previously been used to analyse relationships among *Cylindrocladium* spp. These include protein profiles (Crous et al 1993b), RAPDs (Victor et al 1997) and Restriction fragment length polymorphisms (RFLP) (Crous et al 1997b). Previous results by Jeng et al (1997) showed that isolates of *Cy. scoparium* and *Cy. floridanum* could be distinguished by DNA sequence analysis of the 5.8S ribosomal RNA gene and flanking internally transcribed spacers (ITS). More recently data obtained from mating studies were combined with the analysis of ITS sequences in the *Cy. candelabrum* species complex (Part 2), emphasising the low number of informative characters available in the DNA sequence data of the ITS region.

In a study aimed at differentiating species in the *Gibberella fujikuroi* species complex, O'Donnell et al (1998) employed sequence data of the nuclear 28S rDNA, mitochondrial small subunit (SSU) and β-tubulin gene. From these data it was shown that the β-tubulin gene yielded the most variation of all areas sequenced, making it useful for determining phylogeny in newly diverged groups. Degenerate primers based on conserved regions in the HMG (high mobility group) box in the *mt a-1*

mating type gene of *Neurospora crassa* Shear & B.O. Dodge have successfully been employed to amplify partial *MAT-2* (*mt a-1*) sequences from other species in the pyrenomycetes (Arie et al 1997, Turgeon 1998, Witthuhn et al 1999).

Based on the clear advantages of these techniques to separate closely related species, the aim of the present study was to use these sequences to infer the phylogeny of *Cy. scoparium* and other small-spored, heterothallic *Cylindrocladium* species.

Materials and Methods

Isolates

Cylindrocladium scoparium isolates studied were either isolated from from symptomatic material, or obtained from the American Type Culture Collection (ATCC 46300 and ATCC 38227) (Table I). All isolates were identified using the methods reported by Crous et al (1997b) and those in Part 2.

Table I. Isolates used in this study.

Species	Culture no.	Collector	Host	Origin
Cy. scoparium	STE-U 496	A.C. Alfenas	Unknown	U.S.A.
	STE-U 497	A.C. Alfenas	Unknown	U.S.A.
	STE-U 654	A.C. Alfenas	Unknown	U.S.A.
	STE-U 655	A.C. Alfenas	Unknown	U.S.A.
	STE-U 1720	N.E. El-Gholl	*Rosa* sp.	Florida, U.S.A.
	STE-U 1721	N.E. El-Gholl	*Conocarpus erectus*	Florida, U.S.A.
	STE-U 1722	N.E. El-Gholl	*Dodonea viscosa*	Florida, U.S.A.
	STE-U 1723	N.E. El-Gholl	*Nandina domestica*	Florida, U.S.A.
	ATCC 38227	S.A. Alfieri	*Mahonia bealei*	Florida, U.S.A.
	ATCC 46300	D.M. Benson	*Leucothoe catesbaei*	N. Carolina, U.S.A.
Cy. pauciramosum	STE-U 416	S. de Buisson	*Eucalyptus grandis*	N. Province, South Africa.
	STE-U 925	M.J. Wingfield	Soil	Santa Catarina, Brazil
	STE-U 972	P.W. Crous	*Eucalyptus grandis*	Western Cape, South Africa
Cy. candelabrum	STE-U 1677	A.C. Alfenas	*Eucalyptus* sp.	Amazonas, Brazil
	STE-U 1674	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil
	STE-U 1951	A.C. Alfenas	Soil	Brazil
Cy. insulare	STE-U 616	M.J. Wingfield	Soil	Amazonas, Brazil
	STE-U 768	P.W. Crous	Soil	Tamatave, Madagascar
	STE-U 954	M.J. Wingfield	Soil	Veracruz, Mexico
Cy. mexicanum	STE-U 927	M.J. Wingfield	Soil	Yucatan, Mexico
	STE-U 941	M.J. Wingfield	Soil	Campeche, Mexico
Cy. ovatum	UFV 90	A.C. Alfenas	Soil	Brazil
	STE-U 2232	P.W. Crous	*Eucalyptus* sp.	Brazil
Cy. multiseptatum	STE-U 1589	M.J. Wingfield	*Eucalyptus* sp.	Indonesia
	STE-U 1602	M.J. Wingfield	*Eucalyptus* sp.	Indonesia

Sexual compatibility

Isolates were mated in all possible combinations. This was achieved by removing 3 mm diam agar plugs from the periphery of actively growing cultures and placing them on carnation leaf agar plates as described by Crous et al (1997a). Two different isolates were placed in a Petri dish with carnation leaves between them. Plates were subsequently incubated for 2 mo at 22°C as explained in Part 2. Successful matings were regarded as those isolate combinations that produced perithecia with fertile, extruding ascospores. Perithecia were harvested and ascospores cultured on 2% malt extract agar (MEA) (Biolab, Midrand, South Africa).

Isolation of DNA

Single conidial and ascospore isolates were grown on MEA plates and plugs transferred into 500 ml Erlenmeyer flasks containing 100 ml liquid MEA broth. Flasks were shaken at 25°C and 125 rpm for approximately 7 d. Mycelium was collected by filtration (Whatman no. 1 filter paper) and DNA was extracted as described by Crous et al (1993b).

RAPD analysis

PCR reactions (25 µl total volume) comprised of 1.5 units Biotaq (Bioline, London, U.K.) with the buffer as recommended by the manufacturer, 1 mM deoxynucleoside triphosphates, 4 mM $MgCl_2$, 0.5 µM primer oligonucleotide and approximately 10 to 30 ng of fungal genomic DNA. Reactions were performed on a Rapidcycler (Idaho Technology, Idaho, U.S.A.). RAPD reaction conditions consisted of the following: an initial denaturation for 30 s at 96°C, followed by 40 cycles of 30 s at 96°C, 30 s at 38°C and 30 s at 72°C. A final elongation step of 2 min at 72°C was included.

Amplified DNA fragments were separated on 1.6% (w/v) CE agarose gels (Boehringer Mannheim, South Africa), with ethidium bromide (1µg/ml) using 0.5 X TBE buffer and run at a constant voltage of 60 V. Fragments were visualised and photographed under ultraviolet light. Thirteen decameric oligonucleotides (OPE 02, 03, 04, 07, 09, 10, 11, 13, 15, 16, 17, OPM 06, OPY 20, Operon Technologies Inc., U.S.A.) were screened. One primer, OPE 17 (CTA CTG CCG T) was selected for further analysis after yielding polymorphic bands separating both parental isolates.

DNA fingerprints were evaluated by visual inspection of the photographs of the gels. Bands that were observed as intense bands were used for analysis. The data were scored on the presence or absence of fragments within each individual sample. Possible recombination observed in the parental isolates could be seen in progeny as determined by the co-segregation of bands that were polymorphic in the parents.

PCR amplifications

HMG box

The strategy of Arie et al (1997) was followed, using two degenerate primers based on the *Neurospora crassa mt a-1* HMG box, (NcHMG1 CCY CGY CCY CCY AAY GCN TAY AT and NCHMG2 CGN GGR TTR TAR CGR TAR TNR GG). DNA fragments were visualised on an agarose gel and photographed under ultraviolet light. Although several *Cylindrocladium* species were tested with the degenerate primers the clearest band was obtained from a homothallic species, *Cy. colhounii.* Fragments with an approximate size of 300 base pairs [based on known sequences from *Neurospora crassa* (Staben & Yanofsky 1990)] were subsequently cut from the gel with a clean scalpel. DNA was recovered from the agarose matrix using Wizard PCR Preps (Promega Corporation, Madison, Wisconsin). This was sequenced directly after purification. The amino acid translation from the sequence obtained was compared to the *N. crassa mt a-1* HMG sequence obtained from GenBank (M54787) (Staben & Yanofsky 1990) in order to confirm its identity. This sequence was used to design ColHMG1 (CCA GAT GCT GAA GCA GCT CAA CC) and ColHMG2 (GCT TCT TGA TGA GCT CAG CC). Fragments of approximately 170 base pairs were amplified and sequenced with these primers.

A range of different species in the genus *Cylindrocladium* from both mating types were tested for specific PCR of amplification of a *MAT-2* HMG box fragment using primers ColHMG1 and ColHMG2 under the following conditions: an initial denaturation for 2 min at 96°C, followed by 35 cycles of 15 s at 96°C, 30 s at 55°C and 35 s at 75°C. A final elongation step of 4 min at 75°C was included. PCR amplifications were performed on a Rapidcycler (Idaho Technology, Idaho, U.S.A.). Amplified DNA fragments were separated on 1.6% (w/v) CE agarose gels (Boehringer Mannheim, South Africa), with ethidium bromide (1 µg/ml) using 0.5 X TBE buffer and run at a constant voltage of 60 V.

β-tubulin gene

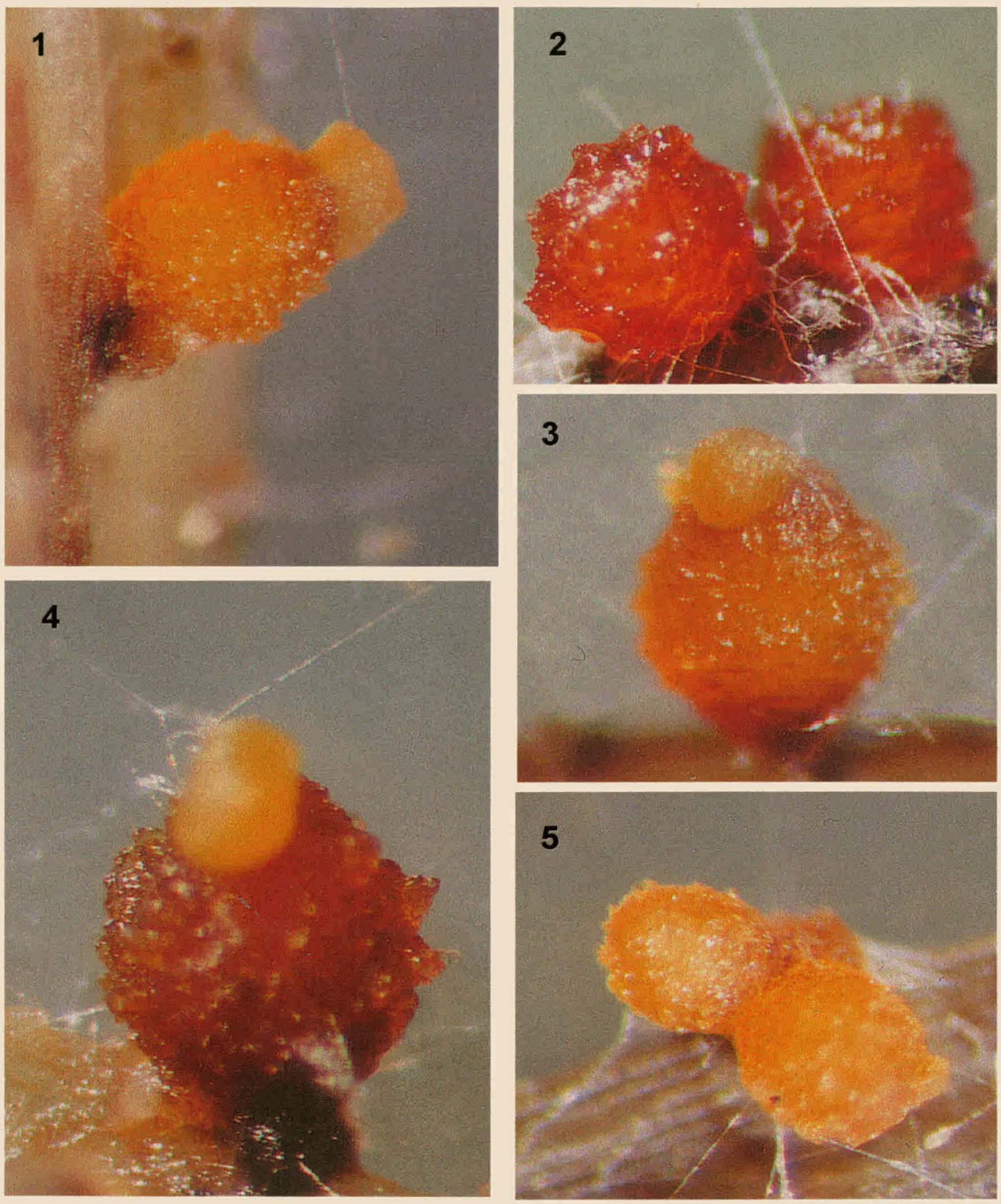
A 600 bp fragment was amplified with primers T1 (O'Donnell & Cigelnik 1997) and Bt2b (Glass & Donaldson 1995). Amplification and visualisation conditions were the same as for the HMG box.

ITS and 5.8S

The ITS1 and ITS2 internally transcribed spacers as well as the 5.8S ribosomal gene were amplified, yielding a fragment consisting of 537 bp. DNA was amplified using the primers ITS1 and ITS4 (White et al 1990). Amplification and visualisation conditions were the same as for the HMG box.

Sequence analysis

Initially both mating types of each species were tested for amplification with the primers ColHMG1 and ColHMG2. After the *MAT-2* mating types were identified as those isolates yielding a fragment of approximately 300 bp, two isolates belonging to this mating type were used for further comparisons. Additional isolates belonging to the opposite mating type (based on the absence of the *MAT-2* sequence) were used for the β-tubulin and ITS data sets. DNA was extracted as described by Crous et al (1993b) and PCR performed as mentioned previously. PCR products were purified using Wizard PCR Preps (Promega Corporation, Madison, Wisconsin). Both strands of the PCR product were sequenced using the ABI Prism 377 DNA Sequencer (Perkin-Elmer, Connecticut, U.S.A.). Sequencing conditions were as described in Part 2. Alignments of sequences were done with the computer package Malign version 2.7 (Wheeler & Gladstein 1991) and appended manually. These were included in the Appendix (Alignments 1-3). Phylogenetic analysis of aligned DNA sequences was performed using PAUP* version 4.0b1 (Swofford 1998) and printed with the help of Treeview version 1.5 (Page 1996). Unweighted parsimony analysis was performed using the branch and bound search option. Gaps were treated as a fifth character, but in order to remove ambiguities only the first position was coded as such. Subsequent gap positions were coded as missing data. . Confidence intervals for nodes were determined using 1000 bootstrap replications and the branch and bound search option for the β-tubulin and combined data sets. Due to the high number of possible trees the bootstrap values of the ITS data set was determined by means of a heuristic search with 1000 random additions and 1000 bootstrap replications.



Figs. 1-5. Variation in colour of perithecia from matings in *Cy. scoparium*. 1. Yellow perithecia from a cross of STE-U1720 X STE-U 1722. 2. Red immature perithecia from a cross between the two type species (ATCC 38227 X ATCC 46300). 3-5. Range of yellow to red perithecia from a cross of STE-U 1720 X ATCC 46300.

Results

Sexual compatibility

Crous et al (1993a) and Overmeyer et al (1996) previously reported that mating compatibility was low for *Cy. scoparium*. This was also true in the present study. From a total of ten isolates, including the reference isolates obtained from ATCC, only five isolates (STE-U 1720, STE-U 1722, STE-U 1723, ATCC 38227, ATCC 46300) could be crossed successfully. In the case of successful crosses fertile perithecia appeared after two to three wk. Successful crosses were: STE-U 1720 X STE-U 1722, STE-U 1720 X STE-U 1723, STE-U 1720 X ATCC 46300 and ATCC 38227 X ATCC 46300.

A successful mating between isolates STE-U 1720 and STE-U 1722 was selected for further study. Perithecia were found to be pale yellow to light orange in this cross (Figs. 1-5). Isolate STE-U 1720 also successfully mated with the reference isolate ATCC 46300 and this cross yielded perithecia ranging from pale yellow to orange brown in colour (Fig. 1-5). Viable progeny confirmed that these isolates belonged to the same biological species, namely *Cy. scoparium*.

After several unsuccessful attempts, a fertile cross could be observed between the two reference isolates (ATCC 46300 and ATCC 38227). Perithecial colour in this instance was as previously described, dark orange to red-brown (Figs. 1-5) (Crous et al 1993a, Overmeyer et al 1996). Ascospores were recovered from the mating between isolate STE-U 1720 and STE-U 1722. In addition to the fifteen ascospores used in th

RAPD analysis

The 15 randomly chosen ascospores were also used in the RAPD study. Primers were screened against the two parental isolates in order to find polymorphic bands between them. Most primers yielded profiles that appeared to be highly monomorphic. Only one primer showed clear polymorphic bands between the two parents, OPE 17 (Fig. 6). The markers shown in Fig. 6 co-segregated in three of the fifteen progeny (lanes 3, 7 and 17). Additional polymorphic bands in parent 1 (STE-U 1720) also co-segregated with the indicated polymorphic band (see arrow, Fig. 6) in parent 2 (STE-U 1722), further supporting the hypothesis that genetic material was derived from both parents. These data suggest that the ascospore progeny is the result of a true heterothallic cross and Mendelian segregation.

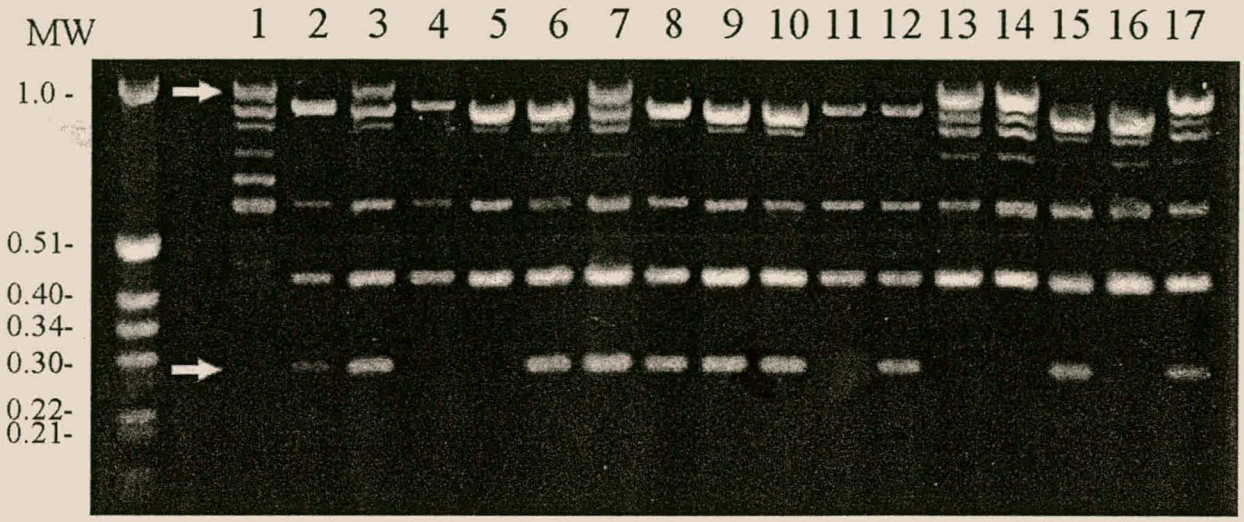


Fig. 6. Electropherogram showing RAPD profiles obtained with primer OPE 17. The two unique polymorphic bands are indicated (arrows). Lambda DNA size marker (kb) is also shown. Amplification products from parental isolates were loaded in lane 1 (STE-U 1720) and 2 (STE-U 1722). Products from ascospore progeny (A1-A15) are shown in lanes 3-17.

Phylogeny

Three regions of the genome were used for phylogenetic comparisons. The *Cylindrocladium* specific primers obtained from the *MAT-2* HMG box of an isolate of *Cy. colhounii* yielded products from several other *Cylindrocladium* species. Partial HMG box sequences from the *MAT-2* mating types of the small-spored heterothallic species, *Cy. scoparium, Cy. candelabrum, Cy. insulare, Cy. pauciramosum* and *Cy. ovatum* were also obtained. Where possible two isolates from disparate geographic areas were used for each species, in order to allow for intraspecific variation. In addition to this, the ITS ribosomal region and part of the β-tubulin gene were amplified and used for comparisons. Sequences of the opposite mating type for each species were also added to the β-tubulin and ITS data sets.

Two isolates from the multiseptate, large-spored species, *Cy. multiseptatum* Crous & M.J. Wingf., were included in order to investigate intrageneric phylogeny. The sequences of *Fusarium subglutinans* deposited by O'Donnell et al (1998), were obtained (GenBank accession numbers ITS: U34559, β-tubulin: U34417), and used as outgroups in the ITS and β-tubulin data sets. A sequence of the *Fusarium oxysporum* Shltdl.:Fr. (O-17) obtained from Genbank (AB005040) was used as outgroup for the partial *MAT-2* HMG data set. The results were presented as phylogenetic trees (Figs. 7-9).

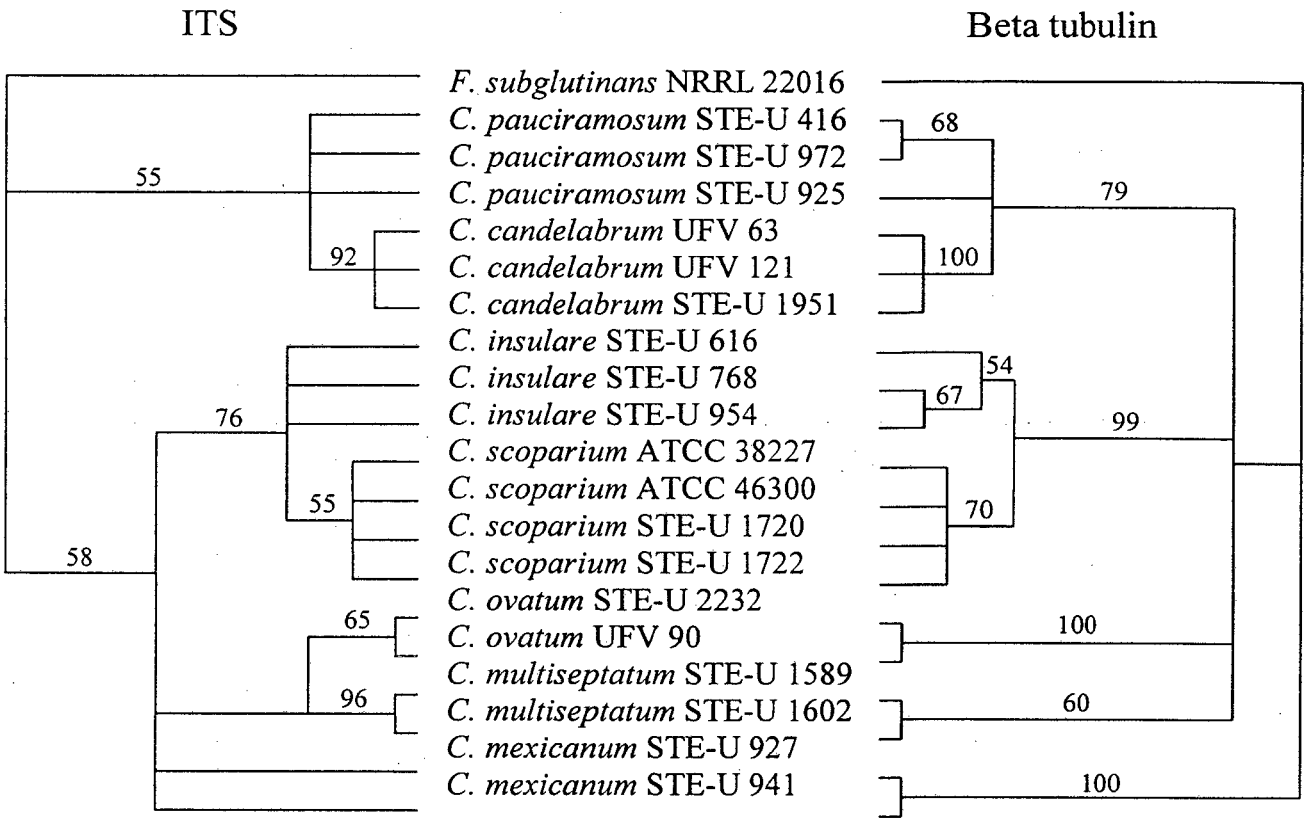


Fig. 7. Concordance of two selected most parsimonious trees generated from aligned sequences of the 5.8S gene and flanking ITS regions (done with a heuristic search with 1000 random addition sequences, 186 trees, 86 steps, CI=0.965, RI=0.941, RC=0.908) as well as the β-tubulin gene (with a branch and bound search, 27 trees, 320 steps CI=0.844 , RI=0.854 , RC=0.721) in PAUP* version 4.0b1. Clade stability was assessed with 1000 bootstrap replications and values above 50% are shown.

The ITS data set consisted of 489 nucleotide characters, of which 14 were parsimony informative, while the β-tubulin data set contained 107 parsimony informative sites out of 540 nucleotide characters. The area of the β-tubulin gene sequenced was found to have three introns containing 93 informative sites. Only 15% of informative sites were in the coding regions. Substitutions in the exons were favouring third base substitutions with 65% of all variable characters in this position, while 16% and 19% were in the first and second bases respectively.

Trees obtained from only the coding regions of the β-tubulin gene could not distinguish between the species *Cy. insulare* and *Cy. scoparium* as well as *Cy. pauciramosum* and *Cy. candelabrum* with any meaningful bootstrap support (results not shown), but were still concordant with a tree from the total β-tubulin data set (Fig. 7). A partition-homogeneity analysis performed on PAUP* version 4.0b1 revealed an underlying similarity in the phylogeny (P = 0.84) of the trees obtained with ITS and β-tubulin data sets. A similar analysis also indicated that the three introns in the β-

tubulin data set provided concordant phylogenies (P=0.56). The β-tubulin dta set will be discussed in more detail in Part 5. The disparity in the number of informative charactersin the ITS and β-tubulin data sets is reflected in the bootstrap values revealed in Fig. 7. Nodes generally had lower support in the ITS data set than in the β-tubulin data set. A closer relationship of the Brazilian isolate of *Cy. pauciramosum* (STE-U 925), with the apparent sibling species *Cy. candelabrum* is also evident from the β-tubulin data set. Both these taxa were shown to be biological species (Part 2), but a closer relationship between isolates from similar geographical origins is suggested from these data. This will be discussed in more detail in Part 4.

The topology for the tree based on the *MAT-2* HMG box sequences (Fig. 8) confirmed the results discussed above. However, although isolates of *Cy. ovatum* were shown to be distinct from other isolates, relationships between this species and other species were not concordant in all data sets. The use of *Fusarium subglutinans* and *Fusarium oxysporum MAT-2* HMG box protein sequences obtained from GenBank (accession number AFO 25888) was used to confirm the identity of the sequences amplified. The high variation of the nucleotide sequences obtained for these *Fusarium* species made sequence alignment difficult. Therefore, sequences from the two isolates of *Cy. multiseptatum,* shown to group distantly in the ITS and β-tubulin data sets, were used as outgroup sequences. The *MAT-2* HMG box data set consisted of 171 nucleotide characters, with 27 of these characters being parsimony informative. In a similar fashion to the ITS data set, it was not possible to distinguish between isolates of *Cy. scoparium* and *Cy. insulare*. However, it was possible to separate both these species after analysis of the β-tubulin data, albeit with weak bootstrap support (50-70%).

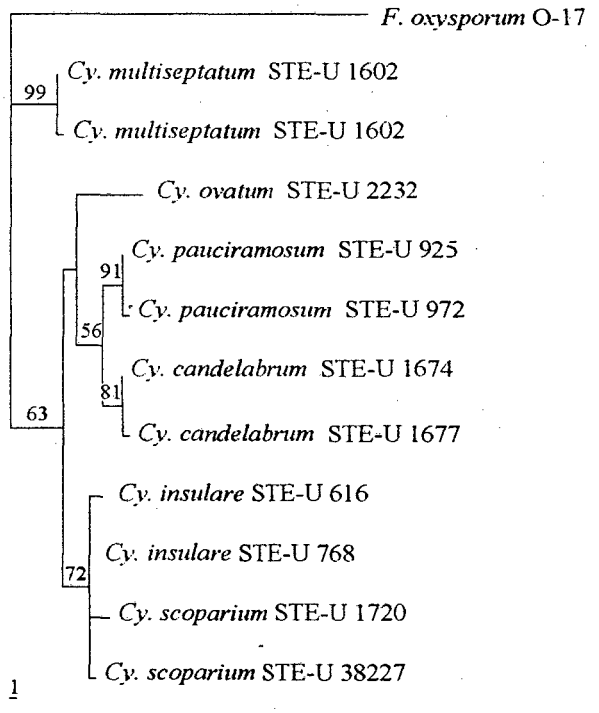


Fig. 8. One of 13 most parsimonious trees (48 steps CI = 0.917, RI = 0.920, RC = 0.843) generated by the branch and bound algorithm in PAUP* version 4.0b1 based on sequences of the *MAT-2* HMG box. Clade stability was assessed with 1000 bootstrap replications (values above 50% are shown) and *F. oxysporum* was used as outgroup

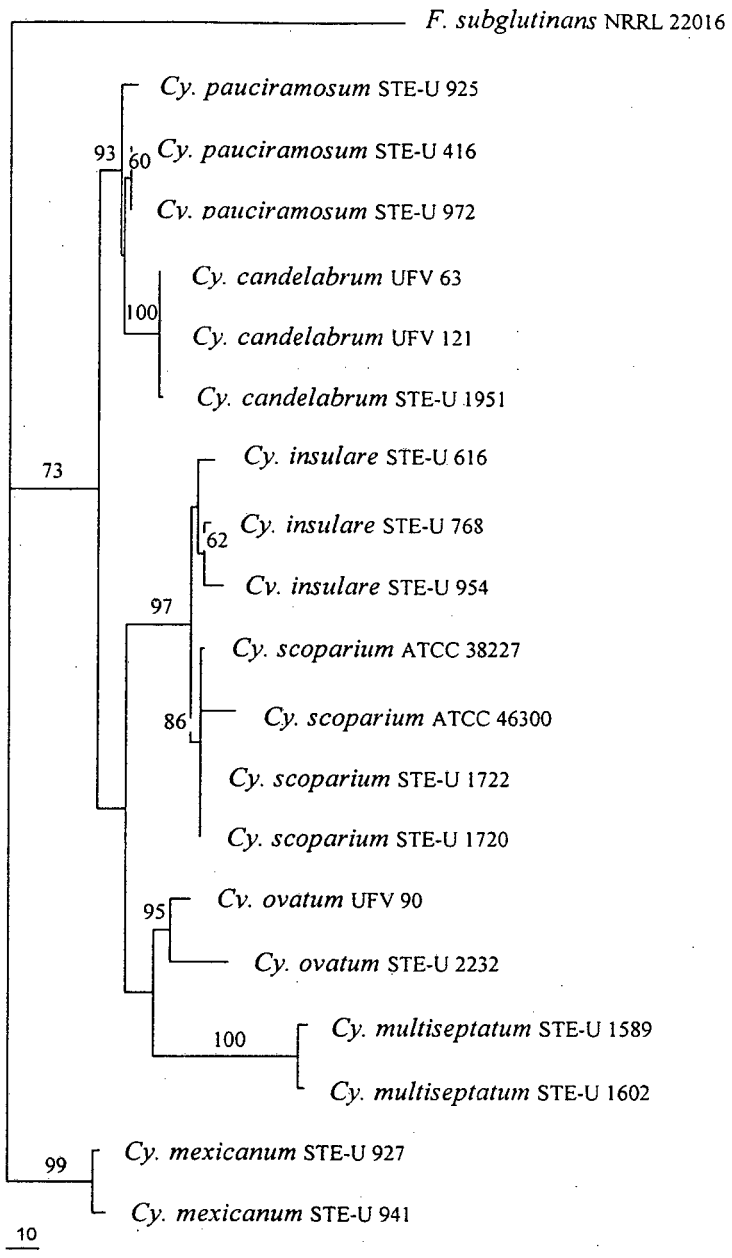


Fig. 9. Dendrogram of combined ITS and β-tubulin data set. One of 20 most parsimonious trees (531 steps CI = 0.857, RI = 0.824, RC = 0.706) generated with a branch and bound algorithm in PAUP* version 4.0b1 from aligned sequences of combined data set of the 5.8S gene and flanking ITS regions as well as the β-tubulin gene. Ten steps are indicated by the bar. Clade stability was assessed with 1000 bootstrap replications and values above 50 % are shown. *Fusarium subglutinans* sequences (GenBank accession numbers ITS:U34559, β-tubulin:U34417) were used as outgroups.

A final analysis was done with a combination of both ITS and β-tubulin data sets (Fig. 9). The partition homogeneity test performed earlier indicated the possibility that these data sets would reinforce each other. This data set yielded 20 most parsimonious trees and consisted of 1026 nucleotide characters with 135 being parsimony informative. This confirmed the topology seen in the earlier dendrograms.

However higher bootstrap support for a separation of *Cy. scoparium* and *Cy. insulare* was observed. The high similarity previously mentioned in the RAPD data between STE-U 1720 and STE-U 1722 is also reflected.

Isolates of *Cy. multiseptatum* were shown to be distant from the other small-spored species in agreement with the difference in morphology. Isolates from *Cy. mexicanum,* the fourth species described under the *Cy. candelabrum* species complex, also grouped distantly compared to the other small-spored species. Neighbor-joining and maximum-likelihood trees for all data sets (results not shown) were concordant with those obtained through maximum parsimony.

Discussion

The results obtained in the present study have confirmed that *Cy. scoparium* has a biallelic heterothallic mating system. Furthermore, sequence data from all three genomic regions used also support *Cy. scoparium* as a morphological and biological species, distinct from other morphologically similar small-spored *Cylindrocladium* spp.

The results of the mating study are in direct contrast with those previously obtained (Overmeyer et al 1996), where a system involving genetic material from only one parent was suggested in *Cy. scoparium.* Using RAPD markers, recombinant profiles obtained from both the parental isolates (STE-U 1720 and STE-U 1722) were observed in the F1 generation. A phylogenetic analysis of RAPD data obtained by Overmeyer et al (1996), however, showed all progeny to group with one parent. In addition to this, no back-cross was reported with strain ATCC 38227. However, F1 isolates were reported to intercross, indicating the existence of both mating types in the sample used. The absence of protoperithecia reported by Overmeyer et al (1996), and observed in this study, indicate that isolate ATCC 38227 has lost the ability to act as a hermaphrodite in a cross. This fact, combined with the low fertility observed in our study could explain why Overmeyer et al (1996) were unsuccessful in backcrossing ascospore progeny with ATCC 38227.

Furthermore, RAPD results obtained from 15 ascospores in the present study indicate that both parents contributed to the genetic make-up of the progeny. The designation of all isolates as either *MAT-1* or *MAT-2*, using DNA sequence data, their

novel RAPD profiles as well as their mating behavior with tester strains, is further proof that a biallelic heterothallic system exists in *Cy. scoparium*.

In order to determine the phylogenetic relationships between other heterothallic, small-spored *Cylindrocladium* species and *Cy. scoparium*, several genomic DNA regions were sequenced and analyzed. This study evaluated the phylogenetic trees obtained from the *MAT-2* gene HMG box, β-tubulin and the ribosomal ITS region. From the results presented here it is clear that, in spite of their similar morphology, these species can be differentiated on the basis of DNA phylogeny. Although only an area of 170 base pairs was obtained from the HMG box, trees were similar in topology compared to those obtained from β-tubulin and ITS sequences.

The results further indicate that *Cy. scoparium* is very closely related to *Cy. insulare*. Only one area of the genome tested, β-tubulin, could distinguish isolates of these two species. This could not be done with high bootstrap support, however. In a combined data set of both ITS and β-tubulin sequences higher bootstrap values were observed (Fig. 9). A closer relationship between the two isolates selected for the mating studies (STE-U 1720 and 1722) is also evident with relatively high bootstrap support in the combined data set. This is in agreement with the high amount of monophyly observed with the RAPD markers. Additionally, the variation in perithecial colour observed between crosses of these isolates and those involving the ATCC reference isolates support this observation. This finding also underlines the fact that in some heterothallic species of *Calonectria* variation can occur regarding perithecial colour, thus reducing the usefulness of this feature for species identification (Crous & Wingfield 1994).

The β-tubulin based tree grouped isolate STE-U 925 of *Cy. pauciramosum* with isolates of *Cy. candelabrum*. All of these isolates were collected in Brazil. In other studies where β-tubulin sequences were obtained from a wider range of *Cy. pauciramosum* isolates (Part 4), clusters correlated with geographical origin, but also confirmed a close relationship among various South American species, and between *Cy. pauciramosum* and *Cy. candelabrum* in particular. The high similarity shown between these two species indicate that they probably are sibling species.

Other than rDNA ITS sequences, DNA sequences obtained from genes such as β-tubulin and *MAT-2* appear to be more variable and yielded much higher resolution for

interspecies differentiation. However, more information is needed regarding intraspecies variation and the relationship between some of the closely related species in *Cylindrocladium*, before these results can be seen as comprehensive.

Differing characters found for other *Cylindrocladium* species, such as optimum growth temperature (Crous & Wingfield 1994, Part 2), fungicide profiles (Jayasinghe & Wijesundera 1995) and pathogenicity (Alfieri et al 1972, Blum et al 1992, Crous et al 1993c) highlight the need for accurate identification of even seemingly closely related species. The fact that *Cy. scoparium* is regularly confused with morphologically similar species further underlines this requirement. This is exemplified by recent new reports of one of the species in the *Cy. candelabrum* species complex, *Cy. pauciramosum* from Italy (Polizzi & Crous 1999) and Florida (Koike et al 1999). The apparent lack of resolution in morphological characters in this genus necessitates the use of sexual compatibility (where applicable) as well as molecular characters in order to identify morphologically similar species.

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4. Comparison of female fertility and β-tubulin DNA sequences in isolates of *Cylindrocladium pauciramosum*

Abstract

Cylindrocladium pauciramosum isolates were obtained from nurseries in South Africa, Italy and the U.S.A. The percentages of hermaphrodites and the different mating types were evaluated in these isolates. This enabled the determination of the effective population for the different areas studied. All nurseries had isolates with mating type ratios significantly different from an expected 1:1 ratio. In the South African nursery, the *MAT-1* mating type was dominant, while the *MAT-2* was more common in other samples. This was consistent with one or more founder effects. The high percentage of hermaphrodites also suggested that recent introductions had occurred in nurseries in Italy and the U.S.A. DNA sequence comparisons of the 5' end of the β-tubulin gene obtained for a set of *Cy. pauciramosum* isolates collected from various geographic regions yielded different amounts of variation. All isolates from South Africa, U.S.A. and Australia had identical sequences. In the Italian sample, two groups were observed, one of which was identical to the sequences obtained from isolates in the other areas. Finally, a group of isolates obtained from South and Central America had the highest variation of all isolates investigated and also included isolates that had shared characters with another biological species, *Cy. candelabrum*.

Introduction

Cylindrocladium species are associated with *Calonectria* teleomorphs (Rossman 1979). Species are distinguished based on the morphological features of the anamorph, such as conidium, vesicle and phialide morphology, as well as cultural characteristics. Morphological features of the teleomorph tend to be more conserved and species identification based on these characters alone is generally not possible (Crous & Wingfield 1994).

Cylindrocladium candelabrum is a well-known root and leaf pathogen of numerous hosts. This species has regularly been confused with another species, *Cy. scoparium* Morgan (Doidge 1950, Botha & Crous 1992, Polizzi & Azzaro 1996). In

order to distinguish these two species, *Cy. scoparium* was delimited as having ellipsoidal to pyriform vesicles, while *Cy. candelabrum* was circumscribed as having ellipsoidal to obpyriform vesicles (Crous et al 1993). Mating studies have shown both these species to be distinct and heterothallic (Crous et al 1993, Part 2).

In Part 2 the existence of four genetically isolated mating populations within the boundaries of the existing morphological definition of *Cy. candelabrum* was demonstrated. DNA sequencing of the ribosomal ITS regions confirmed these to be separate entities and consequently four species were described. One of these species, described as *Cy. pauciramosum,* was described from isolates originating in Australia, Brazil, Colombia, Mexico and South Africa.

Published records indicate that *Cy. pauciramosum* has been associated with diseases of plants in South Africa for several years, but incorrectly referred to as *Cy. scoparium* (Doidge 1950, Darvas et al 1978, Lamprecht 1986, Botha & Crous 1992) and *Cy. candelabrum* (Crous et al 1993). Previous reports of a new disease attributed to *Cy. scoparium* from nurseries in Sicily, Italy (Polizzi & Azzaro 1996) were subsequently shown to be caused by *Cy. pauciramosum* (Polizzi & Crous 1999). In addition to this, another recent report confirmed the recent introduction of this fungus into Florida, U.S.A. (Koike et al 1999).

The phylogenetic relationship of *Cy. scoparium* to other heterothallic small-spored *Cylindrocladium* species was recently investigated by means of DNA sequence comparisons (Part 3). Although previous work on these fungi could distinguish closely related species based on small differences in the sequence of the 5.8S rDNA and flanking internal transcribed spacers (ITS1 and ITS2) (Jeng et al 1997, Part 3), the low number of informative characters made phylogenetic determinations difficult. The use of DNA sequences obtained from additional areas, such as the β-tubulin gene and the HMG box of the *MAT-2* mating type gene yielded higher variation and could distinguish most species previously defined based on other characters (Part 2).

Cylindrocladium pauciramosum is self-sterile, and female structures consist of protoperithecia that can be spermatized by conidia or hyphae from opposite mating type isolates. A typical heterothallic ascomycete has been defined as a self-sterile hermaphrodite, capable of producing the female reproductive structures as well as male gametes (Leslie & Klein 1996). Generally these male functions can be performed by asexual spores, sexual spores or mycelia. Observations in *Gibberella*

fujikuroi have shown that the female function is lost regularly (Leslie 1995). These female sterile isolates can act only as males and were proposed to have a vegetative advantage during asexual reproduction because no resources would be required for the production of female reproductive structures (Leslie & Klein 1996). The opposite scenario was proposed for conditions favouring sex, resulting in a higher percentage of hermaphrodites (Leslie & Klein 1996). The ratios of both mating types and of female steriles and hermaphrodites can be used to determine the importance of sexual replication and the effective population (N_e), giving an estimate of a finite population' s size as first proposed by Wright (1931). These principles were reviewed by Caballero (1994) and adapted for haploids (Leslie & Klein 1996). Recent work by Mansuetus et al (1997) and Britz et al (1998) made use of these assumptions in order to gain information on the effective population size and sexual dynamics of mating populations in the *Gibberella fujikuroi* complex.

The goals of this study were to firstly determine the ratios of both mating types in the newly introduced populations of *Cy. pauciramosum* in Sicily (Polizzi & Azzaro 1996) and California (Koike et al 1999) and to compare these with a sample of the South African population. Additionally, the presumed founder populations introduced into disease free nurseries are compared with respect to fertility and mating type ratio. This would provide the necessary data to determine the mating type and inbreeding effective populations in the nurseries sampled. A final aim was to obtain data relating to infraspecific variation of *Cy. pauciramosum* based on DNA sequences of the β-tubulin gene of isolates collected from a wide geographical area.

Materials and Methods

Isolates

Isolates of *Cy. pauciramosum* (Table I) were either obtained from symptomatic plant material, or baited from soil samples. Soil samples were collected and treated according to Crous et al (1997). Collectors are indicated in Table I. All isolates were identified using the morphological concepts, mating types and keys as defined in earlier studies (Crous et al 1997, Part 3). For the purpose of this study mating capability of isolates was assumed not to be influenced by the host from which they were isolated, because species in the genus have been found not to be host specific and are essentially soil borne (Part 6).

South African isolates of *Cy. pauciramosum* were obtained from the culture collection at the Department of Plant Pathology at the University of Stellenbosch (STE-U). These were collected throughout South Africa over a period from 1990-1995 and were obtained from diseased plant material as well as from soil. Because a recent subset from this collection all produced successful crosses, it was assumed that the techniques used to preserve cultures did not adversely affect mating ability (Part 2). An additional sample of 50 isolates was obtained from crown and root rot symptoms on cherry, *Prunus* sp., plants (one isolate / plant) from a small nursery in Stellenbosch to which this disease was recently introduced (C. Linde pers. comm.).

Italian isolates were obtained from a number of nurseries in Italy (Polizzi & Crous 1999). A total count of 50 isolates was spread between several nurseries. In a similar manner, 50 isolates were collected from crown and root rot symptoms of heath, *Erica capensis* Salter from a single nursery in California, U.S.A.

Sexual compatibility

Two mating tester strains of the opposing mating type (*MAT-1* = STE-U 416, *MAT-2* = STE-971) were selected for their high levels of fertility during previous mating experiments (Parts 2 and 3). Single isolates were grown on Petri dishes containing malt extract agar (MEA) (Biolab, Midrand, South Africa) for 2-4 wk until sporulation. One ml of sterile water was added to each Petri dish and conidia were dislodged with the help of a sterile glass rod. The conidial suspension was removed with a micropipette. Cultures were spermatised by applying the conidial suspension to Petri dishes containing CLA with 2-4-wk-old growth. The selected cultures were spermatized with both tester strains. In addition to this, the tester strains were individually spermatized with all test isolates. Plates were packed in stacks of 10, sealed in plastic bags and incubated on the laboratory bench at 22°C. Successful crosses were determined after 2 mo of incubation and were selected as those isolate combinations that produced perithecia with extruding, fertile ascospores.

Statistical analysis

The effective population numbers were calculated according to methods of Leslie and Klein (1996). The effective population number based on mating type ($N_{e(mt)}$) was determined as $N_{e(mt)} = (4N_{MAT\text{-}1}N_{MAT\text{-}2})/(N_{MAT\text{-}1} + N_{MAT\text{-}2})$ with $N_{MAT\text{-}1}$ the number of *MAT-1* strains and $N_{MAT\text{-}2}$ the number of *MAT-2* mating type strains. These are parameters to estimate genetic drift and inbreeding in populations. The inbreeding effective

population ($N_{e(f)}$) is based on the probability of identity due to common ancestry and determined as $N_{e(f)} = (4\ N^2\ N_h)/(N + N_h)^2$ with N being the total number of individuals and N_h the total number of hermaphrodites.

Isolation of DNA

Single conidial isolates selected for DNA comparison (Table II) were grown on MEA plates. Mycelial mats were removed from the plates by means of a sterile scalpel and ground to a powder by means of liquid nitrogen and a mortar an pestle. Approximately 40 mg of ground mycelium was added to 2 ml microtubes containing 600 µl of extraction buffer. The extraction buffer consisted of 1% SDS, 50 mM Tris-HCl (pH 8.0), 150 mM NaCl and 100 mM EDTA. Subsequently, the protocol was followed as suggested for the Wizard Genomic DNA Purification kit (Promega, Madison, U.S.A.).

PCR amplifications and sequencing

Reactions (total volume 25 µl) comprised of 1.5 units Biotaq (Bioline, London, U.K.) with the buffer as supplied by the manufacturer, 1 mM deoxynucleoside triphosphates, 4 mM $MgCl_2$, 0.5 µM primer oligonucleotide and approximately 10 to 30 ng of fungal genomic DNA as target. Reactions were performed on a Rapidcycler (Idaho Technology Idaho, U.S.A.). Reaction conditions consisted of the following: an initial denaturation for 2 min at 96°C, followed by 30 cycles of 15 s at 96°C, 30 s at 55°C and 35 s at 75°C with a slope of 1.0. A last elongation step of 2 min at 75°C was included. A 600 bp fragment was amplified using primers T1 (O' Donnell & Cigelnik 1997) and Bt2b (Glass & Donaldson 1995). PCR fragments were sequenced as described previously (Part 2).

Phylogenetic analysis

Sequence comparisons based on DNA sequences of the β-tubulin gene have previously been used to investigate phylogeny in *Cy. scoparium, Cy. pauciramosum* and related species (Part 3). In the present study an investigation on the variation in *Cy. pauciramosum* was undertaken. *Cy. candelabrum, Cy. multiseptatum* and *Fusarium subglutinans* were used as outgroups. As far as possible six isolates from disparate regions within a country and representing different mating types were used for comparison. The isolates selected for phylogenetic analysis are shown in Table II. Alignments of sequences were done with the computer package Malign version 2.7 (Wheeler & Gladstein 1991) and assessed manually. These are included in the

Appendix (Alignment 2). Phylogenetic analysis of aligned DNA sequences was performed using PAUP* Version 4.0b1 (Swofford 1998). Gaps were treated as a fifth base. Confidence intervals were determined using a 1000 bootstrap replications.

Table II. Isolates of *Cy. pauciramosum* and other species used for sequencing.

Species	Original no.	Collector	Host	Origin
Cy. pauciramosum	STE-U 143	P. W. Crous	*Eucalyptus grandis*	Mpumalanga, South Africa
	STE-U 416	S. de Buisson	*Eucalyptus grandis*	Northern Province, South Africa
	STE-U 344	P.W. Crous	*Eucalyptus grandis*	KwaZulu Natal, South Africa
	STE-U 925	M.J. Wingfield	Soil	Santa Catarina, Brazil
	STE-U 951	M.J. Wingfield	Soil	Veracruz, Mexico
	STE-U 971	P.W. Crous	*Eucalyptus grandis*	Western Cape, South Africa
	STE-U 972	P.W. Crous	*Eucalyptus grandis*	Western Cape, South Africa.
	STE-U 1160	M.J. Wingfield	Soil	Córdoba, Colombia
	STE-U 1670	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil
	STE-U 1671	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil
	STE-U 1691	D. Hutton	*Fragraria* sp.	Queensland, Australia
	STE-U 1692	D. Hutton	*Fragraria* sp.	Queensland, Australia
	STE-U 1990	S. Koike	*Erica* sp.	California, U.S.A.
	STE-U 2030	S. Koike	*Erica* sp.	California, U.S.A.
	DISTEF-G 2	G. Polizzi	*Polygala myrtifolia*	Catania, Sicily, Italy
	DISTEF-G 6	G. Polizzi	*Callistemon citrinus*	Messina, Sicily, Italy
	DISTEF-G 60	G. Polizzi	*Myrtus communis*	Catania, Sicily, Italy
	DISTEF-G 62	G. Polizzi	*Callistemon citrinus*	Messina, Sicily, Italy
	DISTEF-G 84	G. Polizzi	*Acacia retinodes*	Messina, Sicily, Italy
	DISTEF-G 126	G. Polizzi	*Arbutus unedo*	Catania, Sicily, Italy
	DISTEF-G 127	G. Polizzi	*Callistemon citrinus*	Messina, Sicily, Italy
	DISTEF-G 128	G. Polizzi	*Callistemon citrinus*	Messina, Sicily, Italy
	DISTEF-G 192	G. Polizzi	*Polygala myrtifolia*	Catanzaro, Calabria, Italy
	DISTEF-G 196	G. Polizzi	*Polygala myrtifolia*	Catanzaro, Calabria, Italy
Cy. candelabrum	STE-U 1677	A.C. Alfenas	*Eucalyptus* sp.	Amazonas, Brazil
	STE-U 1674	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil
	STE-U 1951	A.C. Alfenas	Soil	Brazil
	UFV 89	A.C. Alfenas	Soil	Brazil
Cy. mexicanum	STE-U 927	M.J. Wingfield	Soil	Yucatan, Mexico
	STE-U 941	M.J. Wingfield	Soil	Campeche, Mexico
Cy. multiseptatum	STE-U 1589	M.J. Wingfield	*Eucalyptus* sp.	Indonesia
	STE-U 1602	M.J. Wingfield	*Eucalyptus* sp.	Indonesia

Results

Sexual compatibility

Effective populations and ratios based on numbers of mating types and hermaphrodites of the *Cy. pauciramosum* samples obtained from the selected areas are shown in Table III. These values reflect differences in the profiles for the different nurseries. Samples from a group of various areas in South Africa, where the disease has been well established, tended to have a mating type ratio of approximately 1:1. All other samples, representing areas where the pathogen is thought to be recently introduced, yielded ratios that significantly favoured one mating type. In the Stellenbosch nursery the ratio favoured the *MAT-1* mating type, while the nurseries in California and Sicily had more *MAT-2* isolates present. Additionally, only one mating type, *MAT-2,* was present in Californian nursery. These figures differ appreciably

from those obtained by other workers for species of the *Gibberella fujikuroi* complex (Leslie & Klein 1996, Mansuetus et al 1997, Britz et al 1998). Here the highest mating type ratio was approximately of 1:2.

Table III. Comparison of population distribution of mating types and hermaphrodites between three geographic areas.

Geographic origin	Ratio of mating types[1]	N_e (effective population)[3]		
		$N_{fs}:N_h$[2]	$N_{e(mt)}$[4]	$N_{e(f)}$[5]
South Africa				
Stellenbosch nursery	48:8	31:25	49.0	85.3
Rest of South Africa	21:23	29:15	99.7	75.8
United States				
Californian nursery	0:50	4:46	0	99.8
Italy				
Various nurseries	13:41	12:42	73.1	98.4

[1] The ratio of mating types based shown as *MAT-1:MAT-2* (mating types determined previously according to work done in Part 3).

[2] The ratio of female sterile:hermaphrodites in the population.

[3] The effective population number based on the numbers of males (N_{fs}) and hermaphrodites (N_h) as percentage of the actual count.

[4] Effective population number based on mating type (given as percentage of total population).

[5] Inbreeding effective number based on numbers of males and hermaphrodites (given as percentage of total population).

Equations were all derived from Leslie and Klein (1996).

Effective population size, based on mating types ($N_{e(mt)}$), of between 49% and 99% of the total count was inferred where both mating types of the *Cy. pauciramosum* isolates were present. In contrast to the effective populations based on mating types, higher effective populations based on the presence of hermaphrodites were found. Other effective population values differed between 76% and 98% of the total population. High percentages were found for nurseries in California and Italy (98-99%), in spite of a mating type bias in these samples. Mating type ratios found for the hermaphrodites were also comparable to those of the total sample in all cases (data not shown).

β-tubulin sequence analysis

Based on preliminary results obtained in Part 3 a number of isolates were selected in order to investigate the variation of the β-tubulin DNA sequence for a number of isolates within *Cy. pauciramosum*. A heuristic search using PAUP* 4.0b1 with 500 random additions and 1000 bootstrap repetitions yielded ten most parsimonious trees. One of these trees is shown in Fig. 1.

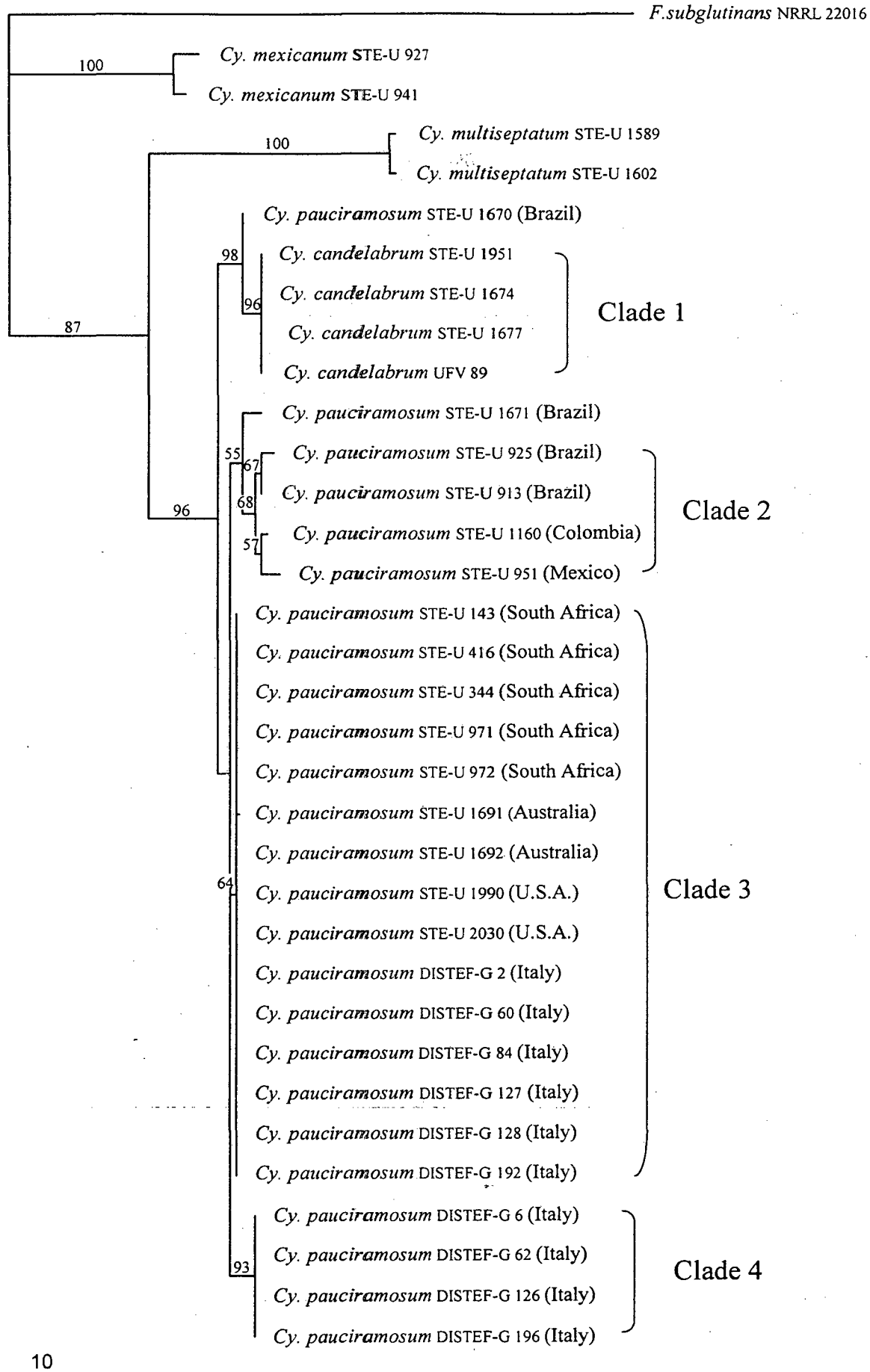

Fig. 1. Phylogram of DNA sequences from the 5' end of the β-tubulin gene. One of 10 most parsimonious trees (266 steps, CI=0.925 RI=0.905 RC=0.837) generated by the heuristic algorithm in PAUP* version 4 based on sequences of the β-tubulin gene. Ten steps are indicated by the bar. Clade stability is assessed by 1000 bootstrap samplings (shown above branches).

All variable characters in the DNA alignments were single base pair substitutions, less than a third of these being transversions. From a comparison between *Cy. candelabrum* and *Cy. pauciramosum* 27 variable characters were found out of a data set of 521 unordered characters. Only 18 of these were parsimony informative. This is comparable to the low, but consistent amount of variation previously seen between species of *Cylindrocladium* in the ITS1 and ITS2 spacers flanking the 5.8S ribosomal RNA gene (Crous et al 1999, Part 2). Variable characters were almost exclusively situated in the non-coding regions of the β-tubulin gene. Only 2 characters (base pairs 273 and 348) were inside the coding regions (Table IV).

The low number of informative characters were emphasised in the low bootstrap values (Fig. 1). A Neigbor Joining comparison done with 1000 bootstrap replications in PAUP* yielded higher values (75-90%) and similar topology. In order to investigate the variation at sequence level the different base pair substitutions are presented as single characters in Table IV with the clades as indicated in Fig. 1.

Cylindrocladium candelabrum isolates obtained from Brazil (Clade 1, Fig. 1) all had identical sequences. Although this species is closely related to *Cy. pauciramosum*, these two species have already been shown to differ biologically and genetically (Parts 2 and 3). The *Cy. candelabrum* isolates (Clade 1) shared a total of nine variable sites of which three (base pairs 57, 232 and 409) were unique for all isolates in this group. The remaining five variable sites were shared by isolates in clade 2 with an isolate of *Cy. pauciramosum,* STE-U 1670. This isolate clustered with *Cy. candelabrum* (Fig. 1), but still grouped separate and also had one unique variable site (base pair 227). Only one variable site separated clades 1, 2 and STE-U 1670 (base pair 198).

Variation was found for other individual *Cy. pauciramosum* isolates from South America and Mexico. Three variable characters were found in Clade 2. Of these, base pair 198 was shared with clade 1 and STE-U 1670, and base pair 420 with STE-U 1671. Although variation occurred between South American and Mexican isolates no variable characters were shared with any of the isolates from the other geographic regions (South Africa, Australia and Italy).

Isolates in Clade 3, selected from the South African, Italian and California populations had identical sequences and clustered together with low bootstrap support. This group is supported by one unique character at base pair 95 (Table IV).

A different group of Italian isolates were supported by four unique base pair substitutions (Clade 4). This grouping is shown to be distinct with high (93%) bootstrap support (Fig. 1).

Table IV. The 27 variable characters in the comparison of β-tubulin DNA sequence data from isolates of *Cy. pauciramosum Cy. candelabrum* species, compared to the groups seen in Fig. 1, and their areas of origin. Base pairs are numbered from the start of deposited sequences (Appendix, Alignment 4).

Base pair no.	Original state	Derived state	Group (seen in Fig. 1)	Geographic origins
57	C	T	Clade 1	Brazil
63	C	G	STE-U 925	Brazil
75	A	G	STE-U 1671	Brazil
83	C	G	STE-U 925	Brazil
95	A	G	Clade 3	Australia, California, South Africa, Italy
138	C	T	Clade 1, STE-U 1670	Brazil
143	T	C	STE-U 951	Mexico
181	T	C	Clade 1, STE-U 1670	Brazil
195	T	C	Clade 1, STE-U 1670	Brazil
198	A	C	Clade 1, STE-U 1670, Clade 2	Brazil
212	G	A	STE-U 951, STE-U 1160	Mexico, Colombia
215	A	G	STE-U 913, STE-U 925	Brazil
217	T	G	STE-U 1671	Brazil
219	A	G	Clade 2	Brazil
225	A	G	STE-U 951	Mexico
227	T	C	STE-U 1670	Brazil
232	G	C	Clade 1	Brazil
273	T	C	Clade 1, STE-U 1670	Brazil
348	C	T	Clade 4	Italy
387	C	G	Clade 4	Italy
394	C	T	Clade 4	Italy
397	G	A	STE-U 1160	Colombia
406	G	T	Clade 1, STE-U 1670	Brazil
409	A	G	Clade 1	Brazil
413	C	G	Clade 4	Italy
417	C	T	STE-U 951	Mexico
420	C	A	Clade 2, STE-U 1671	Brazil

Discussion

The results presented here showed fundamental differences in the profiles of the populations sampled. In effect, all the nursery populations amounted to founder populations and some could have gone through several population bottlenecks. This is reflected in the varying ratios of mating types found in the different nurseries in the different geographic areas. The only population that approached a 1:1 mating type ratio was the sample where the disease has been well established in South Africa (Table III). This was collected over a wide area and a time period of several years.

The Italian sample used in the present study resembled a number of isolates spread over a number of nurseries in Sicily and Southern Italy. Preliminary results obtained from an additional number of isolates collected in single nurseries such as Carubba,

Barcellona and Milazzo indicate that the founder effects seen in the nurseries of Stellenbosch (South Africa) and California (U.S.A.) were also consistent in these circumstances (results not shown). Indications are that in some Italian nurseries only one mating type has been introduced. All the Italian samples had the same mating type bias correlating with a single source, the nursery in Carubba. This nursery has been established as the point of entry for new material in the region and could have had a persistent inoculum (Sicily and Southern Italy). Further analysis of these additional samples will enable a clearer picture of the population variation between single nurseries in Italy.

The high ratios of hermaphrodites in samples supports hypothesised recent introductions (Polizzi & Azzaro 1996, Koike et al 1999). However, the percentage of hermaphrodites found in the various nurseries is still consistent with a population that is sexually reproductive (Leslie & Klein 1996, Britz et al 1998). One would expect the percentage of hermaphrodites to drop if a single mating type were to persist in each nursery. The application of good nursery practices entails the immediate removal of diseased material. This has the potential to create several bottlenecks as the remaining populations must result from small starter populations. The influx of new diseased material containing the opposite mating type could further rapidly influence population structure in these nurseries.

Plant pathogens are normally introduced into nurseries by infected plant material or soil. The most important survival structures of *Cylindrocladium* spp. are microsclerotia which can survive for periods of up to 15 years and longer in soil (Thies & Patton 1970, Sobers & Litrell 1974). Under suitable climatic conditions germination and subsequent infection of roots and leaves occurs (Anderson et al 1962, Sharma et al 1990). The conidia form on infected plant material and are splash dispersed between closely placed plants (Mohanan & Sharma 1986). In the case of sexual reproduction, the ascospores can also be an additional source of inoculum and are generally wind dispersed (Crous et al 1991). The profiles of the mating type distributions found in this study are consistent with the effects seen for a small initial inoculum, probably by asexual propagules. The fact that only one mating type can be found in the nursery samples from California, as well as the strong bias towards one mating type, suggests that sexual replication has a small role to play under these circumstances.

Genetic variation, based on DNA sequencing data, was detected between different isolates of *Cy. pauciramosum*. Although the gene phylogeny as reflected from the tree obtained from the partial sequences of the β-tubulin gene may not accurately reflect the species phylogeny (Doyle 1992, Maddison 1997), recent analysis of different loci have produced concordant phylogenies for *Cy. pauciramosum* and closely related species (Part 3).

Shared characters were found between a number of *Cy. pauciramosum* isolates and isolates of *Cy. candelabrum*. These *Cy. pauciramosum* isolates include the isolates in Clade 2 as well as STE-U 1670 (Fig. 1). All of these isolates were collected in South and Central America. This suggests a population of *Cy. candelabrum* being sexually isolated from the more variable mother population of *Cy. pauciramosum*. In addition to this, it would imply that these two taxa are sibling species.

The high variation amongst South and Central American isolates of *Cy. pauciramosum* is consistent with an endemic population in this area. Attempts to obtain a larger sample to include in this study have thus far proved unsuccessful as all samplings contained mainly *Cy. candelabrum* isolates. These results could imply a South African population introduced from elsewhere. The identical DNA sequences obtained from the South African isolates certainly allows this possibility. DNA sequences obtained from isolates collected from a wide variety of locations, including Australia, South Africa, Italy and California were also identical and could indicate a collective origin for these populations. There is anecdotal evidence of importation of South African nursery material into Italian nurseries and this would agree with results presented here. The occurrence of another distinct group of DNA sequences obtained from isolates in the Italian population complicates this issue. It is possible that there has been more than one introduction of this species into this area.

Because the relatively small sample sizes utilised in this study could influence the results, it must be emphasised that this is a first approximation of the variation present in populations of *Cy. pauciramosum*. A more detailed study of genetic and mating markers will allow more comprehensive conclusions to be drawn. In spite of this, these results emphasise the importance of identification of the members of morphologically closely related species in the *Cylindrocladium candelabrum* species complex in order to aid phytosanitation programmes and aid disease control.

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5. Phylogeny of *Calonectria* based on β-tubulin DNA sequence comparisons

Abstract

The phylogeny of the genus *Calonectria* was analysed by means of DNA sequence comparisons. This was done by amplifying the 5' end of the β-tubulin gene from isolates representative of 30 *Calonectria* species. A neighbor-joining analysis was performed on a total data set of 86 isolates, while a representative subset of isolates was analysed by means of maximum parsimony. The analyses yielded dendrograms with concordant topology. Many clades, containing small numbers of isolates were strongly supported by bootstrap. However, relationships between these clades were often ambiguous. A number of phylogenetic placements based on DNA data did not always agree with preconceived morphological relationships. Two large groupings were evident and both contained small-spored one-septate species. The only morphological character that correlated with DNA based phlyogenies was vesicle shape.

Introduction

The genus *Calonectria* De Not. resides in the euascomycete order Hypocreales and has been characterised as having *Cylindrocladium* Morgan anamorphs (Rossman 1979, Crous & Wingfield 1994). Members of this genus are defined as species with brightly coloured ascocarps that change colour when placed in a 3% KOH solution (KOH+), have a warty wall surface, darkened stromatic bases, as well as *Cylindrocladium* anamorphs (Rossman 1993, Rossman et al 1999). *Cylindrocladium* anamorphs are the form most frequently encountered in nature and are also morphologically the most informative. Thus, most of the species in *Calonectria* are distinguished based on morphological features of their anamorphs.

Conflicting opinions have arisen regarding the use of the stipes eminating from the conidiophores and specifically the shape of its terminal vesicle as a taxonomic character. This character was rejected by some authors (Hunter & Barnett 1978, Rossman 1983), but others found it to give reliable taxonomic results (Sobers & Alfieri 1972, Peerally 1991). Crous et al (1992) demonstrated that the osmotic potential of the medium influences vesicle shape. Thus vesicle shape was proposed to be a reliable character only when it is used under standardised conditions.

Consequently, this criterion has been combined with other morphological characters in order to delimit *Cylindrocladium* species (Crous & Wingfield 1994).

Several *Cylindrocladium* species have been described with variable morphological characters despite the use of standardised growth conditions. One such character is conidial septation. Hence only predominant septation has been used as an important character in past descriptions (Crous & Wingfield 1994). Further studies have also shown intraspecific variation in other characters such as conidial size and vesicle shape (Crous & Peerally 1996, Crous et al 1998).

Because various morphological characters overlap in *Cylindrocladium,* frequent misidentifications occur, and different biological species are commonly lumped together under broad morphological species concepts. One example is the *Cy. candelabrum* Viégas species complex. Besides the fact that it is regularly confused with other species such as *Cy. floridanum* Sobers & C.P. Seym., *Cy ovatum* El-Gholl et al and *Cy. scoparium* Morgan, a high amount of plasticity within the limits originally defined for its vesicle shape has been reported (Crous et al 1993a). A subsequent study revealed the presence of several distinct mating populations previously identified as *Cy. candelabrum* (Part 2). The use of mating tester strains was advocated in order to differentiate between these biological species, but due to the practical limitations of this approach, molecular characters became increasingly significant. In agreement with the contemporary trend in systematics, such molecular characters have also been applied to *Calonectria* taxonomy. These include the use of aminopeptidase substrate specificities (Stevens et al 1990), total protein electrophoresis (Crous et al 1993a) isoenzyme comparisons (El-Gholl et al 1997), DNA hybridisation based techniques (Crous et al 1993b, Victor et al 1997) as well as PCR-based methods (Victor et al 1997). These techniques have been helpful in delimiting several new species (Crous et al 1997a, Victor et al 1997, Crous et al 1999) subsequent to the monograph by Crous and Wingfield (1994).

The first study using DNA sequence comparisons to distinguish species of *Cylindrocladium* was that of Jeng et al (1997), where isolates of *Cy. floridanum* were compared with *Cy. scoparium* using the DNA sequences obtained from the ITS-5.8S ribosomal RNA area. Although these authors found differences between the two species, subsequent work showed that these differences were consistent between other *Cylindrocladium* species, and that the number of variable characters in this

region was low (Part 2). This necessitated the use of DNA sequences from additional genomic regions in order to infer a phylogeny for these taxa.

DNA sequences obtained from the β-tubulin gene have been employed to predict a phylogeny for closely related species in the *Gibberella fujikuroi* (Sawada) Wollenw. species complex (O'Donnell et al 1998). Several unlinked loci were used in a study by O'Donnell et al (1998), and the β-tubulin gene yielded the most variation of all areas sequenced, possibly making it useful for determining phylogeny in recently diverged groups. The β-tubulin gene product is an important component of microtubules, the major constituents of the cytoskeleton and mitotic spindles. The fact that mutations in this gene can confer resistance to the fungicide benomyl, implies that a significant body of sequencing data are already available for comparisons in fungi (Koenraad & Jones 1993, Yan & Dickman 1996). The utility of the β-tubulin gene sequence in determining phylogenetic relationships has also been demonstrated at various taxonomic levels (Schardl et al 1994, Tsai et al 1994, Donaldson et al 1995, Baldauf & Doolittle 1997).

Gene phylogeny may not necessarily be an accurate reflection of species phylogeny (Doyle 1992, Maddison 1997). One problem could be posed by the presence of several copies of the β-tubulin gene under different selection constraints. Several copies of this gene have been encountered in plants (Snustad et al 1992), and more than one copy have also been reported in fungi, such as the two divergent copies in *Colletotrichum graminicola* (Panaccione & Hanau 1990), and five in *Epichloë* species (Schardl et al 1994, Tsai et al 1994). However, ascomycetes generally appear to have lower copy numbers and several species have been described with only one β-tubulin gene (Neff et al 1983, Orbach et al 1986, Smith et al 1988).

The present study of *Calonectria* has shown that the gene phylogeny obtained from the 5' end of the β-tubulin is concordant with that obtained from the ITS flanking sequences of the 5.8 S rRNA gene, as well as the HMG box of the *MAT-2* gene (Part 3). These results indicated that the β-tubulin gene could be suitable for determining the phylogeny of this closely related group of fungi. The aims of this study were to utilise the DNA sequences of the 5' end of the β-tubulin gene in order to obtain a phylogeny for species in *Calonectria,* and to investigate species relationships at a larger scale than in previous studies. Inclusion of biological species such as those forming part of the *Cy. candelabrum* species complex (Part 2) would also enable a

comparison of the morphological, phylogenetic and biological species concepts in this genus.

Materials and Methods

Isolates

Strains were either obtained from culture collections (Table I) or isolated from infected plant material or soil samples (Crous et al 1997b). These have been deposited in the culture collection of the Department of Plant Pathology, University of Stellenbosch (STE-U).

Isolation of DNA

Single conidial isolates were grown on malt extract agar (MEA) (Biolab, Midrand, South Africa) plates. Mycelial mats were cut from the plates using a sterile scalpel and ground to a powder with liquid nitrogen and a mortar and pestle. Approximately 40 mg of ground mycelia was added to 2 ml microtubes containing 600 µl of extraction buffer. The extraction buffer consisted of 1% SDS, 50 mM Tris-HCl (pH 8.0), 150 mM NaCl and 100 mM EDTA. The subsequent protocol was followed as suggested for the Wizard Genomic DNA Purification kit (Promega, Madison, U.S.A.).

PCR amplifications and sequencing

A wide variety of isolates were used for sequencing (Table I). Reactions (total volume 25 µl) comprised of 1.5 units Biotaq (Bioline, London, U.K.) with the buffer as recommended by the manufacturer, 1 mM deoxynucleoside triphosphates, 4 mM $MgCl_2$, 0.5 µM primer oligonucleotide and approximately 10 to 30 ng of fungal genomic DNA as target. These were performed on a Rapidcycler (Idaho Technology Idaho, U.S.A.). Reaction conditions consisted of the following: an initial denaturation for 2 min at 96°C, followed by 30 cycles of 15 s at 96°C, 30 s at 55°C and 35 s at 75°C with a slope of 1.0. A last elongation step of 2 min at 75°C was included. A 600 bp fragment encompassing the first three introns and exons and part of the fourth exon of the β-tubulin gene was amplified with the use of primers T1 (O'Donnell & Cigelnik 1997) and Bt2b (Glass & Donaldson 1995). PCR fragments were sequenced as described previously (Part 3). DNA sequences of isolates of*Cy. floridanum,Cy. spathiphylli* and a number of unknowns (CBS 413.67, STE-U 599, 682, 1150, 1484, 2712, 2350, IMI and IMI 354529, UFV 76) previously sequenced by J.C. Kang was also included in this study for a more complete analysis.

Table I. Isolates of *Cylindrocladium* spp. studied.

amorph	Teleomorph	No.	Collector	Substrate	Origin	Date isolated
. *avesiculatum*	*Ca.* avesiculata	ATCC 38226	S.A. Alfieri	*Ilex vomitoria*	Florida, U.S.A.	1971
. *candelabrum*	*Ca. scoparia*	STE-U 1674	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil	Jul. 1990
		STE-U 1677	A.C. Alfenas	*Eucalyptus* sp.	Amazonas, Brazil	1991
		STE-U 1951	A.C. Alfenas	*Eucalyptus* sp.	Brazil	Jun. 1998
		UFV 89	A.C. Alfenas	*Eucalyptus* sp.	Brazil	1990
. *citri*	Unknown	CBS 186.36	H.S. Fawcett	*Citrus sinensis*	Florida, U.S.A.	Jan. 1932
. *colhounii*	*Ca. colhounii*	STE-U 681	M.J. Wingfield	Soil	Thailand	Nov. 1993
		STE-U 705	M.J. Wingfield	Soil	KwaZulu-Natal, S. Africa	Nov. 1993
		STE-U 1237	P.W. Crous	*Eucalyptus sp.*	KwaZulu-Natal, S. Africa	Oct. 1995
		STE-U 1339	M.J. Wingfield	Soil	Indonesia	Mar. 1996
. *curvisporum*	Unknown	STE-U 763	P.W. Crous	Soil	Madagascar	Apr. 1994
		STE-U 765	P.W. Crous	Soil	Madagascar	Apr. 1994
. *flexuosum*	*Ca. clavata*	STE-U 2536	N.E. El-Gholl	*Callistemon viminalis*	Florida, U.S.A.	Apr. 1978
. *floridanum*	*Ca. kyotensis*	ATCC 18834	T. Terashita	*Robinia pseudoacacia*	Japan	1968
		ATCC 18882	R.H. Morrison	Peach roots	Florida, U.S.A.	1967
		CBS 413.67	W .Gerlach	*Paphiopedilum callosum*	Celle, Germany	Oct. 1967
		STE-U 682	M.J. Wingfield	Soil	Thailand	Aug. 1993
		STE-U 2350	M.J. Wingfield	Soil	Hong Kong	1998
		IMI 354528	M. Aragaki	*Araucaria heterophylla*	Hawaii	1987
		IMI 354529	M. Aragaki	*Araucaria heterophylla*	Hawaii	1987
		UFV 76	A.C. Alfenas	*Pinus* sp.	Canada	1990
. *gracile*	Unknown	ATCC 22833	C.S. Hodges	*Pinus caribeae*	Brazil	Mar. 1971
		IMI 167580	A. Peerally	*Camellia sinensis*	Mauritius	1970
		PC 551197	Bugnicourt	*Argyreia splendens*	Vietnam	1937
		STE-U 623	M.J. Wingfield	Soil	Amazonas, Brazil	Apr. 1993
		STE-U 1586	P.W. Crous	Soil	Amazonas, Brazil	1996
. *graciloideum*	*Ca. gracilipes*	STE-U 1153	M.J. Wingfield	Soil	Colombia	Jun. 1996
. *hawksworthii*	Unknown	MUCL 30866	A. Peerally	*Nelumbo necifera*	Mauritius	1990
. *macroconidiale*	*Ca. macroconidialis*	STE-U 307	P.W. Crous	*Eucalyptus grandis*	Mpumalanga, S. Africa	Mar. 1990
		STE-U 413	P.W. Crous	Soil	Mpumalanga, S. Africa	May 1990
. *heptaseptatum*	Unknown	FTCC 1002	N.E. El-Gholl	*Rumohrae adiantiformis*	Florida, U.S.A.	Unknown
		FTCC 1003	N.E. El-Gholl	*Rumohrae adiantiformis*	Florida, U.S.A.	Unknown
		STE-U 2344	N.E. El-Gholl	*Rumohrae adiantiformis*	Florida, U.S.A.	Mar. 1999
. *insulare*	*Ca. insularis*	STE-U 616	M.J. Wingfield	Soil	Amazonas, Brazil	Apr. 1993
		STE-U 768	P.W. Crous	Soil	Madagascar	Apr. 1994
		STE-U 954	M.J. Wingfield	Soil	Veracruz, Mexico	Apr. 1994
. *leucothoes*	Unknown	ATCC 64824	N.E. El-Gholl	*Leucothoe axillaris*	Florida, U.S.A.	1988
		P97.2605	N.E. El-Gholl	*Leucothoe* sp.	Florida, U.S.A	1997
. *mexicanum*	*Ca. mexicana*	STE-U 927	M.J. Wingfield	Soil	Yucatan, Mexico	Apr. 1994
		STE-U 941	M.J. Wingfield	Soil	Holpechén, Mexico	Apr. 1994
. *multiseptatum*	*Ca. multiseptata*	STE-U 1589	M.J. Wingfield	*Eucalyptus* sp.	Indonesia	Jan. 1997
		STE-U 1602	M.J. Wingfield	*Eucalyptus* sp.	Indonesia	Jan. 1997
. *naviculatum*	*Ca. naviculata*	STE-U 627	M.J. Wingfield	Soil	Amazonas, Brazil	Apr. 1993
		STE-U 628	M.J. Wingfield	Soil	Amazonas, Brazil	Apr. 1993
. *ovatum*	*Ca. ovata*	UFV 90	M.J. Wingfield	Soil	Amazonas, Brazil	1990
. *parasiticum*	*Ca. ilicicola*	ATCC 46133	S.A. Alfieri	*Cissus rhombifolia*	Florida, U.S.A.	1981
		CBS 190.50	K.B. Boedijn J. Reitsma	*Solanum tuberosum*	Java, Indonesia	Feb. 1948
		STE-U 723	M.J. Wingfield	Soil	Colombia	Jan. 1994
. *pauciramosum*	*Ca. pauciramosa*	STE-U 416	S. de Buisson	*Eucalyptus grandis*	N. Province	Jun. 1990
		STE-U 972	P.W. Crous	Soil	W. Cape	Nov. 1994
		STE-U 925	M.J. Wingfield	Soil	Santa Catarina, Brazil	Apr. 1994
. *penicilloides*	Unknown	CBS 174.55	M. Ookubu	*Prunus* sp.	Hatizyo, Japan	Jan. 1952
. *pseudogracile*	*Ca. gracilis*	AR 2677	A.Y. Rossman	*Manilkara* sp.	Amazonas, Brazil	Unknown
		STE-U 1588	P.W. Crous	Soil	Amazonas, Brazil	1997
. *pteridis*	*Ca. pteridis*	STE-U 2190	P.W. Crous	*Eucalyptus* sp.	Amazonas, Brazil	Oct. 1996
		STE-U 2869	P.W. Crous	*Eucalyptus* sp.	Brazil	1997
		UFV 43	J.C. Dianese	Unknown	Minas Gerais, Brazil	Unknown

Table I. Isolates of *Cylindrocladium* spp. studied (continued).

amorph	Teleomorph	No.	Collector	Substrate	Origin	Date isolated
quinqueseptatum	*Ca. quinqueseptata*	ATCC 16550	Unknown	*Scolopendrium* sp.	Solomon Islands	1965
		STE-U 516	M.J. Wingfield	*Eucalyptus* sp.	Thailand	Aug. 1992
		STE-U 759	P.W. Crous	*Eucalyptus* sp.	Madagascar	Jan. 1994
spathiphylli	*Ca. spathiphylli*	ATCC 44730	S.A. Alfieri	*Spathiphyllum* sp.	Florida, U.S.A.	1982
		STE-U 1624	M.J. Wingfield	Soil	Ecuador	Jun. 1997
		STE-U 1641	M.J. Wingfield	Soil	Ecuador	Jun. 1997
		STE-U 2186	K.I. Kavowas	*Heliconia psitacorum*	Florida, U.S.A.	1986
		STE-U 2188	A. Thompson	*Spathiphyllum* sp.	Mpumalanga, S. Africa	Feb. 1998
rumohrae	*Ca. rumohrae*	UFV 215	A.C. Alfenas	*Rumohrae adiantiformis*	Panama	Jan. 1997
		UFV 218	A.C. Alfenas	*Rumohrae adiantiformis*	Panama	Jan. 1997
		STE-U 1603	R. Pieters	*Adiantum* sp.	The Netherlands	Jan. 1996
scoparium	*Ca. morganii*	ATCC 38227	S.A. Alfieri	*Mahonia bealei*	Florida, U.S.A.	1970
		ATCC 46300	D.M. Benson	*Leucothoe catesbaei*	North Carolina, U.S.A.	1981
		STE-U 1720	N.E. El-Gholl	*Rosa* sp.	Florida, U.S.A.	Jan. 1998
		STE-U 1722	N.E. El-Gholl	*Dodonea viscosa*	Florida, U.S.A	Jan. 1998
spathulatum	*Ca. spathulata*	AR 1844	C.S. Hodges	*Eucalyptus grandis*	Minas Gerais, Brazil	Unknown
		ATCC 62616	N.E. El-Gholl	*Eucalyptus viminalis*	Brazil	1985
theae	*Ca. indusiata*	ATCC 48895	N.E. El-Gholl	*Rhododendron* sp.	Florida, U.S.A.	Unknown
		UFV 16	N.E. El-Gholl	*Rhododendron* sp.	Minas Gerais, Brazil	Unknown
variabile	*Ca. variabilis*	AR 2675	F.C. de Albuquerque	*Didymopanax morototoni*	Pará, Brazil	1990
		UFV 28	A.C. Alfenas	*Eucalyptus* sp.	Minas Gerais, Brazil	Unknown
lindrocladium sp.	*Calonectria* sp.	STE-U 2321	J. Taylor	Soil	Madagascar	Dec. 1998
		STE-U 2322	J. Roux	Soil	Congo	Dec. 1998
		STE-U 2347	N.E. El-Gholl	*Rumohrae adiantiformis*	Florida, U.S.A.	May 1999
		STE-U 599	P.W. Crous	Soil	Brazil	Jan. 1993
		STE-U 1150	M.J. Wingfield	Soil	Colombia	Jan. 1995
		STE-U 1484	P.W. Crous	Soil	Brazil	Aug. 1998
		STE-U 2712	M.J. Wingfield	*Eucalyptus grandis*	Colombia	1998

Phylogenetic analysis

Alignments of sequences were done with the computer package Malign version 2.7 (Wheeler & Gladstein 1991) and assessed manually and are included in the Appendix (Alignment 5). A number of isolates Phylogenetic analysis of aligned DNA sequences was performed using PAUP* 4.0b1 (Swofford 1998) and printed with the help of Treeview Version 1.5 (Page 1996). The large number of indels found in the three non-coding regions proved to be problematic for alignment. Twenty-four highly ambiguous characters in the third intron (base pair 542-567) were excluded from the analysis. Analyses were also done both with gaps treated as a "missing" and as a "fifth base" in PAUP*4.0b1. Finally, in order to limit the influence of large gaps consisting of several characters only the first character of a multi-character gap was coded. Subsequent gap characters were coded as missing data. The former treatment yielded 104 and the latter 1 most parsimonious trees after addition of 1000 random sequences using a heuristic search algorithm. Confidence intervals were determined using 1000 bootstrap replications. . Decay indices were determined with Autodecay Version 4.0 (Eriksson 1998). Data sets were also assessed by using neighbor-joining with uncorrected ("p") distance methods and ties were broken

randomly in PAUP* 4.0b1. The outgroup sequence was obtained from GenBank (*Fusarium subglutinans,* accession number, U34417).

Results

Sequences of the complete open reading frame of the β-tubulin gene from *Gibberella fujikuroi* (*tub2*) were obtained from GenBank (Accession no. U27303). After comparisons with the partial gene sequences obtained from *Calonectria* a similar arrangement for the coding and non-coding regions was observed in this species. Both of these species had three introns and exons in the genomic DNA area amplified. This confirmed the close relationship between these species.

Due to the number of sequences used and the high amount of possible most parsimonious trees, the neighbor-joining analysis method of Saitou and Nei (1987) was applied to a complete data set containing DNA sequence data sets obtained from more than one isolate per species, where possible. This data set consisted of 92 ingroup taxa with 582 total characters of which 316 were parsimony informative. The PCR fragments of the partial β-tubulin gene obtained from the different *Cylindrocladium* species had a variation of 31 base pairs in length. The regions used for analysis differed from 509 to 540 base pairs, while the outgroup *F. subglutinans* had the shortest length (494 base pairs). The tree obtained after 1000 bootstrap repetitions showed a number of clades within two larger clades (Fig. 1). Clade A included the largest number of species, as well as subclades 1-8. Clade B encompassed a smaller number of species (clades 9 and 10). In addition to this, it was evident that most isolates of the same morphological species grouped together with strong bootstrap support.

In order to perform a cladistic analysis a reduced data set of taxa containing a single isolate of each morphological species was used. This data set consisted of 30 ingroup taxa with 579 characters. Twenty four highly ambiguous characters at the end of the third intron were excluded. This left 170 variable parsimony informative characters. A heuristic search with 1000 random additions yielded 104 most parsimonious trees when gaps were treated as missing and a single most parsimonious tree when gaps were treated as a fifth base (Fig. 2). The topology of all these trees were similar, but lower bootstrap support for branches were found when gaps were ignored. The topology of the tree in Fig. 2 is mainly concordant with that of the neighbor-joining tree in Fig. 1 and shows close relationships for the same morphological species. Two large clades are again evident from this tree.

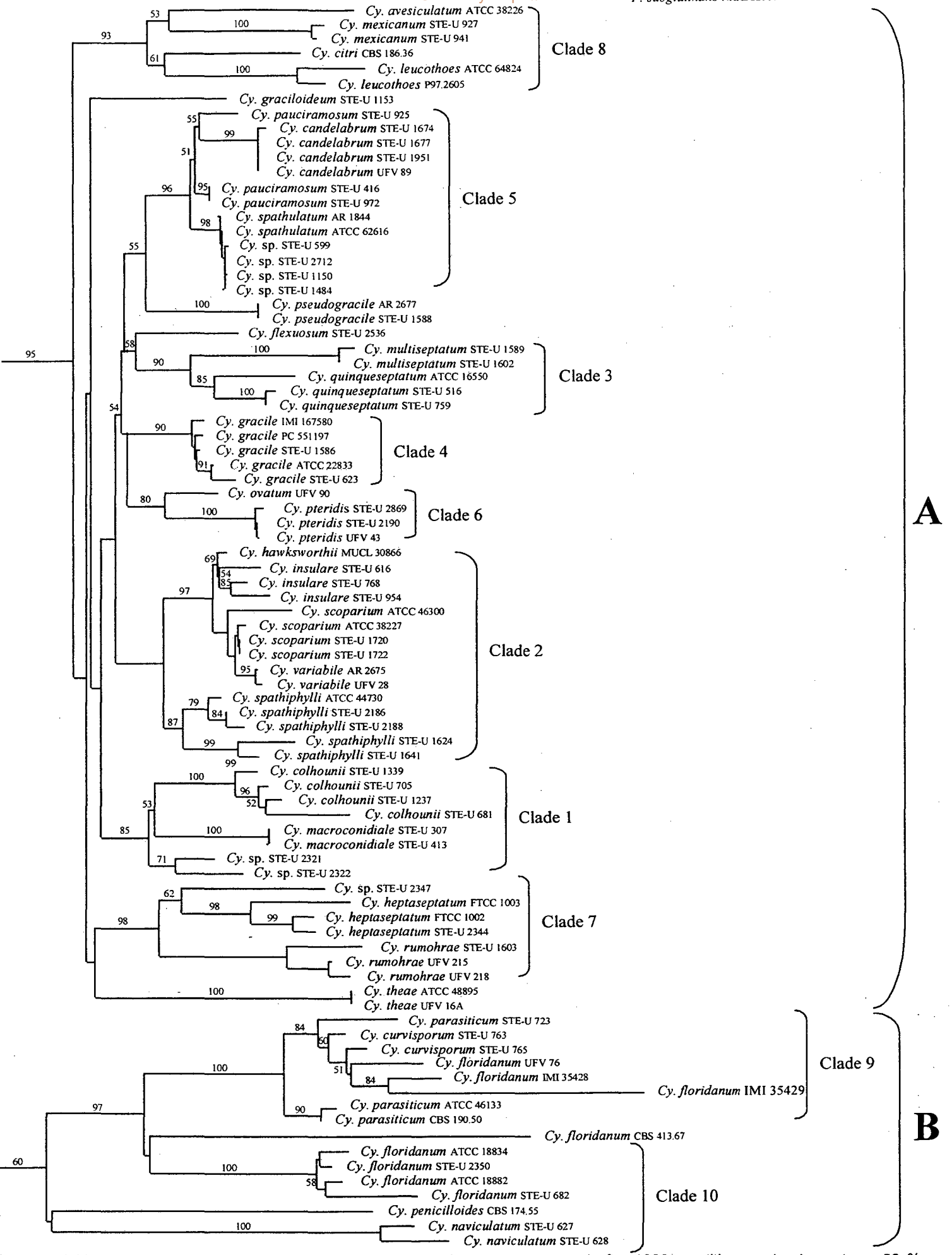

Fig.1. Neighbor-joining tree of total group of taxa. Bootstrap values were assessed after 1000 repetitions and values above 50 % are shown. Clades supported by bootstrap values are indicated by brackets. A *Fusarium subglutinans* sequence (Genbank accession number: U34417) was used as outgroup.

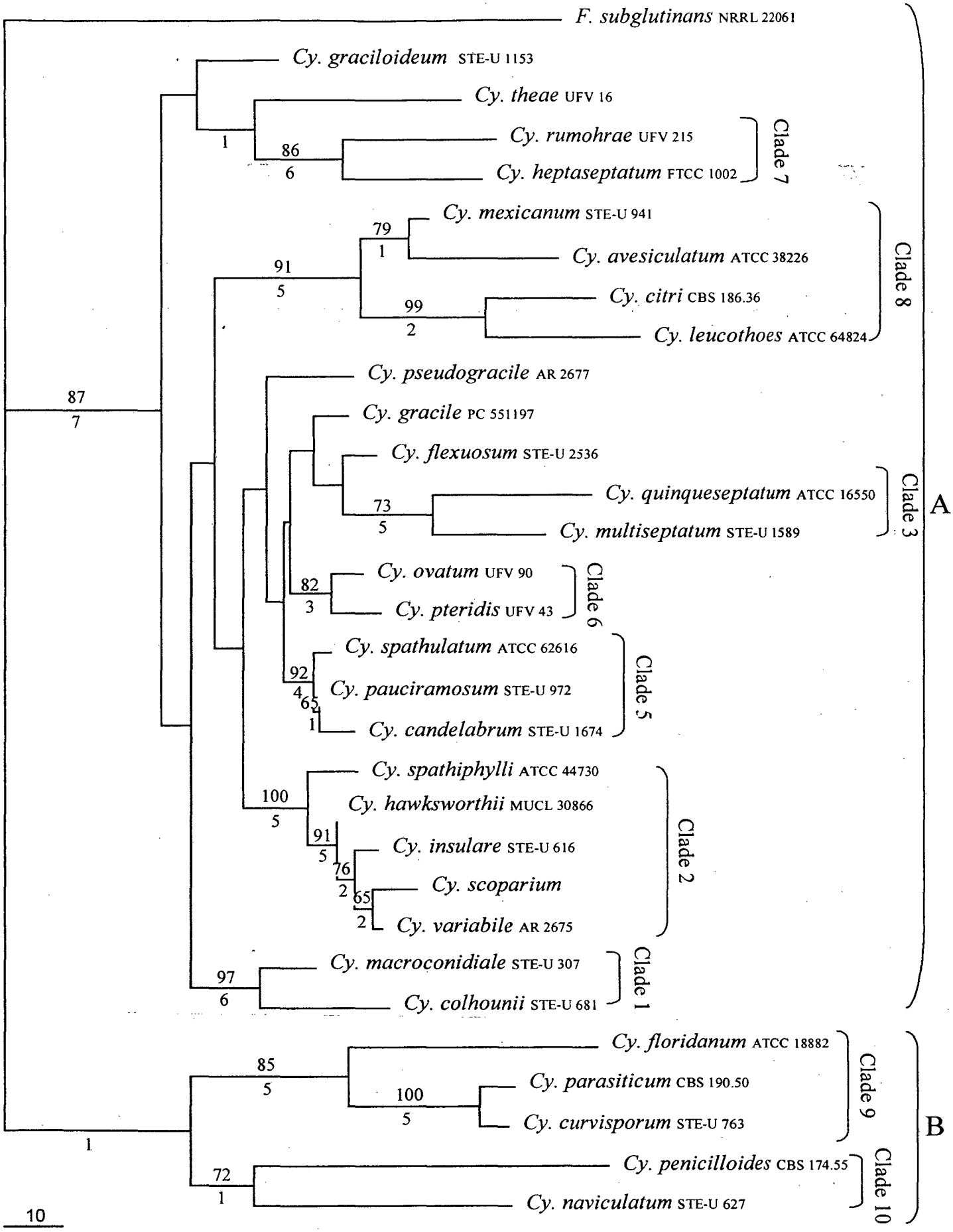

Fig. 2. Parsimonious tree obtained from a subset of *Calonectria* isolates. The most parsimonious tree (958 steps CI = 0.568, RI = 0.551, RC = 0.313) generated with a heuristic algorithm in PAUP* version 4.0b1 from aligned sequences of the 5' end of the β-tubulin gene. Ten steps are indicated by the bar. Gaps were treated as a fifth base. Clade stability was assessed with 1000 bootstrap replications and values above 50 % are shown. Decay indices are shown below branches. A *Fusarium subglutinans* sequence (Genbank accession number: U34417) was used as outgroup.

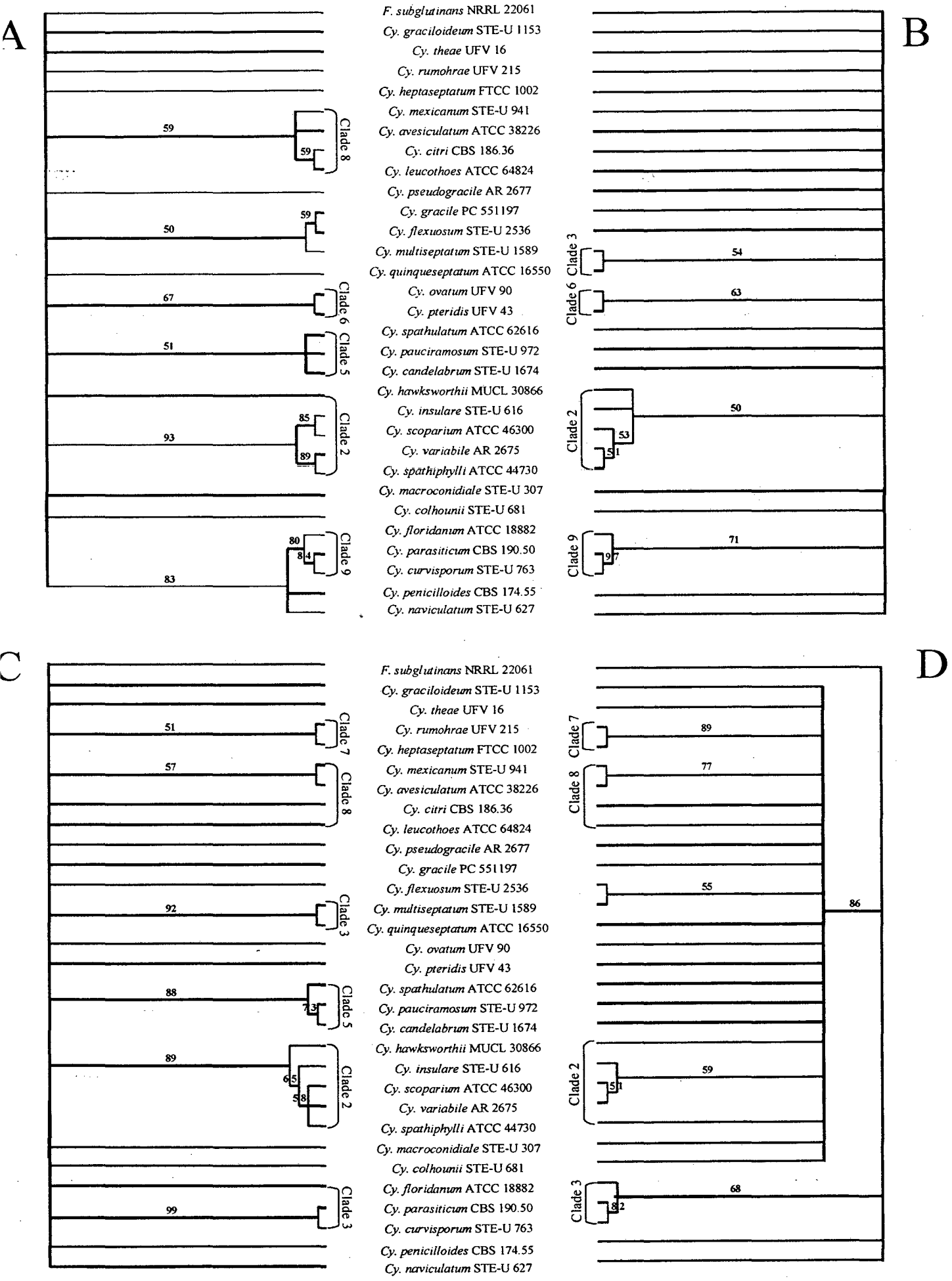

Fig. 3. Neighbor-joining trees of selected areas in the β-tubulin DNA sequence data set. A. intron 1 B. intron 2 C. intron 3 D. coding sequence. Clade stability was assessed after 1000 repetitions.

Several smaller clades are apparent that generally conform to those observed in the neighbor-joining tree (Fig. 1). However, like the neighbor-joining tree no strong bootstrap support was evident for relationships between several clades.

In order to test whether specific areas in the DNA fragments sequenced specifically influenced the compositions of the dendrograms (Figs. 1 and 2) separate analyses for each of the introns found in the area of β-tubulin sequenced were performed. The large number of possible most parsimonious topologies made a cladistic analysis difficult and the neighbor-joining method was used (Fig. 3A-D). The first intron consisted of 167 characters, with 96 informative sites, the second had 74 characters with 52 informative sites and the third 112 characters with 78 informative sites. The protein coding area was also subjected to the same analysis (Fig. 3D). This data set consisted of 230 characters with 45 informative sites.

The separate analyses yielded a number of clades weakly supported by bootstrap values (Fig. 3A-D). A higher number of clades observed in Figs. 1 and 2 were supported in analyses of the three different introns. The protein sequences also provided support for the two large clades A and B observed in Figs. 1 and 2. Only one clade (clade 1) was supported in the neighbor-joining (Fig. 1) and heuristic trees (Fig. 2) but not in any of the separate analyses (Fig. 3). Several clades were supported in more than one of the areas analysed, but in some instances a smaller number of species were supported e.g. clade 2 (Fig. 3A-D). Finally, a close relationship is suggested between previously unsupported clades such as *Cy. multiseptatum* and *Cy. flexuosum* (Fig. 3A, D). The bootstrap support for this relationship was low in Fig 3 and although the most parsimonious tree in Fig. 2 supported this relationship, it was not supported by bootstrap values in that analysis.

Discussion

This study presents the first attempt to consider the phylogeny of all described species in the genus *Cylindrocladium*. Previous studies have used smaller subsets of isolates in order to investigate morphologically defined groups, such as those species with multiseptate conidia (Crous et al 1999) and heterothallic species with small conidia (Part 3). Several of these studies have corroborated morphological species concepts (Crous et al 1997b, Crous et al 1999, Part 3) and also showed the presence of additional genetic groups within morphologically defined taxa (Part 2). Some of these seemingly closely related fungi have also been found to group

distantly in DNA sequence based phylogenies, such as *Cy. mexicanum* Crous & C.L. Schoch, originally described as part of the *Cy. candelabrum* species complex (Part 3). The current study tests whether species in the genus have evolutionary relationships not realised in previous, less encompassing studies.

The β-tubulin DNA sequence based phylogeny of *Cylindrocladium* species has both confirmed some, but contradicted other taxonomic concepts for the genus. Several clades received strong bootstrap support (Figs. 1-3). However, the relationships between most of these indicated clades were not supported by statistical data and remained unresolved. In spite of this, several conclusions could be made.

In the first large clade (A) the isolate representing *Cy. graciloideum* Crous & G.R.A. Mchau formed a distinct branch, basal to clades 1-6. Clade 1 comprises species from the *Cy. colhounii* Peerally species complex. *Cy. macroconidiale* Crous et al was previously described as a large-spored variant of *Cy. colhounii* (Crous & Wingfield 1994) and has only recently been proposed as a separate species based on sequence and morphological data (Crous et al 1999). Isolates STE-U 2231 and 2232 could not be identified as either *Cy. macroconidiale* or *Cy. colhounii* by means of sequence data and possibly represent one or two new phylogenetic species. Although these isolates had smaller conidia than other isolates of *Cy. colhounii,* their taxonomic placement remained unclear. They clustered distantly from the other isolates, but are retained as *Cy. colhounii* for the present.

Cylindrocladium species with ellipsoid and globose vesicles were grouped within clade 2 (Fig. 1). Two well-supported subclades could also be distinguished. In the first, the close relationship between isolates of *Cy. scoparium* and *Cy. variabile* Crous et al was surprising, since they both have distinctive characters. *Cy. scoparium* is heterothallic with exclusively one-septate macroconidia, while *Cy. variabile* is a homothallic species with microconidia and predominantly three-septate macroconidia. Other morphologically distinctive species included in this group are *Cy. insulare* Crous & C.L. Schoch and *Cy. hawksworthii* Peerally. The most notable difference between these two species is the presence of curved conidia in *Cy. hawksworthii.* Preliminary mating studies confirmed the DNA sequence based phylogeny and showed both species to be sexually compatible (results not shown). This calls into question the value of curved conidia as a distinguishing character for species of *Cylindrocladium.* The second sub-clade consisted of isolates of *Cy. spathiphylli* Schoult. et al This cluster contained isolates with two mating strategies

(homo- and heterothallic). Although they are morphologically indistinct, the groups containing isolates with either of these mating strategies could clearly be differentiated based on DNA sequence comparisons.

A number of clades (3, 6 and 7) contained isolates from two distinct morphological species with bootstrap support. In one of these clades (clade 7) isolate P99.0545 had intermediate morphological features between *Cy. heptaseptatum* Sobers et al and *Cy. rumohrae* El-Gholl & Alfenas. The statistical analysis (Fig. 1) only showed low bootstrap support for a similarity with *Cy. heptaseptatum.* This species could thus not be identified with any certainty and could not be delimited as a new species. The species clustering in clades 3 and 7 shared morphological characters such as multiseptate conidia and clavate vesicles. However, the isolates of *Cy. ovatum* El-Gholl et al and *Cy. pteridis* F.A. Wolf in clade 6 had clear differences in vesicle shape and spore size and were never previously considered to be closely related.

Clade 4 contained isolates previously identified as *Cy. gracile* (Bugnic.) Boesew. and *Cy. clavatum* Hodges & L.C. May (ATCC 22833). Variation between various strains were evident. However, these species were recently synonymised on morphological characters (Crous et al 1999) and these results supported this.

Clade 5 contained a number of species with spathulate to obpyriform vesicles. Isolates of two distinct biological species, *Cy. candelabrum* and *Cy. pauciramosum* Crous & C.L. Schoch were included in this group. *Cy. pauciramosum* isolates also exhibited prominent intraspecies variation and one isolate (STE-U 925) showed similarities to *Cy. candelabrum.* In addition to this, a large number of unknown isolates that were obtained from various locations in South America, tentatively identified as a possible new species, clustered strongly with isolates of *Cy. spathulatum* El-Gholl et al These isolates were provisionally identified as *Cy. reteaudii* (STE-U 1150 and STE-U 2712) and were found to be associated with a serious disease of eucalypts in Colombia. After sequence comparisons were made they were found to share the same sequences with those obtained from the type species of *Cy. spathulatum.* On the basis of statistical analysis and re-examination of their morphological characters they were reclassified as *Cy. spathulatum.*

A number of species with variable morphological features were represented in clade 8. Some of these species had umbonate vesicles, (*Cy. mexicanum* and *Cy. leucothoes* El-Gholl et al), but the additional two species had distinctly clavate [*Cy.*

citri (Fawcett & Klotz) Boedijn & Reitsma] or clavate to avesiculate vesicles (*Cy. avesiculatum* Gill et al). As was true for clade 6, these species were not previously considered to be closely related based on morphology.

In addition to those species forming part of well supported clades, several species could not be positioned on the tree with any statistical support (Figs. 1 and 2). Isolates representing the morphological species *Cy. flexuosum* Crous, *Cy. theae* (Petch) Subram. and *Cy. pseudogracile* Crous grouped separately within the first large clade, but without any strong indications of their relationships to other species. However, their distinctiveness as separate species were supported by these data.

The second large clade (B) consisted of clades 9 and 10, as well as additional groups consisting of isolates of a single species. Clade 9 contained isolates from three morphological species - *Cy. floridanum, Cy. parasiticum* Crous et al and *Cy. curvisporum* Crous & Victor. The differentiation for those isolates seen in Fig. 1 is not distinct and will have to be re-evaluated in future. All of these species have sphaeropendunculate vesicles, with differences in conidial shape and septation. The second clade (clade 10) consisted of the type culture of *Cy. floridanum* (ATCC 18882) and additional isolates identified as *Cy. floridanum.* Another isolate of *Cy. floridanum* (UFV 76) also clustered separately from any of the clades. These data distinguished at least three distinctive groups within *Cy. floridanum,* supporting the results of previous studies in this complex (Jeng et al 1997, Victor et al 1997).

This study represents the first instance where it has been possible to investigate the phylogenetic relationship of *Cy. penicilloides* (Tubaki) Tubaki to other species. *Cy. penicilloides* was initially described without any mention of its vesicle morphology (Tubaki 1958). Furthermore its ex-type culture is infertile and no dried specimens could be located. Data from the present study confirmed that it is a distinct species without clear indication of its phylogenetic placement. Similarly, isolates of *Cy. naviculatum* Crous & M.J. Wingf. formed part of the larger clade (B) but could not be placed phylogenetically.

This study has provided an opportunity to compare the morphological species and biological concepts previously used for species in *Cylindrocladium* with a phylogenetic species concept. A similar species concept, based on propositions made earlier by Nixon and Wheeler (1990) has previously been applied on isolates in the *Gibberella fujikuroi* complex by O'Donnell et al (1998). The biological species

described in Part 2 provided a convenient "bench mark" enabling comparison with other species concepts. The existence of biological species within the confines of morphological species delimitations of *Cylindrocladium* was discussed earlier and only slight morphological differentiations was possible for these species (Part 2). Results of Part 3 confirmed the delimitations of these biological concepts as was also validated in the current study. The only morphological characters that agreed to some extent with the DNA based phylogeny presented here was vesicle shape. This was not surprising, as Crous and Wingfield (1994) showed that vesicle shape is an important character, but it had to be assessed under controlled conditions. However, most clades did not exclusively have one vesicle shape and the clavate shape appeared to be present in several clades with unresolved relationships.

In general, this study has emphasised that most morphological and biological species of *Cylindrocladium* represent separate phylogenetic entities. These data were also helpful in confirming identifications of isolates with intermediate or indeterminate morphological characters. Several questions, however, remain unresolved. This includes the close phylogenetic relationships seen between some species previously considered to be distinct based on morphological characters.

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6. Phylogeny of *Calonectria* and selected hypocrealean genera with cylindrical macroconidia*

Abstract

Calonectria is characterised by having brightly coloured, warty perithecia and *Cylindrocladium* anamorphs. Other hypocrealean genera in this complex have a similar perithecial anatomy and anamorph morphology, except those of *Cylindrocladiella* spp. which are smooth-walled and clearly distinct. The aim of this study was to employ DNA sequence analysis to determine the phylogeny of *Calonectria* to other hypocrealean genera with cylindrical macroconidia. The taxonomy of species in *Cylindrocladiella* was also investigated. *Calonectria* was found to form a monophyletic lineage, and this was also true for the anamorph genera *Cylindrocladiella*, *Cylindrocarpon*, *Curvicladium*, *Gliocephalotrichum*, *Gliocladiopsis* and *Xenocylindrocladium*. Although some of these genera have been associated with nectriaceous teleomorphs, *Nectria* sensu stricto is restricted to species with *Tubercularia* anamorphs. Based on molecular data and the distinct anamorph form genera, new teleomorph genera are proposed for *Cylindrocladiella* (*Nectricladiella*), *Gliocladiopsis* (*Glionectria*) and *Xenocylindrocladium* (*Xenocalonectria*). The data also provide support for recognition of previously erected holomorphs for *Cylindrocarpon* (*Neonectria*) and *Gliocephalotrichum* (*Leuconectria*). To date no teleomorph has been reported for *Curvicladium*, although our results suggest that *C. cigneum* is closely related to *Xenocalonectria*. Eight species of *Cylindrocladiella* are recognised, with two having teleomorphs in *Nectricladiella*, namely *N. camelliae* (*Ce. microcylindrica*) and *N. infestans* (*Ce. infestans*).

Introduction

The ascomycete order *Hypocreales* includes fungi found in a variety of ecological niches that are of agricultural, medical and industrial importance. These fungi are characterized by unitunicate asci produced in typically ostiolate, brightly or lightly coloured perithecia, hyaline ascospores and a hamathecium of apical paraphyses

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that disintegrate at maturity (Rogerson 1970, Rossman et al 1999). It is noteworthy that a large number of anamorph genera are associated with the *Hypocreales* (Samuels & Seifert 1987). These can be described as moniliaceous and typically phialidic; conidia are held in lightly to brightly coloured slime (Samuels & Seifert 1987). The importance of anamorph morphology in taxonomic studies is emphasized by the fact that in many economically important species this form is more frequently encountered than the teleomorph, and is thus often the only way to identify a species.

In the *Hypocreales, Nectria* (Fr.) Fr. has included more species than any other genus, with more than 600 described. Traditionally all species having fleshy, uniloculate ascocarps with a hypocrealean centrum with hyaline, non-apiculate, bicellular ascospores, and phialidic anamorphs have been included in *Nectria* (Rossman 1993). In this generic definition, ascospore morphology and septation dominated. Other genera were segregated from *Nectria* on the basis of single characters, including ascospore septation and pigmentation, and synnematous anamorphs. *Calonectria* De Not. (*Ca.*), one of the segregate genera that is of special interest to the current work, was described for species having multiseptate ascospores (Saccardo 1883).

Booth (1959) was the first to use a combination of characters that included anatomy of the perithecial wall, ecology and anamorphs in describing informal taxonomic groups in *Nectria sensu lato*. Subsequent authors (e.g. Samuels 1976, Samuels et al 1991, Brayford & Samuels 1993, Samuels & Brayford 1993) followed Booth in recognizing informal groups within the large genus *Nectria*. In a recent revision of genera of the *Hypocreales* (Rossman et al 1999), many of these groups were given generic status and additional genera were described. *Nectria sensu stricto* was restricted to the type species, *Nectria cinnabarina* (Tode : Fr.) Fr., and species similar to it. Rossman et al (1999) split the large and polyphyletic genus *Nectria* into several smaller genera within two families, the Nectriaceae and the Bionectriaceae. *Calonectria* was included in the Nectriaceae, but was differentiated from *Nectria sensu stricto* on the basis of ascocarp morphology and anatomy, the occurrence of a *Cylindrocladium* Morgan (*Cy.*) anamorph, and basic differences in biology. Although the singular character of ascospore morphology was regarded as less important (Rossman 1983, Crous & Wingfield 1994), ascospores of *Calonectria* are distinct from those of *Nectria*.

In a study based on the sequence alignments of the nuclear large-subunit ribosomal DNA obtained from several genera in the *Hypocreales*, Rehner and Samuels (1995) found some species to group together with *Calonectria.* These authors showed that species of *Calonectria* grouped closely to *Leuconectria clusiae* Rossman et al (anamorph: *Gliocephalotrichum bulbilium* J.J. Ellis & Hesselt.), as well as to *Nectria radicicola* Gerlach & L. Nilsson [anamorph: *Cylindrocarpon destructans* (Zinssm.) Scholten], with two typical species of *Nectria*, *N. pseudotrichia* Berk. & M.A. Curtis [anamorph: *Tubercularia lateritia* (Berk.) Seifert] and *N. cinnabarina*, forming part of this subclade, but grouping more distantly. This phylogeny generally confirmed morphological observations, where similarities were found between the *Gliocephalotrichum* and *Cylindrocladium* anamorphs of *Leuconectria* and *Calonectria* (Rossman & Samuels 1993), the most notable similarities being the formation of cylindrical conidia and brown pigment diffusing in the agar.

In addition to *Gliocephalotrichum,* several other anamorph form-genera are similar to *Cylindrocladium* in producing cylindrical macroconidia, phialidic conidiogenous cells and slimy conidia. Among these are *Cylindrocladiella* Boesew. (*Ce.*), *Gliocladiopsis* S.B. Saksena, *Xenocylindrocladium* Decock et al and *Curvicladium* Decock & Crous. Of these, only *Cylindrocladiella* (Boesewinkel 1982) and *Xenocylindrocladium* (Decock et al 1997) have been linked to teleomorphs, both forming part of *Nectria sensu lato.* We have included representatives of these genera in the present evaluation of holomorphs having cylindrical conidia.

Anamorphs have assumed an increasingly important role in the delimitation of genera of the *Hypocreales* (Rossman et al 1999), to the extent that they have replaced ascospores as the single most important phylogenetically informative character. The advent of data derived from sequences of the rDNA gene has provided independent support for the phylogenetic significance of anamorphs. These data have indicated that some anamorphs that have the 'hypocrealean phenotype' do, in fact, cluster with sexually reproducing genera of the *Hypocreales* (e.g. Spatafora & Blackwell 1993, Rehner & Samuels 1994, 1995, Glenn et al 1996; O'Donnell et al 1998). Moreover, individual anamorph species that are either not known to reproduce sexually, or that are encountered frequently in the absence of sexual reproduction (i.e. perithecia) can be phylogenetically related to sexually reproducing holomorphs (Kuhls et al 1996, 1997).

Additional anamorph genera and species are likely to be linked to the *Hypocreales* as additional DNA sequence data become available. Considering this and recent trends in favour of discarding the phenetically based form-genera of the deuteromycetes (Sutton, 1993), Rossman (1993, this volume) proposed that each hypocrealean teleomorph genus should potentially be linked to one anamorph genus. This is in step with a more holomorphic approach, encompassing both teleomorph and anamorph (Hawksworth, 1993). However, the generic concepts as currently applied still have a strong influence from Saccardo's original taxonomic system (Rossman, 1996, this volume), and detailed cultural and molecular studies are required to clarify anamorph/teleomorph relationships and attain a genus for genus phylogeny as far as possible.

The revision of genera of the *Hypocreales* proposed by Rossman et al (1999) was acknowledged by the authors as a 'starting point' rather than a final statement on the *Hypocreales*. They acknowledged that many of the genera that they delimited are still poly- or paraphyletic, and that new genera remain to be described as new species are discovered through exploration. Most of the genera that were recognized by Rossman et al (1999) have not been assessed using DNA characters. In the present work we consider holomorphs of nectriaceous ascomycetes that have cylindrical conidia whose anamorphs are classified in several genera. These ascomycetes are united by the formation of small, red perithecia that are situated on a small basal stroma, occur singly or in clusters, and have pigments that change colour in 3% KOH. Species of *Calonectria* are characterized by warted perithecia, and clavate, long-stemmed asci without a visible apical discharge mechanism, and large (≤ 25 µm), 1- to multiseptate, hyaline, smooth, fusiform ascospores with obtuse ends that aggregate in the upper third of the ascus. Based on teleomorph morphology alone, however, species of *Calonectria* can only be identified to species complexes, and the anamorph is required for identification at species level. The perithecial wall anatomy of *Calonectria* is not unique, but is also shared by teleomorphs of some *Cylindrocarpon* (*destructans*-complex), *Xenocylindrocladium* and *Gliocladiopsis* species. The latter are primarily distinguished from *Calonectria* based on their ascus and ascospore morphology. That said, teleomorphs of the latter three genera would be difficult if not impossible to distinguish without knowledge of their respective anamorphs. In contrast, the teleomorphs of *Cylindrocladiella* spp. are quite distinct from those discussed above, as they have a smooth, relatively thin-walled *Cosmospora*-like perithecia that easily collapse laterally when dry, a less well-developed basal stroma, and smaller ascospores.

Materials and Methods

Isolates

Strains were either obtained from other culture collections or isolated from infected plant material or soil samples (Crous *et al.,* 1997) and deposited in the culture collection of the Department of Plant Pathology, University of Stellenbosch, South Africa (acronym STE-U, Table 1). Hypocrealean genera are abbreviated as follows: *Calonectria* – *Ca.*; *Cylindrocladium* – *Cy.*; *Cylindrocladiella* – *Ce.*, and *Cylindrocarpon* – *Co.*

Acronyms used to denote culture collections of institutions and individuals from which isolates were obtained include: ATCC – American Type Culture Collection, Virginia, U.S.A.; A.R. – A.R. (A. Y. Rossman), C. T. R. (C. T. Rogerson) and G. J. S. (G. J. Samuels), United States Department of Agriculture, A.R.S., Beltsville, Maryland, U.S.A.; IMI – CABI Bioscience, Bakeham Lane, Egham, U.K.; IMUR – Institute of Mycology, University of Recife, Brazil; MUCL – Mycothèque, Laboratoire de Mycologie Systématique et Appliqée, Université Louvain-la-Neuve, Belgium; STE-U – (see above), and UFV – (A. C. Alfenas), Department of Plant Pathology, University of Viçosa, Viçosa, Minas Gerais, Brazil.

Morphological comparisons

Isolates were cultured on 2% malt extract agar (MEA) (Biolab, Midrand, South Africa), plated onto carnation-leaf agar (CLA) (Fisher *et al.*, 1982; Crous *et al.*, 1992), incubated at 25°C under near-ultraviolet light, and examined after 7 d. Only material growing on carnation leaves was examined. Mounts were prepared in lactophenol, examined using Nomarski interference phase contrast and bright-field phase contrast microscopy, and measurements made at x 1000 magnification. The 95% confidence intervals were determined from at least 30 observations and the minimum and maximum ranges given in parentheses. Cardinal temperature requirements for growth and cultural characteristics were determined after 6 d on MEA, using procedures described by Crous and Wingfield (1994). Colony colours were coded according to Rayner (1970). Sections of perithecia were cut at 10 µm thickness on a CM1100 Cryostat microtome (Leica, Heidelberg, Germany).

Table I. Isolates used in this study.

Anamorph	Teleomorph	Original no.	Collector	Host	Origin
Cylindrocladium scoparium	*Calonectria morganii*	ATCC 38227	S.A. Alfieri	*Mahonia bealei*	Florida, U.S.A.
		ATCC 46300	D.M. Benson	*Leucothoe catesbaei*	North Carolina, U.S.A.
Cylindrocladium floridanum	*Calonectria kyotensis*	ATCC 18882	R.H. Morrison	Peach roots	Florida, U.S.A.
		ATCC 18834	T. Terashita	*Robinia pseudoacacia*	Japan
Cylindrocladium candelabrum	*Calonectria scoparia*	STE-U 1677	A.C. Alfenas	*Eucalyptus* sp.	Amazonas, Brazil
		STE-U 1674	A.C. Alfenas	*Eucalyptus* sp.	Bahia, Brazil
Cylindrocladium multiseptatum	*Calonectria multiseptata*	STE-U 1589	M.J. Wingfield	*Eucalyptus* sp.	Sumatra, Indonesia
		STE-U 1602	M.J. Wingfield	*Eucalyptus* sp.	Sumatra, Indonesia
Cylindrocladiella novae-zelandiae	None described	ATCC 44815	H.J. Boesewinkel	*Rhododendron indicum*	New Zealand
Cylindrocladiella elegans	None described	STE-U 518	P.W. Crous	Litter	Western Cape, South Africa
Cylindrocladiella parva	None described	ATCC 28272	H.J. Boesewinkel	*Telopea speciossima*	New Zealand
		STE-U 373	P.W. Crous	*Pinus radiata*	Western Cape, South Africa
Cylindrocladiella peruviana	None described	IMUR 1843	M.P. Herrera	Ants	Brazil
		STE-U 395	P.W. Crous	*Acacia mearnsii*	KwaZulu Natal, South Africa
Cylindrocladiella lageniformis	None described	UFV 115	A.C. Alfenas	*Eucalyptus* sp.	Brazil
Cylindrocladiella infestans	*Nectricladiella infestans*	ATCC 44816	H.J. Boesewinkel	*Pinus pinea*	New Zealand
		IMI 299376	K.B. Boedijn & J. Reitsma	*Arenga pinnata*	Indonesia
		STE-U 708	M.J. Wingfield	Soil	Hong Kong
		STE-U 2319	J.E. Taylor	Soil	Madagascar
Cylindrocladiella microcylindrica	*Nectricladiella camelliae*	ATCC 38571	W.A. Shipton	*Pinus pinea*	Australia
		STE-U 683	M.J. Wingfield	Soil	Thailand
		STE-U 918	Unknown	Soil	Salta, Argentina
Cylindrocladiella camelliae	None described	STE-U 234	P.W. Crous	*Eucalyptus grandis*	Northern Province, South Africa
		STE-U 277	P.W. Crous	*Eucalyptus grandis*	Northern Province, South Africa
Cylindrocarpon macroconidialis	*Neonectria radicicola* var. *macroconidialis*	GJS 83-162	G.J. Samuels	*Astelia* sp.	New Zealand
Cylindrocarpon destructans	*Neonectria radicicola* var. *radicicola*	AR 2553	A.Y. Rossman	Bark	Venezuela
		CTR 71-322	G.J. Samuels	Host unknown	Venezuela
Cylindrocarpon destructans var. *coprosmae*	*Neonectria radicicola* var. *coprosmae*	CTR 73-152	G.J. Samuels	*Cosmospora* sp.	New Zealand
		GJS_85-182	G.J. Samuels	Unknown	New Zealand
Gliocladiopsis tenuis	*Glionectria tenuis*	STE-U 706	M.J. Wingfield	Soil	Hong Kong
Gliocladiopsis sumatrensis	None described	STE-U 1351	M.J. Wingfield	Soil	Sumatra, Indonesia
Gliocladiopsis irregularis	None described	STE-U 718	A.C. Alfenas	Soil	Sumatra, Indonesia
Curvicladium cigneum	None described	STE-U 1595	C. Decock	Leaf of angiosperm	French Guiana
Xenocylindrocladium serpens	*Xenocalonectria serpens*	STE-U 1144	G.L. Hennebert	Bark of unknown tree	Ecuador

DNA extraction and sequencing

Single conidial isolates were grown on MEA plates. Mycelial mats were removed from the plates and ground to a powder with the help of liquid nitrogen and a mortarand pestle. Approximately 40 mg of ground mycelium was added to 2 ml microtubes containing 600 µl of extraction buffer. The extraction buffer consisted of 1% SDS, 50 mM Tris-HCl (pH 8.0), 150 mM NaCl and 100 mM EDTA. The subsequent protocol was followed as suggested for the Wizard Genomic DNA Purification kit (Promega, Madison, U.S.A.).

Reactions (total volume 25 µl) comprised of 1.5 units Biotaq (Bioline, London, U.K.) with the buffer as recommended by the manufacturer, 1 mM deoxynucleoside triphosphates, 4 mM $MgCl_2$, 0.5 µM primer oligonucleotide and approximately 10 to 30 ng of fungal genomic DNA as target. Reactions were performed on a Rapidcycler (Idaho Technology, Idaho, U.S.A.). Reaction conditions consisted of the following: an initial denaturation for 2 min at 96°C, followed by 30 cycles of 15 s at 96°C, 30 s at 55°C and 35 s at 75°C with a slope of 1.0. A last elongation step of 2 min at 75°C was included. DNA was amplified using the primers ITS1 and ITS4 (White et al 1990). The region amplified was the 5.8S ribosomal gene and the two internal transcribed spacers (ITS1 and ITS2). An approximately 540 bp fragment was amplified. The PCR products were sequenced using the ABI Prism 377 DNA Sequencer (Perkin-Elmer, Norwalk, Connecticut). Sequencing conditions were as described in Part 2.

Phylogenetic analysis

Sequences were aligned with the computer package Malign version 2.7 (Wheeler & Gladstein 1991) and adjusted manually. Phylogenetic analysis of aligned DNA sequences was performed using PAUP* Version 4.0b1 (Swofford 1998) and printed with the help of Treeview Version 1.5 (Page 1996). In order to limit the influence of large gaps consisting of several characters only the first character of a multi-character gap was coded. Subsequent gap characters were coded as missing data. Having done this, the analyses were done treating these single character gaps as fifth characters. A number of strains representing different species in each genus were selected for the generic analysis (Fig. 1). In this instance a heuristic search option with 1000 random addition sequences was used. The analysis for species with *Cylindrocladiella* anamorphs were performed using the branch and bound search option. Confidence intervals were determined using 1000 bootstrap

replications in all cases. Decay indices were determined with Autodecay Version 4.0 (Eriksson 1998). A partition homogeneity test was performed in PAUP* Version 4.0b1 in order to test whether phylogenies obtained from the ITS and β-tubulin data sets differed significantly. This was done heuristically with 1000 replications. Data sets were also analyzed by using Neighbor-Joining with uncorrected ("p") and maximum-likelihood distance methods in PAUP* Version 4.0b1.

Taxonomy

A phylogenetic analysis of all species in this study, based on the DNA sequence of the two flanking internally transcribed spacers (ITS1 and ITS2) and the 5.8S ribosomal RNA gene is shown in Fig. 1. When gaps were coded as missing the number of possible most parsimonious trees was in excess of 1000. With gaps treated as a fifth character only one most parsimonious tree was found. No difference in the number of most parsimonious trees was found when all subsequent gap characters after the first gap character was coded as missing. However, this reduced the number of parsimony informative sites from 163 to 139. All species clustered in accordance with their distinctive anamorphs and the groupings evident from this are discussed in more detail below.

Calonectria/Cylindrocladium, Curvicladium, Nectria/Xenocylindrocladium

The type species of *Calonectria* is *Ca. daldiniana* De Not., now considered a synonym of *Ca. pyrochroa* (Desm.) Sacc. (Rossman 1979a). *Calonectria* encompasses species with brightly coloured ascocarps that become red in 3% KOH solution (KOH+), have a thick perithecial wall that consists of large cells and have a darkened stromatic base. Ascospores of *Calonectria* tend to be longer than 25 µm, are fusiform, and usually phragmosporous. *Cylindrocladium* spp. have been linked to *Calonectria* teleomorphs exclusively (Rossman 1993). Rossman (1979b) redisposed many species ascribed to *Calonectria*.

The anamorph genus *Cylindrocladium* was originally based on *C. scoparium* Morgan, a species that was collected from a dead pod of honey locust (*Gleditsia triacanthos* L.) in Ohio, U.S.A. (Morgan 1892). Species in this genus are well-known plant pathogens and have been isolated from all continents in tropical and subtropical zones world-wide (Crous & Wingfield 1994). Species concepts in *Cylindrocladium* have been defined based on the dimensions and septation of conidia, phialide shape, stipe length, cultural characteristics, as well as the shape and diameter of the

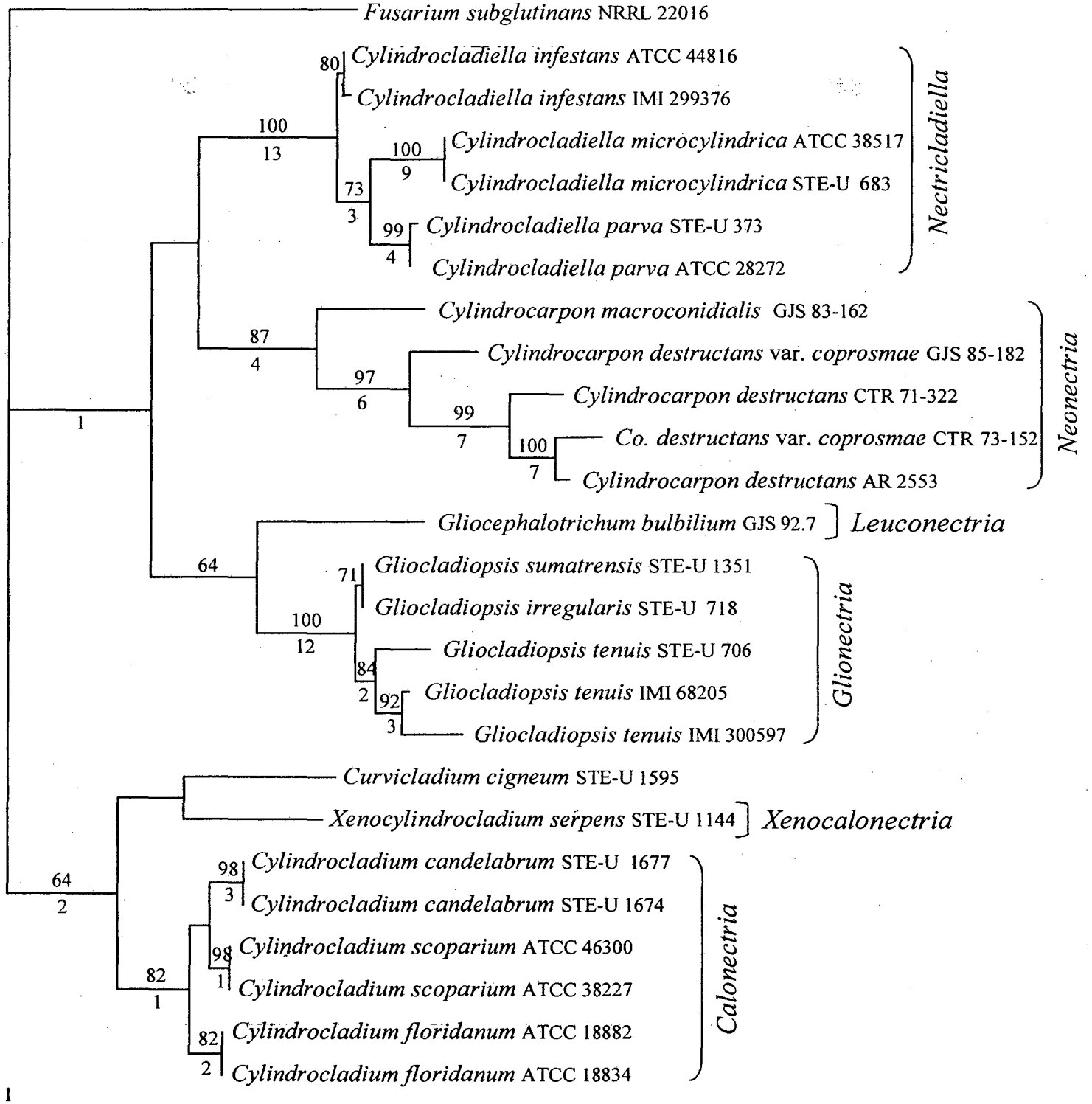

Fig. 1. One of four most parsimonious trees (405 steps CI =0.681 RC =0.554 RI =0.812) obtained with a heuristic search in PAUP* version 4.0b1 and 1000 random addition sequences. Bootstrap values are shown above branches and decay indices below. Characters used were based on a data set comprising of ITS1 and 2 as well as the 5.8S ribosomal gene DNA sequences.

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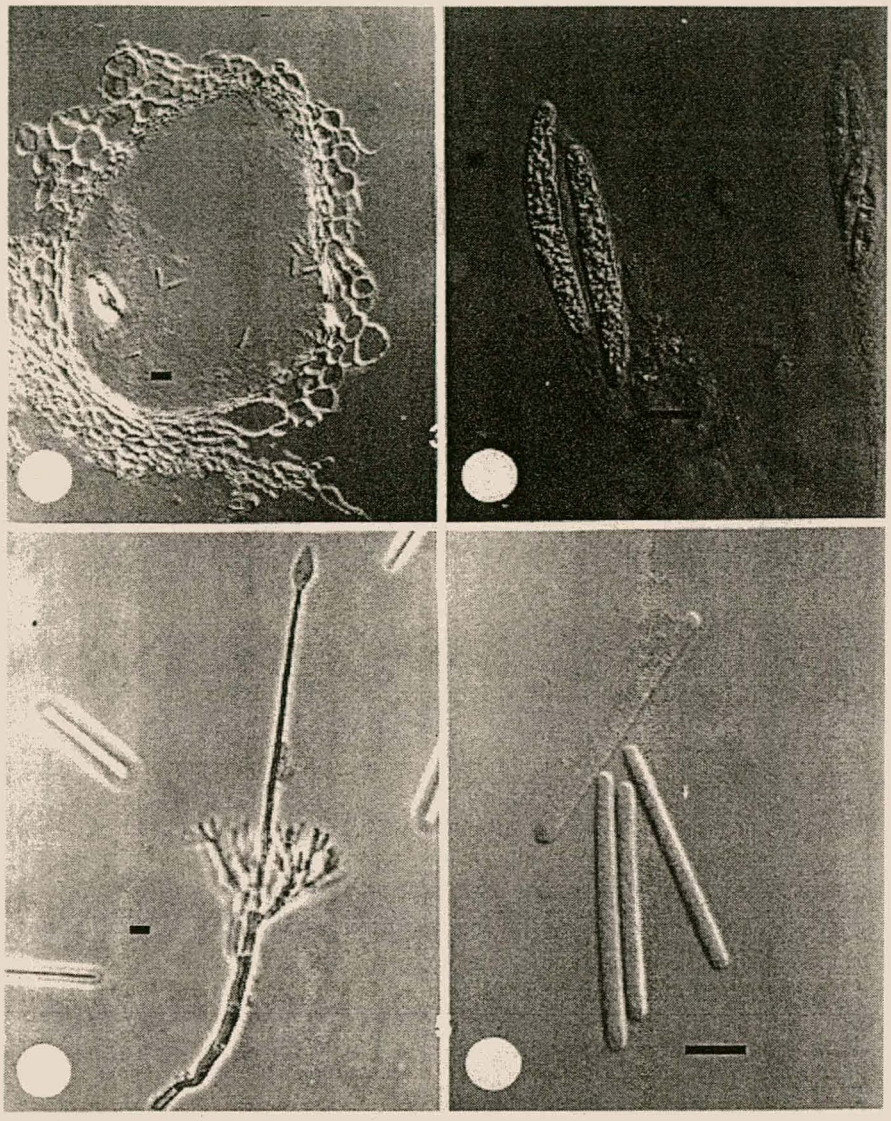
terminal vesicle found on stipes eminating from the conidiophores (Figs. 2-5) (Crous & Wingfield, 1994).



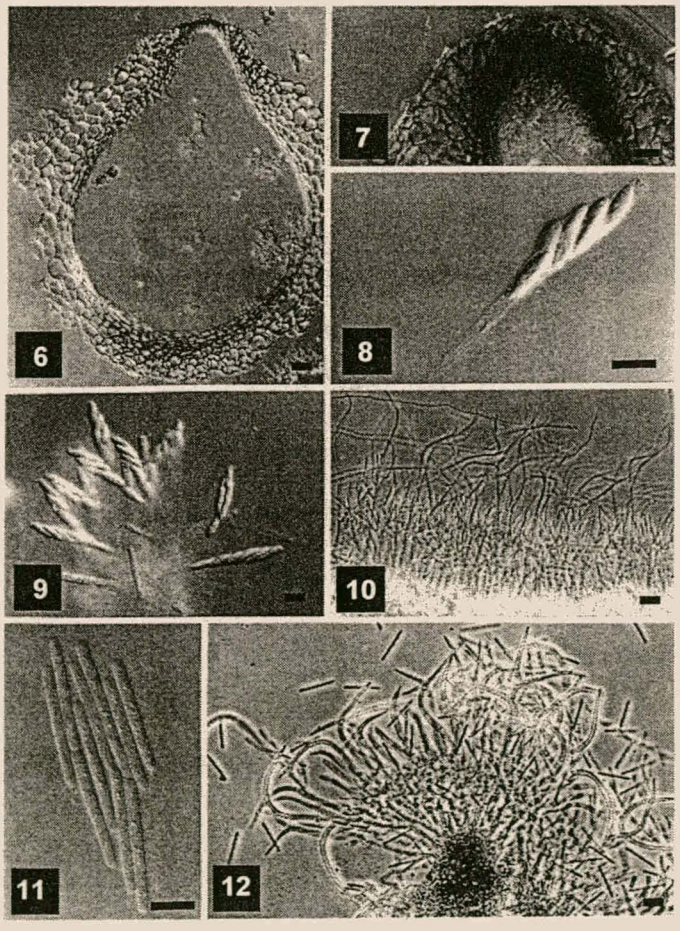
Figs. 2-5. *Calonectria mexicana* and its anamorph *Cylindrocladium mexicanum*. 2. Vertical section through a perithecium. 3. Asci with ascospores. 4. Conidiophore with extending stipe and terminal vesicle. 5. One-septate conidia. Bars = 10 µm.

Previous studies, using sequence data obtained from ITS, β-tubulin and the HMG box of *MAT-2*, showed that concordant phylogenies could be derived from the gene trees based on different loci in this genus (Crous et al 1999, Part 3). Some of these species were also shown to have interfertility barriers, thus complying with a biological species concept (Part 1). Although these results generally coincided with morphological species concepts, in some cases several phylogenetic species (based on DNA sequence data) and biological species could be described within the parameters of a morphological species.

Two new hyphomycete genera with penicillate conidiophores and unique stipe elongations were described that also appeared to be morphologically closely related

to *Cylindrocladium* (Decock et al 1997, Decock & Crous 1998). *Xenocylindrocladium serpens* was described from Ecuador as the type species of this genus, while its teleomorph, distinct from *Calonectria,* was described in *Nectria* as *N. serpens* Decock *et al.* (Decock et al 1997). A similar fungus, *Curvicladium cigneum* Decock & Crous, was later described as yet another new genus in this complex, characterized by curved, rough, sparsely septate stipe extensions (Decock & Crous 1998). No teleomorph has yet been reported for *Curvicladium* (Fig. 12).

The species of *Calonectria* included in this study all produced *Cylindrocladium* anamorphs characteristic of this genus, and formed a clearly distinct clade, strongly supported by high bootstrap values (Fig. 1). The *Calonectria* clade was shown to be closely related to *Xenocylindrocladium* and *Curvicladium* (Fig. 1). Their close proximity to *Calonectria* suggests a shared ancestor. This hypothesis will still have to be tested further, however, using additional gene trees.



Figs. 6-12. *Nectria serpens* and *Curvicladium cigneum*. 6-11. *Xenocalonectria serpens* and its anamorph *Xenocylindrocladium serpens*. 6. Vertical section through perithecium. 7. Ostiolar region of perithecium. 8-9. Cylindrical asci with apical apparatus. 10. Conidiophores with stipe extensions. 11. One-septate conidia. *eum*. 12. Conidiophores and conidia of *Curvicladium cigneum*. Bars = 10 μm.

Based on the phylogenetic distance shown in Fig. 1, as well as distinct morphological differences in the anamorph of *Xenocylindrocladium*, we propose the following new holomorph genus:

Xenocalonectria Crous & C.L. Schoch gen. nov.
Anamorphe: *Xenocylindrocladium* Decock, Hennebert & Crous
Typus: *Xenocalonectria serpens* (Decock, Hennebert & Crous) Crous & C.L. Schoch
Perithecia superficialia, solitaria vel aggregata, globosa ad subglobosa, verrucosa, lutea usque ad rubra, cum basi obscure rubra stromatica, KOH+; pariete perithecii ex duabus regionibus composito: strato exteriore ex *textura globulosa* cum parietibus crassitunicata, strato interiore ex cellulis compressis texturae angularis; periphyses ostioli hyalinae, tubulares cum apicibus rotundatis. Asci unitunicati, octospori, cylindrici basi elongata, apice applanato et apparatu apicali refringente. Ascosporae in parte superiore asci aggregatae, hyalinae, late vel anguste ellipsoideae, leves, medio uniseptatae.

Perithecia superficial, solitary or in clusters, globose to subglobose, warted, yellow to red and with a dark red stromatic base, KOH+; perithecial wall consisting of two regions: outer layer of thick-walled *textura globulosa*, inner layer of compressed cells of *textura angularis*; ostiolar periphyses hyaline, tubular with rounded ends. Asci unitunicate, 8-spored, cylindrical, with long basal stalks, a flattened apex, and a refractive apical apparatus. Ascospores aggregated in the upper third of the ascus, hyaline, broadly to narrowly ellipsoidal, smooth, medianly 1-septate. Anamorph is *Xenocylindrocladium*.

Xenocalonectria serpens (Decock, Hennebert & Crous) Crous & C.L. Schoch, *comb.nov.* — (Figs. 6-11).
≡ *Nectria serpens* Decock, Hennebert & Crous, Mycol. Res. 101: 788. 1997.
Anamorph: *Xenocylindrocladium serpens* Decock, Hennebert & Crous, Mycol. Res. 101: 788. 1997.

Holotypes. ECUADOR. SUCUMBIOS: Reserva de Producción Faunistica, Cuyabeno, Tierra firme, bark of a fallen tree trunk, Jul. 1993, *G.L. Hennebert*, MUCL 39315a, holotype of teleomorph, MUCL 39315b, holotype of anamorph (culture ex-type: MUCL 39315 = STE-U 1144).

This species was described in full by Decock *et al.* (1997). Ascospores aggregated in the upper third of the ascus, hyaline, broadly to narrowly ellipsoidal, smooth, with granular contents, (8-)12-20(-25) x 4-5(-6) µm, medianly 1-septate, becoming constricted at the septum, and developing up to 2 septa with age. Macroconidia

cylindrical, hyaline, straight with rounded ends, 1-septate, (24-)27-33(-36) x 2.5-3(-3.5) µm.

Cultures. Colony colour (reverse) 13K, amber brown (Rayner 1970). Chlamydospores in extensive numbers, with medium to extensive sporulation on aerial mycelium.

Cardinal temperature requirements for growth. Minimum above 5°C, optimum 25-30°C, maximum below 35°C.

Substrate. Bark of fallen trees.

Nectria/Cylindrocarpon

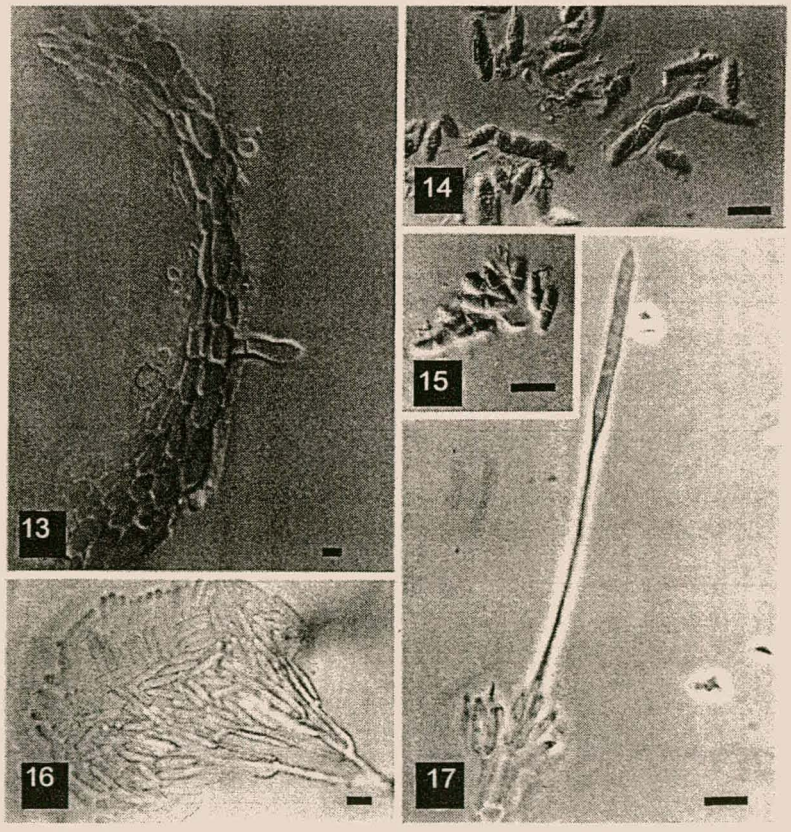
Perithecial anatomy in *N. radicicola* and its relatives is similar to that of *Calonectria* (Samuels & Brayford 1990). Samuels and Seifert (1987) commented on the similarity between *Cylindrocladium* and the *Cylindrocarpon* Wollenw. anamorphs of *N. radicicola* and closely related species. *Calonectria* and the nectriaceous species centred around *N. radicicola* are distinguished primarily by the respective occurrence of *Cylindrocladium* and *Cylindrocarpon* anamorphs, as well as on their distinct ascus and ascospore morphology (Samuels & Brayford 1990). Ascospores of the *radicicola*-group are, however, much smaller than those of *Calonectria* spp. Rossman et al (1999) referred many holomorphs having *Cylindrocarpon* anamorphs to *Neonectria* Wr. *Nectria radicicola* (which was not transferred to *Neonectria*) and its relatives, all of which have *Cylindrocarpon* anamorphs, cluster in a clade (Fig. 1) that is sister to *Cylindrocladiella*. Whether *N. radicicola* is representative of all holomorphs having *Cylindrocarpon* anamorphs (*Neonectria*) is currently being evaluated (F. Mantiri & G. Samuels pers. comm.).

Nectria/Cylindrocladiella

A new anamorph genus was erected in 1982 to accommodate five small-spored species of *Cylindrocladium* (Boesewinkel, 1982). This new genus, *Cylindrocladiella,* was reported to have different conidiophore branching patterns, conidial shapes, dimensions as well as cultural characteristics. The recognition of *Nectria camelliae* Shipton as the teleomorph for one of these species made a strong case for the delimitation of the new genus. More recent studies have confirmed the genera *Cylindrocladium* and *Cylindrocladiella* to be distinct (Crous & Wingfield, 1993; Crous

et al 1994, Victor et al 1998). Samuels et al (1991) allocated *N. camelliae* (anamorph: *Ce. infestans*) to *Nectria* subg. *Dialonectria,* while Rossman et al (1999), in a re-evaluation of the group, placed it in *Cosmospora* as *C. camelliae* (Shipton) Rossman & Samuels, based on its perithecial morphology and anatomy. As presently defined by Rossman et al (1999), *Cosmospora* is heterogeneous in having diverse anamorphs, including *Cylindrocladiella*. In comparison to *Calonectria* spp., the perithecial wall of *Cosmospora camelliae* is smooth, narrow, and its ascospores are much smaller.

Victor et al (1998) recognised seven species in *Cylindrocladiella.* All these species could be distinguished based on RFLP and AT-DNA data, as well as morphology. The AT-DNA data showed differences in the profiles of the ex-type isolates of *Cosmospora camelliae* (ATCC 38571; teleomorph) and *Ce. infestans* (ATCC 44816; anamorph). One restriction enzyme also showed differences in the RFLP profiles, but cultural and morphological characters have shown little variation other than conidial length (Victor et al 1998).



Figs. 13-17. *Nectricladiella infestans* and its *Cylindrocladiella microcylindrica* anamorph. 13. Vertical setum through a perithecium, showing smooth wall and hyphal mute, brown seta. 14. Broken asci and ascospores 15. Ascospores. 16. Conidium and conidia. 17. Conidiophore with stipe extensions and terminal cylindrical vesicle. Bars = 10 µm.

The *Nectria/Cylindrocladiella* clade has strong bootstrap support (Fig. 1). Relationships between the groupings *Nectria/Cylindrocladiella* and *Neonectria* are equivocal because the clade that includes these two groups received only weak

bootstrap support. However, both groups are strongly supported as separate entities in accordance with their different anamorphs. Two areas of the genome were utilised in order to investigate relationships in those species with *Cylindrocladiella* anamorphs. When the phylogenies derived from data sets obtained from the ITS regions flanking the 5.8S ribosomal RNA gene as well as the 5' end of the β-tubulin gene were compared in a partition homogeneity test, they were not found to differ significantly (P = 0.33, where P < 0.05 denotes significance) (Fig. 18). The number of parsimony informative sites in the ITS data set (25) were much less than those in the β-tubulin data set (109). A similar trend occurred in *Calonectria* species (Part 2).

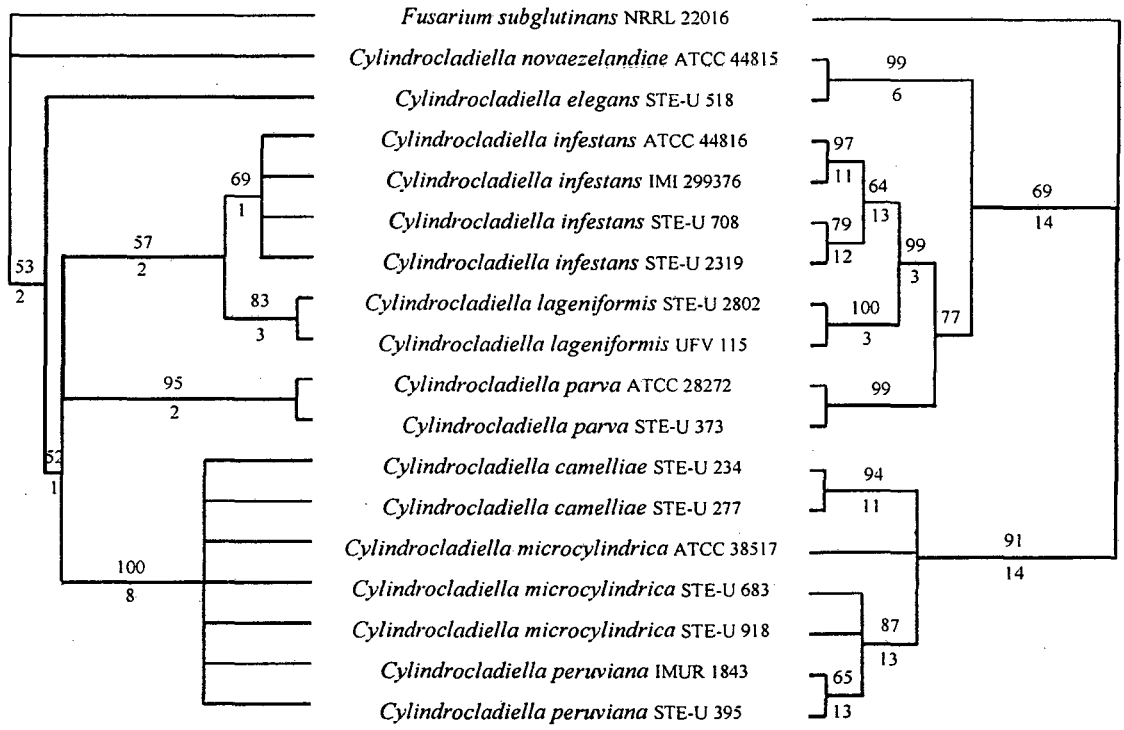


Fig. 18. Concordance of two most parsimonious trees obtained from the ITS (left) and β-tubulin (right) data sets. The ITS data set yielded one most parsimonious tree and β-tubulin yielded four. Trees were obtained with a branch and bound search in PAUP* version 4.0b1 and 1000 random addition sequences. Bootstrap values are shown above branches and decay indices below.

The DNA sequence data of both ITS and β-tubulin loci have shown clear differences between two groups of isolates identified as *Ce. infestans* (Fig. 18). One group is characterised by the culture on which the name *Cosmospora camelliae* is based, while the other is characterised by the culture on which the name *Ce. infestans* is based. Furthermore, an isolate from the "anamorph type grouping", recently obtained from Madagascar, produced a teleomorph in culture. The clear differences shown in the molecular data, based on two DNA sequence data sets and the

previous characters described by Victor *et al.* (1998), suggest that *Ce. infestans* contains more than one genetically distinct taxon. These are described as new below.

Cylindrocladiella microcylindrica, *Ce. peruviana* (Bat., J.L. Bezerra & S. Herrera) Boesew. and *Ce. camelliae* (Venkataram & C.S.V. Ram) Boesew. were shown to cluster together in the tree based on the ITS data (Fig. 18). Likewise, the β-tubulin data set showed support for a distinct grouping of these species, but could differentiate between them (Fig. 18). Previously, Crous and Wingfield (1993) synonymized *Ce. peruviana* with *Ce. camelliae* based on similarity in morphology. Conidiophores of both of these species have ellipsoid to lanceolate vesicles and similar conidial dimensions as well as similar temperature growth relationships, but Victor et al (1998) separated them based on differences in RFLP profiles as well as vesicle width and taper. The data in Figs. 1 and 18 show that this close relationship is also reflected in the molecular characters used here. The β-tubulin data set supported their separation. Further variation in this clade based on the β-tubulin sequences was also evident. Although molecular data confirmed *Ce. camelliae* and *Ce. peruviana* to be different, isolates of the third species, *Ce. microcylindrica*, exhibited similarities to these two taxa, and more isolates will have to be studied to clearly resolve the boundaries among these species.

The relationships of the other species in the genus, *Ce. elegans* Crous & M.J. Wingf., *Ce. novaezelandiae* (Boesew.) Boesew., *Ce. lageniformis* Crous *et al.* and *Ce. parva* (P.J. Anderson) Boesew. were represented as separate entities in both data sets (Fig. 18). A close relationship between *Ce. novaezelandiae* and *Ce. elegans* is only supported by the β-tubulin data set. Based on the distinct clade of *Cylindrocladiella* species identified here, as well as their unique morphological traits, backed up by molecular data, a new holomorphic genus is proposed below.

Nectricladiella Crous & C.L. Schoch gen. nov.
Anamorphe: *Cylindrocladiella* Boesewinkel
Typus: *Nectricladiella camelliae* (Shipton) Crous & C.L. Schoch
Perithecia superficialia, solitaria, stromate basalari egentes, globosa ad obpyriformia, collabentia ubi arida, levia, numerosis setis parvis ex pagina parietis perithecii orientibus; apice et corpore perithecii rubro, basi brunnea, KOH+, ostiolum ex cellulis columnaribus compositum, cum periphysibus hyalinis inconspicuis indutum; pariete

perithecii ex 3-4 stratis texturae angularis composito cum cellulis compressis, hyalinis. Asci unitunicati, octospori, cylindrici, sessiles, tenuitunicati et apice applanato. Ascosporae uniseriatae, superpositae, hyalinae, ellipsoideae ad fusiformes, cum apicibus obtusis, uniseptatae.

Perithecia superficial, solitary, basal stroma absent, globose to obpyriform, collapsing laterally when dry, smooth, with several minute, brown setae arising from the perithecial wall surface, red, KOH+; ostiole consisting of clavate cells, lined with inconspicuous, periphyses; perithecial wall consisting of a single region of 3-4 cell layers of *textura angularis*, which become hyaline and slightly flattened towards the centre. Asci unitunicate, 8-spored, cylindrical, sessile, thin-walled, with a flattened apex, and a refractive apical apparatus. *Ascospores* uniseriate, overlapping, hyaline, ellipsoid to fusoid with obtuse ends, smooth, 1-septate. Anamorph is *Cylindrocladiella*.

Nectricladiella camelliae (Shipton) Crous & C.L. Schoch comb. nov.
≡ *Calonectria camelliae* Shipton & C. Booth, Trans. Br. Mycol. Soc. 69: 59. 1977 (*nom. nud.*).
≡ *Calonectria camelliae* Shipton, Trans. Br. Mycol Soc. 72: 163. 1979.
≡ *Nectria camelliae* (Shipton) Boesewinkel, Can. J. Bot. 60: 2293. 1982.
≡ *Cosmospora camelliae* (Shipton) Rossman & Samuels, Stud. Mycol. 42: 118. 1999.
Anamorph: *Cylindrocladiella microcylindrica* Crous & D. Victor sp. nov.

Etymology. *Micro* + *cylindrica*, named after its smaller conidia and cylindrical vesicles.

Holotypes. AUSTRALIA. QUEENSLAND: Fruit of a rainforest tree, W.A. Shipton, 1973, IMI 174836, holotype of teleomorph PREM 51724, holotype of anamorph (culture ex type: ATCC 38571 = STE-U 2375).

Characteribus culturae, morphologia et temperaturae provento *C. infestanti* similis sed distincta propter conidia minoria. Conidia hyalina, 1-septata, cylindracea, apicibus obtusis, (10-)12-14(-15) x 2(-3) µm.

Perithecia described in full by Shipton (1979). Ascospores hyaline, median septate, unconstricted, oval to ellipsoid, 6.5-10.5 x 2.5-4 µm. Anamorph morphology and

cultural characteristics similar to those of *Ce. infestans*, but conidia shorter (10-)12-14(-15) x 2(-3) µm, than those of the former (10-)14-16(-20) x 2(-3) µm.

Cultures. Colony colour (reverse) 19D, buff yellow (Rayner 1970). Chlamydospores in medium numbers, arranged in chains.

Cardinal temperature requirements for growth. Minimum above 5°C, optimum 25°C, maximum below 35°C.

Substrate. Soil.

Distribution. Australia, Argentina, Brazil, Thailand.

Nectricladiella infestans Crous & C.L. Schoch sp. nov.
Anamorph. Cylindrocladiella infestans Boesewinkel, Can. J. Bot. 60: 2290. 1982.

Holotypes. MADAGASCAR: Rana, isolated from soil, J.E. Taylor, 1998, PREM 56380, holotype of teleomorph (culture ex type: STE-U 2319). NEW ZEALAND: Isolated from *Pinus pinea,* H.J. Boesewinkel, CBS 487.76, holotype of anamorph (culture ex type: ATCC 44816 = STE-U 2380).

Description. Perithecia superficialia, solitaria, sine stromate basale, globosa ad obpyriformia, 150-200 µm alta et lata, collabentia ubi arida, levia, cum numerosis setis parvis ex pagina parietis perithecii orientibus; apice et corpore perithecii rubro, base brunnea, 3% KOH + [bene agens in 3% KOH], parte superiore rubro brunnea facta, base brunneo rubra facta; ostiolum ex cellulis columnaribus compositum, cum periphysis hyalinis inconspicuis; pariete perithecii 10-15 µm lato, ex 3-4 stratis texturae angularis composito; interiore regione hymenii ex 3-4 stratis composita, cum cellulis compressis, hyalinis. Asci unitunicati, octospori, cylindrici, leviter clavati in maturitate, sessiles, cum parietibus tenuibus et apice applanato, apparatu apicale refracto, 35-60 x 4-6 µm. Ascosporae: 8 in uno asco, uniseriatae, superpositae, hyalinae, ellipsoideae ad fusiformes, cum apicibus obtusis, leves, altissimae ad medium septum vel ad regionem leviter superiorem, non constrictae, 8-10(-12) x 3-3.5 µm; ex perithecio extantes, profusae et hyalinae. Morphologia anamorpha et characteristica in cultura Ce. microcylindricae similis sed cum conidiis longioribus, (10-)14-16(-20) x 2(-3) µm.

Perithecia superficial, solitary, basal stroma absent, globose to obpyriform, 150-200 µm high and thick, collapsing when dry, smooth, with several minute, brown setae arising from the perithecial wall surface; apex and perithecial body red, base brown, reacting positive in 3% KOH, upper part turning red-brown, base becoming brown-red; ostiole consisting of columnar cells, lined with inconspicuous, hyaline periphyses; perithecial wall 10-15 µm thick, consisting of 3-4 layers of *textura angularis*; inner hymenium region of 3-4 layers of flattened, hyaline cells. *Asci* unitunicate, 8-spored, cylindrical, becoming slightly clavate at maturity, sessile, thin-walled, with a flattened apex, and a refractive apical apparatus, 35-60 x 4-6 µm. *Ascospores* 8 per ascus, uniseriate, overlapping, hyaline, ellipsoid to fusoid with obtuse ends, smooth, widest at median septum or slightly above, unconstricted, 8-10(-12) x 3-3.5 µm; extruding from perithecia in yellow mass. Anamorph morphology and cultural characteristics similar to those of *Ce. microcylindrica*, but conidia longer, (10-)14-16(-20) x 2(-3) µm.

Habitat. *Arenga pinnata*, *Pinus pinea*, soil.

Distribution. New Zealand, Madagascar, Hong Kong, Indonesia.

Leuconectria/Gliocephalotrichum

The similarities in perithecial anatomy between *Leuconectria* and *Calonectria* have been noted before (Rossman & Samuels 1993). Their *Gliocephalotrichum* and *Cylindrocladium* anamorphs also share several characteristics. Besides having penicillate conidiophores, cylindrical conidia, and forming chlamydospores in culture, both anamorph genera have stipe extensions, even though they originate from different areas on the conidiophores. Cultural characteristics are also similar. Furthermore, both teleomorphs have KOH+, solitary, red perithecia. Perithecia of *Leuconectria* are distinct, however, in having a white covering that is absent in species of *Calonectria*. Thus far, isolates of *Leuconectria* have been obtained from decaying leaves, fruits, or from soil, and nothing is known about their potential status as plant pathogens. It is similar to the other taxa dealt with in this paper in that they occupy similar habitats, all basically being soil fungi that converge in forming more or less similar, small, red perithecia. This is in contrast to *Cylindrocarpon sensu stricto*

(exclusive of the *radicicola* complex), which are primarily lignicolous and canker-forming.

The DNA sequence data employed here support the separation of *Leuconectria* from other genera in this study (Fig. 1). The data were ambiguous about the relationship of *Leuconectria* to other genera that have cylindrical conidia while at the same time confirming the close relationship with *Calonectria* (see also Rehner & Samuels 1995).

Gliocladiopsis

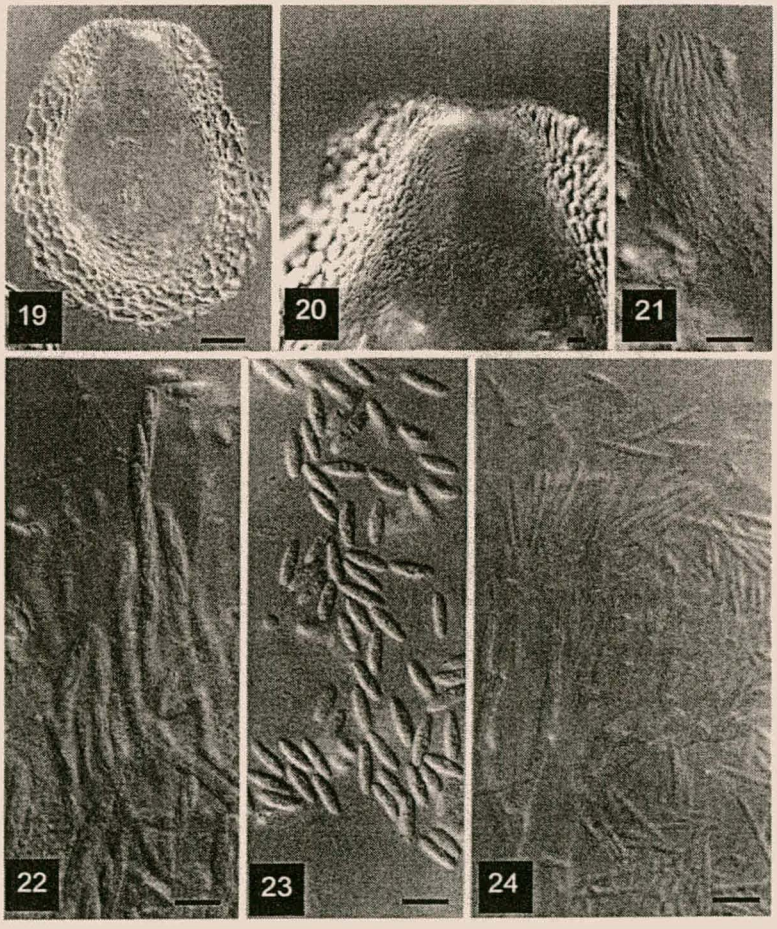
The anamorph genus *Gliocladiopsis* S.B. Saksena (Saksena 1954, Crous & Peerally 1996) closely resembles *Cylindrocladium.* The type species of the genus, *G. sagariensis* S.B. Saksena was shown to be synonymous with *Cylindrocarpon tenue* Bugn. (Barron 1968). Although it had been suggested previously that the genus *Gliocladiopsis* should be retained for species lacking stipe extensions (Crous & Wingfield 1993), Watanabe (1994) synonymised it with *Cylindrocladium* based on the uncertainty of stipe formation. However, studies on *Cylindrocladium* and *Cylindrocladiella* have shown that both these genera regularly produce stipe extensions on their conidiophores under controlled conditions (Crous & Wingfield 1993, Crous & Wingfield 1994), suggesting that the non-stipe forming genus *Gliocladiopsis*, with its multi-branched, penicillate conidiophores should be retained. *Gliocladiopsis* was also represented by a clade. However, as for *Leuconectria*, the relationship of this genus to the other genera selected for this study is still uncertain, due to low bootstrap support for the phylogeny (Fig. 1). The three species described for *Gliocladiopsis* have no known teleomorphs (Saksena 1959, Crous & Wingfield 1993, Crous & Peerally 1996). The present study describes the first teleomorph associated with this genus, which was produced by homothallic cultures obtained from single conidia of *G. tenuis* (Bugn.) Crous & M.J. Wingf. (STE-U 706) on CLA after 2 mo of incubation at 22°C with a 12 h fluorescent white light / dark regime.

Herewith we propose a new holomorph genus for *Gliocladiopsis*. The new genus is based on the distances observed between other genera in the ITS DNA sequence based tree, as well as the distinct anamorph, *Gliocladiopsis*.

Glionectria Crous & C.L. Schoch gen. nov.
Anamorphe: *Gliocladiopsis* S.B. Saksena
Typus: *Glionectria tenuis* Crous & C.L. Schoch

Perithecia superficialia, dense gregaria, stromate tenui basali insidentia, obovoidea ad late obpyriformia, collabentia ubi arida, verrucosa, rubrobrunne basi stromatica atro-rubra, KOH+, pariete perithecii ex duabus regionibus composito: exteriore strato ex *textura globulosa* crassitunicata, interiore strato ex cellulis compressis texturae angularis; periphyses ostioli cylindricae, apicibus rotundatis. Asci unitunicati, octospori, cylindrici, sessiles, cum apice applanato et apparatu apicali refringente. Ascosporae uniseriatae, superpositae, hyalinae, ellipsoidae, leves, medio uniseptatae.

Perithecia superficial, densely gregarious, seated on a thin basal stroma, obovoid to broadly obpyriform, collapsing laterally when dry, warted, red-brown with a dark red stromatic base, changing colour in KOH; perithecial wall consisting of two regions: outer region of thick-walled textura globulosa, inner region of compressed cells of *textura angularis*; ostiolar periphyses tubular with rounded ends. Asci unitunicate, 8-spored, cylindrical, sessile, with a flattened apex, and a refractive apical apparatus. Ascospores uniseriate, overlapping, hyaline, ellipsoidal, smooth, medianly 1-septate Anamorph is *Gliocladiopsis*.



Figs. 19-24. *Glionectria tenuis* and its anamorph *Gliocladiopsis tenuis*. 19. Vertical section through a perithecium. 20,21. Ostiolar region and paraphyses. 22. Cylindrical asci with apical mechanism. 23. One-septate ascopsores. 24. Conidiophore with cylindrical, 1-septate condia. Bars = 10 μm.

Glionectria tenuis Crous & C.L. Schoch sp. nov.

Anamorph. *Gliocladiopsis tenuis* (Bugn.) Crous & M.J. Wingf., Mycol. Res. 97: 446. 1993.

≡ *Cylindrocarpon tenue* Bugn., Encycl. Mycol. 11: 178. 1939.

≡ *Cylindrocladium tenue* (Bugn.) T. Watan., Mycologia 86: 155. 1994.

= *Gliocladiopsis sagariensis* Saksena, Mycologia 46: 663. 1954.

Holotypes. HONG KONG: Soil, M.J. Wingfield, 1993, PREM 56381, holotype of teleomorph, (culture ex type: STE-U 706). INDOCHINA (country unknown): *Indigofera* sp., F. Bugnicourt, Nov. 1936, PC 540, holotype of anamorph (culture ex type: IMI 68205 = STE-U 2403).

Description. Perithecia superficialia, dense gregaria, in stromate basale tenue sedentia, obovidea ad late obpyriformia, collabentia ubi arida, usque ad 400 µm alta et 350 µm lata, verrucosa, cum apice leviter applanata, aurantiaca, corpore et base rubro-brunnea, bene agentia in 3% KOH, apice aurantiaco-rubro facto, corpore perithecii purpureo-rubro et base atro-rubro brunnea. Regione ostiola usque ad 180 µm lata. Pariete perithecii ex duabus regionibus composito: strato exteriore ex 4-5 stratis texturae globulosae cum parietibus crassis composito, usque ad 60 µm lata, compresso ad centrum, [interiore strato] ex 3-4 stratis texturae angularis composito, usqe ad 20 µm lato. Asci unitunicati, octospori, cylindrici, cum apice obtuse rotundato, sessile, cum apparatu apicale refracto, 50-80 x 4-5 µm. Ascosporae uniseriatae, superpositae, hyalinae, leves, ellipsoideae cum apicibus rotundatis, 9-12 x 2.5-3 µm, latissimae ad septum medianum, non constrictae. Conidiophora penicillata, sine extensione stipitis et sine vesiculis terminalibus. Rami conidiophori: primis ramis non septatis, 9-23 x 3-5 µm, secundis ramis non septatis, 10-18 x 2.5-3 µm, tertiis ramis non septatis, 9-14 x 2.5-3.5 µm, quartis ramis raris vel absentibus, non septatis, 9-12 x 2.5-3 µm. Phialides doliiformes ad cymbiformes ad cylindricae, 10-25 x 2.5-3 µm, in verticillis terminalibus dispositae, usque ad 7 in uno ramo, cum collulis parvis. Conidia cylindrica, hyalina, levia, cum apicibus rotundatis, medio uniseptata, (12-)16-19(-23) x 1.5-2(2.5) µm.

Perithecia superficial, densely gregarious, seated on a thin basal stroma, obovoid to broadly obpyriform, collapsing when dry, up to 400 µm high and 350 µm thick, warted, apex slightly flattened, orange, body and base red-brown, reacting positive in 3% KOH, apex becoming orange-red, perithecial body purple-red and base dark red-

brown. Ostiolar region up to 180 µm thick. Perithecial wall consisting of two regions: outer region of 4-5 layers of thick-walled *textura globulosa* up to 60 µm thick, becoming compressed towards the centrum, consisting of 3-4 layers of *textura angularis* up to 20 µm thick. *Asci* unitunicate, 8-spored, cylindrical, with a bluntly rounded apex, sessile, with a refractive apical apparatus, 50-80 x 4-5 µm. *Ascospores* uniseriate, overlapping, hyaline, smooth, ellipsoidal with rounded ends, 9-12 x 2.5-3 µm, widest at median septum, not constricted. *Conidiophores* penicillate, without stipe extensions and terminal vesicles. *Conidiophore branches*: primary branches non-septate, 9-23 x 3-5 µm, secondary branches non-septate, 10-18 x 2.5-4 µm, tertiary branches non-septate, 9-14 x 2.5-3.5 µm, quaternary branches rare to absent, non-septate, 9-12 x 2.5-3 µm. *Phialides* doliiform to cymbiform to cylindrical, 10-25 x 2.5-3 µm, arranged in terminal whorls of up to 7 per branch, with minute collarettes. *Conidia* cylindrical, hyaline, smooth, with rounded ends, medianly 1-septate, (12-)16-19(-23) x 1.5-2(-2.5) µm.

Cultures. Colony colour (reverse) 15"l, sayal brown (Rayner 1970). Chlamydospores in extensive numbers, in clearly delimited, mostly unbranched chains.

Cardinal temperature requirements for growth. Minimum above 5°C, optimum 25-30°C, maximum above 35°C.

Substrate. *Indigofera* sp., *Psidium guajava*, *Shorea robusta*, *Camellia sinensis*, *Chamaedorea elegans*, soil.

Distribution. Brazil, Colombia, Hong Kong, India, Indonesia, Thailand, U.S.A.

Key to genera of the Nectriaceae having cylindrical conidia borne in hyaline or pale yellow masses:

1. Conidiophores penicillate, mononematous..... 4

Conidiophores penicillate or nearly so, sporodochial or synnematous..... 2

2. Stipe extensions present, conidia in hyaline slime; extensions with one apical and basal septum, apical cell curved, pigmented, verruculose..... ..... *Curvicladium*

2. Stipe extensions absent, conidia in hyaline or pale yellow slime;

perithecia solitary to gregarious, warty, wall consisting of two layers; asci cylindrical, sessile, with apical apparatus; ascospores smooth, hyaline, 1-septate.....3

3. Conidiophores frequently divergent, or unbranched with a single conidiogenous cell; macroconidia straight or fusoid, 1-multiseptate, attenuating to rounded ends with a basal abscission scar; microconidia fusoid to ellipsoid, 0-1-septate.....*Neonectria* (*Cylindrocarpon*)

3. Conidiophores always penicillate with more than 2 series of branches, rarely solitary, mostly gregarious; macroconidia cylindrical with rounded ends, 1-septate, straight or curved, abscission scar inconspicuous; microconidia absent.....*Glionectria* (*Gliocladiopsis*)

4. Stipe extensions hyaline, arising above the apical penicillus..... 5

4. Stipe extensions slightly pigmented, forming below the apical penicillus; perithecia warty, wall consisting of two layers; asci narrowly clavate, sessile, with apical apparatus; ascospores smooth, hyaline, 1-septate..... *Leuconectria* (*Gliocephalotrichum*)

5. Perithecium smooth, frequently with a few reduced hyphal setae, body collapsing at maturity; asci cylindrical, sessile, with apical apparatus; ascospores smooth, hyaline, 1-septate; stipe extensions aseptate, thick-walled; conidia shorter than 25 µm; phialide collarettes convergent .....*Nectricladiella* (*Cylindrocladiella*)

5. Perithecium warted, consisting of two layers; asci with long basal stalk; stipe extensions multi-septate, thin-walled; conidia longer than 25 m; phialide collarettes divergent..... 6

6. Asci cylindrical with apical apparatus; ascospores 1-septate; stipe extensions spirally twisted, hyaline, smooth, avesiculate; 1-septate.....*Xenocalonectria* (*Xenocylindrocladium*)

6. Asci clavate without an apical apparatus; ascospores 1-6-septate; stipe extensions straight, terminating in a swollen vesicle of characteristic shape.....*Calonectria* (*Cylindrocladium*)

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7. Appendix - DNA alignments used

Alignment 1. Part 3. ITS1 5.8S ITS2 DNA sequence alignment of selected *Cylindrocladium* species

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                                                                                                                    60
F._subglutinans_NRRL_22061          CCGAGTTTAC AACTCCCAAA CCCC-TGTGA ACATACCAAT T-XGTTGCCT CGGCGGATCA
Cy._candelabrum_STE-U_1674          CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._candelabrum_STE-U_1677          CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._candelabrum_STE-U_1951          XXXXXXXXXX XXXXXCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._insulare_STE-U_616              CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._insulare_STE-U_768              CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._insulare_STE-U_954              CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._mexicanum_STE-U_927             CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._mexicanum_STE-U_941             CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._multiseptatum_STE-U_1589        CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._multiseptatum_STE-U_1602        CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._ovatum_STE-U_2232               XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXCCTGT TTCGTTCCCT CGGCGG-XXX
Cy._ovatum_UFV_90                   CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._pauciramosum_STE-U_416          CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._pauciramosum_STE-U_925          CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._pauciramosum_STE-U_972          CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._scoparium_ATCC_38227            XXXXXXXXXX XXCTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._scoparium_ATCC_46300            CCGAGTTTAC AACTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._scoparium_STE-U_1720            XXXXXXXXXX XXCTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX
Cy._scoparium_STE-U_1722            XXXXXXXXXX XXCTCCCAAA CCCCATGTGA ACATACCTGT TTCGTTCCCT CGGCGG-XXX

                                                                                                                   120
F._subglutinans_NRRL_22061          GCCCGCTCCC GGTAAAACGG GACGGCCCGC CAGAGGACCC C-TAAACTCT GTT-XXTCTA
Cy._candelabrum_STE-U_1674          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._candelabrum_STE-U_1677          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._candelabrum_STE-U_1951          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._insulare_STE-U_616              -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._insulare_STE-U_768              -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._insulare_STE-U_954              -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._mexicanum_STE-U_927             -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._mexicanum_STE-U_941             -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._multiseptatum_STE-U_1589        -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._multiseptatum_STE-U_1602        -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._ovatum_STE-U_2232               -XXXXGGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._ovatum_UFV_90                   -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._pauciramosum_STE-U_416          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._pauciramosum_STE-U_925          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._pauciramosum_STE-U_972          -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._scoparium_ATCC_38227            -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._scoparium_ATCC_46300            -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._scoparium_STE-U_1720            -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT
Cy._scoparium_STE-U_1722            -XXXXTGTCC GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT TTTGAATTTT

                                                                                                                   180
F._subglutinans_NRRL_22061          TATGTAACTT CTGAGTAAAA CCA-XXTAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._candelabrum_STE-U_1674          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._candelabrum_STE-U_1677          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._candelabrum_STE-U_1951          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._insulare_STE-U_616              TCAGTATCTT CTGAGTAAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._insulare_STE-U_768              TCAGTATCTT CTGAGTAAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._insulare_STE-U_954              TCAGTATCTT CTGAGTAAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._mexicanum_STE-U_927             TCAGTATCTT CTGAGTGAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._mexicanum_STE-U_941             TCAGTATCTT CTGAGTGAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._multiseptatum_STE-U_1589        TCAGTATCTT CTGAGTGAAA AAAAAACAA- TAAATAAAAA CTTTCAACAA CGGATCTCTT
Cy._multiseptatum_STE-U_1602        TCAGTATCTT CTGAGTGAAA AAAAAACAA- TAAATAAAAA CTTTCAACAA CGGATCTCTT
Cy._ovatum_STE-U_2232               TCAGTATCTT CTGAGGGAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._ovatum_UFV_90                   TCAGTATCTT CTGAGTGAAA AAAA-XCAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._pauciramosum_STE-U_416          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._pauciramosum_STE-U_925          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._pauciramosum_STE-U_972          TCAGTATCTT CTGAGTAAAA AA-XXXCAAA TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._scoparium_ATCC_38227            TCAGTATCTT CTGAGTAAAA AAAAA-CAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._scoparium_ATCC_46300            TCAGTATCTT CTGAGTAAAA AAAAA-CAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._scoparium_STE-U_1720            TCAGTATCTT CTGAGTAAAA AAAAA-CAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
Cy._scoparium_STE-U_1722            TCAGTATCTT CTGAGTAAAA AAAAA-CAA- TAAATCAAAA CTTTCAACAA CGGATCTCTT
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Cy._candelabrum_STE-U_1674        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._candelabrum_STE-U_1677        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._candelabrum_STE-U_1951        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._insulare_STE-U_616            GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._insulare_STE-U_768            GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._insulare_STE-U_954            GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._mexicanum_STE-U_927           GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._mexicanum_STE-U_941           GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._multiseptatum_STE-U_1589      GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._multiseptatum_STE-U_1602      GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._ovatum_STE-U_2232             GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._ovatum_UFV_90                 GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._pauciramosum_STE-U_416        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._pauciramosum_STE-U_925        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._pauciramosum_STE-U_972        GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._scoparium_ATCC_38227          GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._scoparium_ATCC_46300          GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._scoparium_STE-U_1720          GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
Cy._scoparium_STE-U_1722          GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG TAATGTGAAT TGCAGAATTC
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                                                                                                   300
F._subglutinans_NRRL_22061        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._candelabrum_STE-U_1674        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._candelabrum_STE-U_1677        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._candelabrum_STE-U_1951        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._insulare_STE-U_616            AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._insulare_STE-U_768            AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._insulare_STE-U_954            AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._mexicanum_STE-U_927           AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._mexicanum_STE-U_941           AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._multiseptatum_STE-U_1589      AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._multiseptatum_STE-U_1602      AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._ovatum_STE-U_2232             AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._ovatum_UFV_90                 AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._pauciramosum_STE-U_416        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._pauciramosum_STE-U_925        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._pauciramosum_STE-U_972        AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._scoparium_ATCC_38227          AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._scoparium_ATCC_46300          AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._scoparium_STE-U_1720          AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
Cy._scoparium_STE-U_1722          AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA GTATTCTGGC GGGCATGCCT
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F._subglutinans_NRRL_22061        GTTCGAGCGT CATTTCAACC CTCAAGCCCA GCTTGGTGTT GGGACTCG-C GAG-XXXXXX
Cy._candelabrum_STE-U_1674        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGGCCT
Cy._candelabrum_STE-U_1677        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGGCCT
Cy._candelabrum_STE-U_1951        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGGCCT
Cy._insulare_STE-U_616            GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._insulare_STE-U_768            GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._insulare_STE-U_954            GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._mexicanum_STE-U_927           GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._mexicanum_STE-U_941           GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._multiseptatum_STE-U_1589      GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._multiseptatum_STE-U_1602      GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._ovatum_STE-U_2232             GTTCGAGCGT CATTTCAACC CTCAAGCTCA NCTTGGTGTT GGGGATCGGC AGGGCGTCCT
Cy._ovatum_UFV_90                 GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AGGGCGTCCT
Cy._pauciramosum_STE-U_416        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._pauciramosum_STE-U_925        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._pauciramosum_STE-U_972        GTTCGAGCGT CATTTCAACC CTCAAGCTCA GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._scoparium_ATCC_38227          GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._scoparium_ATCC_46300          GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._scoparium_STE-U_1720          GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
Cy._scoparium_STE-U_1722          GTTCGAGCGT CATTTCAACC CTCAAGCTCT GCTTGGTGTT GGGGATCGGC AAGGCGTCCT
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F._subglutinans_NRRL_22061        TCAAATCGC- XXGTTCCCCA AATTGATTGG CGGTCACG-T CGAGCTTCCA TAGCGTAGTA
Cy._candelabrum_STE-U_1674        CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._candelabrum_STE-U_1677        CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._candelabrum_STE-U_1951        CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._insulare_STE-U_616            CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._insulare_STE-U_768            CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._insulare_STE-U_954            CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._mexicanum_STE-U_927           CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._mexicanum_STE-U_941           CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._multiseptatum_STE-U_1589      CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._multiseptatum_STE-U_1602      CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._ovatum_STE-U_2232             CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGSCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._ovatum_UFV_90                 CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._pauciramosum_STE-U_416        CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._pauciramosum_STE-U_925        CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._pauciramosum_STE-U_972        CCGGGTCGCG CCGTCCCCCA AATTTAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._scoparium_ATCC_38227          CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._scoparium_ATCC_46300          CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._scoparium_STE-U_1720          CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
Cy._scoparium_STE-U_1722          CCGGGTCGCG CCGTCCCCCA AATATAGTGG CGGTCTCGCT GTAGCTTCCT CTGCGTAGTA
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                                                                                                    480
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Cy._candelabrum_STE-U_1674        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GACCACGCCG TAAAACCCCC AACTTTTT-X
Cy._candelabrum_STE-U_1677        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GACCACGCCG TAAAACCCCC AACTTTTT-X
Cy._candelabrum_STE-U_1951        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GACCACGCCG TAAAACCCCC AACTTTTT-X
Cy._insulare_STE-U_616            ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._insulare_STE-U_768            ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._insulare_STE-U_954            ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._mexicanum_STE-U_927           ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTT-X
Cy._mexicanum_STE-U_941           ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTT-X
Cy._multiseptatum_STE-U_1589      ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACNCCG TAAAAACCCC AACTTTTTT-
Cy._multiseptatum_STE-U_1602      ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAAACCCC AACTTTTTT-
Cy._ovatum_STE-U_2232             ATACA-XCCT CGCT-CTGGA GXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
Cy._ovatum_UFV_90                 ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTTT
Cy._pauciramosum_STE-U_416        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTT-X
Cy._pauciramosum_STE-U_925        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTT-X
Cy._pauciramosum_STE-U_972        ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTT-X
Cy._scoparium_ATCC_38227          ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._scoparium_ATCC_46300          ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._scoparium_STE-U_1720          ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-
Cy._scoparium_STE-U_1722          ATACA-XCCT CGCT-CTGGA GTCTCGGTGC GGCCACGCCG TAAAACCCCC AACTTTTTT-

                                   483
F._subglutinans_NRRL_22061        -TGT
Cy._candelabrum_STE-U_1674        CTGG
Cy._candelabrum_STE-U_1677        CTGG
Cy._candelabrum_STE-U_1951        CTGG
Cy._insulare_STE-U_616            CTGG
Cy._insulare_STE-U_768            CTGG
Cy._insulare_STE-U_954            CTGG
Cy._mexicanum_STE-U_927           CTGG
Cy._mexicanum_STE-U_941           CTGG
Cy._multiseptatum_STE-U_1589      CTGG
Cy._multiseptatum_STE-U_1602      CTGG
Cy._ovatum_STE-U_2232             XXXX
Cy._ovatum_UFV_90                 CTGG
Cy._pauciramosum_STE-U_416        CTGG
Cy._pauciramosum_STE-U_925        CTGG
Cy._pauciramosum_STE-U_972        CTGG
Cy._scoparium_ATCC_38227          CTGG
Cy._scoparium_ATCC_46300          CTGG
Cy._scoparium_STE-U_1720          CTGG
Cy._scoparium_STE-U_1722          CTGG
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Alignment 2. Part 3. 5' end of β-tubulin gene DNA sequence alignment from selected *Cylindrocladium* species

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                                                                                                                    60
F._subglutinans_NRRL_22061          GCGTTGAGTT TAT-GGT-XX XXGCCCCTGA TTCTACCCCG C-XXXXTGGG CGGTGGCAGC
Cy._candelabrum_STE-U_1674          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCATCGCT
Cy._candelabrum_STE-U_1677          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCATCGCT
Cy._candelabrum_STE-U_1951          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCATCGCT
Cy._insulare_STE-U_616              ACG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACC
Cy._insulare_STE-U_768              ACG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACC
Cy._insulare_STE-U_954              GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACC
Cy._mexicanum_STE-U_927             GCG-TGCCTT TGTTGCT-XX XXGCCCCTGG TTCTACCCCG CCGTCCCGGT TTCCACCGCT
Cy._mexicanum_STE-U_941             GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGTCCCGGT TTCCACCGCT
Cy._multiseptatum_STE-U_1589        GAG-TGCCTT TGTTGCTTTC TGGCCCCTGA TTCTACCCCG CGGCCCCGGT TTCCACCGCT
Cy._multiseptatum_STE-U_1602        GAG-TGCCTT TGTTGCTTTG CTGCCCCTGA TTCTACCCCG CGGCCCCGGT TTCCACCGCT
Cy._ovatum_STE-U_2232               GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCGCT
Cy._ovatum_UFV_90                   GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCGCT
Cy._pauciramosum_STE-U_416          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCGCT
Cy._pauciramosum_STE-U_925          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCGCT
Cy._pauciramosum_STE-U_972          GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCGCT
Cy._scoparium_ATCC_38227            GGG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACA
Cy._scoparium_ATCC_46300            GCG-TGCCTT GGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACA
Cy._scoparium_STE-U_1720            GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACA
Cy._scoparium_STE-U_1722            GCG-TGCCTT TGTTGCT-XX XXGCCCCTGA TTCTACCCCG CCGCCCCGGT TTCCACCACA

                                                                                                                   120
F._subglutinans_NRRL_22061          TCAACGACAA TGCACGAT-X AG CT-AGCA GCTTTAA-XA TACCTTCTGT CAAGATGAAG
Cy._candelabrum_STE-U_1674          TCGACGACAA -CAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCAGAA CAAGATTGCT
Cy._candelabrum_STE-U_1677          TCGACGACAA -CAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCAGAA CAAGATTGCT
Cy._candelabrum_STE-U_1951          TCGACGACAA -CAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCAGAA CAAGATTGCT
Cy._insulare_STE-U_616              TCGACGACAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._insulare_STE-U_768              TCGACGACAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._insulare_STE-U_954              TCGACGACAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._mexicanum_STE-U_927             ACAACGACAA -CAAAGCCGC AGCCTCGACA ACATGAGCAA GATATCAGGA TATGATGGCT
Cy._mexicanum_STE-U_941             ACAACGACAA -CAAAGCCGC AGCCTCGACA ACATGAGCAA GATATCAGGA TATGATGGCT
Cy._multiseptatum_STE-U_1589        CCGACGAAAA -CAAAGCCGC AACCTCACGA ATGTGA-CGA GATATCAGAA CAAGATTGCT
Cy._multiseptatum_STE-U_1602        CCGACGAAAA -CAAAGCCGC AACCTCACGA ATGTGA-CGA GATATCAGAA CAAGATTGCT
Cy._ovatum_STE-U_2232               TCGACGACAA -CAAAGCCGC AGCCTCACGA ACATGA-CTA GATATCAGAA CGAGATCGST
Cy._ovatum_UFV_90                   TCGACGACAA -CAAAGCCGC AGACTCACGA ACATGA-CGA GATATCAGAA CGAGATTGCT
Cy._pauciramosum_STE-U_416          TCGACGACAA -CAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCAGAA CAAGATTGCT
Cy._pauciramosum_STE-U_925          TGGACGACAA -CAAAGCCGC AGGCTCACGA TCATGA-CGA GATATCAGAA CAAGATTGCT
Cy._pauciramosum_STE-U_972          TCGACGACAA -CAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCAGAA CAAGATTGCT
Cy._scoparium_ATCC_38227            TCGACGAAAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._scoparium_ATCC_46300            TCGACGAAAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._scoparium_STE-U_1720            TCGACGAAAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT
Cy._scoparium_STE-U_1722            TCGACGAAAA -CAAAGCCGC AGCCTCACGA ACATGA-TGT GATATCAGAA CAAGATTGCT

                                                                                                                   180
F._subglutinans_NRRL_22061          AAGCTAATCA GATCTTTTCT CTGCGATAGG TTCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._candelabrum_STE-U_1674          AA-C-CGTGT GCTTCTTTTT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._candelabrum_STE-U_1677          AA-C-CGTGT GCTTCTTTTT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._candelabrum_STE-U_1951          AA-C-CGTGT GCTTCTTTTT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._insulare_STE-U_616              AA-C-CGTGT GCCTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._insulare_STE-U_768              AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._insulare_STE-U_954              AA-C-CGTCT GCTTCTTTCT CGACTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._mexicanum_STE-U_927             AA-C-CGTGT GTTTCTTCCT CAATTCTAGG TTCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._mexicanum_STE-U_941             AA-C-CGTGT GTTTCTTCCT CAATTCTAGG TTCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._multiseptatum_STE-U_1589        AA-C-CTTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGCCAG TGCGTAAGTG
Cy._multiseptatum_STE-U_1602        AA-C-CTTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGCCAG TGCGTAAGTG
Cy._ovatum_STE-U_2232               AA-C-CGTGT GCTTCTTTTT CAATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._ovatum_UFV_90                   AA-C-CGTGT GCTTCTTTCT CAATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._pauciramosum_STE-U_416          AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._pauciramosum_STE-U_925          AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._pauciramosum_STE-U_972          AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTA
Cy._scoparium_ATCC_38227            AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._scoparium_ATCC_46300            AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._scoparium_STE-U_1720            AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG
Cy._scoparium_STE-U_1722            AA-C-CGTGT GCTTCTTTCT CGATTATAGG TCCACCTCCA GACCGGTCAG TGCGTAAGTG

                                                                                                                   240
F._subglutinans_NRRL_22061          CTCATCGCTT CCTCGACGTC GCATGTGGGG -GATGCTCAC -GATGTTT-X -ATCAGGGTA
Cy._candelabrum_STE-U_1674          CCCTTCTCAA CTCCGACCAA ATTCTCACGA CGAGATTCAC TGACAGTTGT CCATAGGGTA
Cy._candelabrum_STE-U_1677          CCCTTCTCAA CTCCGACCAA ATTCTCACGA CGAGATTCAC TGACAGTTGT CCATAGGGTA
Cy._candelabrum_STE-U_1951          CCCTTCTCAA CTCCGACCAA ATTCTCACGA CGAGATTCAC TGACAGTTGT CCATAGGGTA
Cy._insulare_STE-U_616              CTCTTC-XAA CTCCAACGGA ATTCTCACGA CCAGATTCAC TGACAGTTAT CGACAGGGTA
Cy._insulare_STE-U_768              CTCTTC-XAA CTCCAACAAA ATTCTCACGA CCAGATTCAC TGACAGTTAT CGACAGGGTA
Cy._insulare_STE-U_954              CTCTTC-XAA CTCTAACAAA ATTCTCACGA CCAGATTCAC TGACAATTAT CGACAGGGTA
Cy._mexicanum_STE-U_927             CTCCTTGCAA CTCCAACAAC TTTCTCACGG CCATGATCGC TGACAGACGT CGATAGGGTA
Cy._mexicanum_STE-U_941             CTCCTTGCAA CTCCAACAAC TTTCTCACGG CCATGATCTC TGACAGACGT CGATAGGGTA
Cy._multiseptatum_STE-U_1589        CTCCTCTCGA CTCCAACGAT ATTCTTATGA CAAGATTCAC TGACAGTTTT CGATAGGGTA
Cy._multiseptatum_STE-U_1602        CTCCTCTCGA CTCCAACGAT ATTCTTATGA CAAGATTCAC TGACAGTTTT CGATAGGGTA
Cy._ovatum_STE-U_2232               CTTCTCTCGA CTCCAGCAAG ATTTTCACGA CGAGATTCGC TGACAGTTGT CAATAGGGTA
Cy._ovatum_UFV_90                   CTCCTCTCAA CTCCAACAAG ATTCTCACGA CGAGATTCGC TGACAGTTGT CGATAGGGTA
Cy._pauciramosum_STE-U_416          CTCTTCTCAA CTCCAACAAA ATTCTCACGA CGAGATTCAC TGACAGTTGT CGATAGGGTA
Cy._pauciramosum_STE-U_925          CTCTTCTCAA CTCCAACCAA ATTCTCACGA CGAGGTTCGC TGACAGTTGT CGATAGGGTA
Cy._pauciramosum_STE-U_972          CTCTTCTCAA CTCCAACAAA ATTCTCACGA CGAGATTCAC TGACAGTTGT CGATAGGGTA
Cy._scoparium_ATCC_38227            CTCTTC-XAA CTCCAACAAA ATTCTCACGA CCGGATTCAC TGACAGTTAT CGACAGGGTA
Cy._scoparium_ATCC_46300            CTCTTC-XAA CTCCAACAAA ATTCTCACGA CCGGATTCAC TGACAGTTAT CGACAGGGTA
Cy._scoparium_STE-U_1720            CTCTTC-XAA CTCCAACAAA ATTCTCACGA CCGGATTCAC TGACAGTTAT CGACAGGGTA
Cy._scoparium_STE-U_1722            CTCTTC-XAA CTCCAACAAA ATTCTCACGA CCGGATTCAC TGACAGTTAT CGACAGGGTA
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*F._subglutinans*_NRRL_22061	ACCAAATTGG	TGCTGCTTTC	TGGCAAACCA	TCTCTGGCGA	GCACGGCCTC	GACAGCAATG
*Cy._candelabrum*_STE-U_1674	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._candelabrum*_STE-U_1677	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTSTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._candelabrum*_STE-U_1951	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._insulare*_STE-U_616	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._insulare*_STE-U_768	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._insulare*_STE-U_954	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._mexicanum*_STE-U_927	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._mexicanum*_STE-U_941	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._multiseptatum*_STE-U_1589	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	KACAGCAATG
*Cy._multiseptatum*_STE-U_1602	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._ovatum*_STE-U_2232	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._ovatum*_UFV_90	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TCTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._pauciramosum*_STE-U_416	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._pauciramosum*_STE-U_925	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._pauciramosum*_STE-U_972	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._scoparium*_ATCC_38227	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._scoparium*_ATCC_46300	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._scoparium*_STE-U_1720	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG
*Cy._scoparium*_STE-U_1722	ACCAAATTGG	TGCTGCTTTC	TGGCAGACCA	TTTCTGGCGA	GCACGGTCTC	GACAGCAATG

						360
*F._subglutinans*_NRRL_22061	GTGTCTACAA	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAGTGTCTAC	TTCAACGAGG
*Cy._candelabrum*_STE-U_1674	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._candelabrum*_STE-U_1677	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._candelabrum*_STE-U_1951	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._insulare*_STE-U_616	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._insulare*_STE-U_768	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._insulare*_STE-U_954	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._mexicanum*_STE-U_927	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._mexicanum*_STE-U_941	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._multiseptatum*_STE-U_1589	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._multiseptatum*_STE-U_1602	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._ovatum*_STE-U_2232	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._ovatum*_UFV_90	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._pauciramosum*_STE-U_416	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._pauciramosum*_STE-U_925	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._pauciramosum*_STE-U_972	GTGTCTACGC	CGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._scoparium*_ATCC_38227	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._scoparium*_ATCC_46300	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCCACGAGG
*Cy._scoparium*_STE-U_1720	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG
*Cy._scoparium*_STE-U_1722	GTGTCTACGC	TGGTACCTCC	GAGCTCCAGC	TCGAGCGTAT	GAACGTCTAC	TTCAACGAGG

						420
*F._subglutinans*_NRRL_22061	TATGCTTTAA	CAGTC-AATG	-CCAA-GAAT	TCCCAAGCTC	ACA-XXCAAC	T-XXXXXXXX
*Cy._candelabrum*_STE-U_1674	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAATCCGAC	TCACAC-XCA
*Cy._candelabrum*_STE-U_1677	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAATCCGAC	TCACAC-XCA
*Cy._candelabrum*_STE-U_1951	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAATCCGAC	TCACAC-XCA
*Cy._insulare*_STE-U_616	TATGTGAAAA	TCACGCGGTG	TACTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX
*Cy._insulare*_STE-U_768	TATGTGAAAA	CCGCGCGGTG	TACCCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX
*Cy._insulare*_STE-U_954	TGTGTGAAAA	CCGCGCGGTG	TACTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX
*Cy._mexicanum*_STE-U_927	TATGTAAAAA	CCGCTCCAAG	AAATTTCTTT	GTCGGGACGC	CCAAACAAAC	TCACA-XXXX
*Cy._mexicanum*_STE-U_941	TATGTAAAAA	CCGCTCCAAG	AAATTTCTTT	GTCGGGACGC	CCAAACAAAC	TCACACA-CG
*Cy._multiseptatum*_STE-U_1589	TATGCGAAAA	ATCATGAGTG	CGCTCGCTTT	GTGGAGAAAC	ATAGTCAAAC	TGACACACCA
*Cy._multiseptatum*_STE-U_1602	TATGCGAAAA	ATCATGAGTG	CGCTCGCTTT	GTGGAGAAAC	ATAGTCAAAC	TGACACACCA
*Cy._ovatum*_STE-U_2232	TATGTGAAAA	CCACGCCGAG	CACTCCCTTT	ACCGGGAAGC	ACAAGCAAAC	TGACACGC-X
*Cy._ovatum*_UFV_90	TATGTGAAGA	CCACGCGGTG	CACCCCTTTT	GCCGAGAAGC	ACAAGCAAAC	TGACACAC-X
*Cy._pauciramosum*_STE-U_416	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAAGCCAAC	TCACAC-XCA
*Cy._pauciramosum*_STE-U_925	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAAGCCAAC	TCACACA-XA
*Cy._pauciramosum*_STE-U_972	TATGTGAAAA	CCACTCGAAG	CACTCCCTTG	ACCGAGAAGC	ACAAGCCAAC	TCACAC-XCA
*Cy._scoparium*_ATCC_38227	TATGTGAAAA	CCACGCGGTG	TACTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX
*Cy._scoparium*_ATCC_46300	TATGTGAAAA	CCACGCGGTG	TTCTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAN-XXX
*Cy._scoparium*_STE-U_1720	TATGTGAAAA	CCACGCGGTG	TACTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX
*Cy._scoparium*_STE-U_1722	TATGTGAAAA	CCACGCGGTG	TACTCACACG	-CCGAGAGGC	ACAAGCAAAC	TGACAC-XXX

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*F._subglutinans*_NRRL_22061	-XXXXXAGGC	CTCTGGCAAC	AAGTATGTTC	CCCGAGCCGT	CCTCGTCGAT	CTTGAGCCTG
*Cy._candelabrum*_STE-U_1674	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._candelabrum*_STE-U_1677	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._candelabrum*_STE-U_1951	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._insulare*_STE-U_616	-CATGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG
*Cy._insulare*_STE-U_768	-C-TGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG
*Cy._insulare*_STE-U_954	-CATGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG
*Cy._mexicanum*_STE-U_927	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._mexicanum*_STE-U_941	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._multiseptatum*_STE-U_1589	T-GTGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTG-	CCTCGTTGAT	CTTGAGCCCG
*Cy._multiseptatum*_STE-U_1602	T-GTGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTTGAT	CTTGAGCCCG
*Cy._ovatum*_STE-U_2232	-CGTGCAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._ovatum*_UFV_90	-CATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._pauciramosum*_STE-U_416	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._pauciramosum*_STE-U_925	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._pauciramosum*_STE-U_972	TCATGTAGGC	TTCCGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTTGAGCCCG
*Cy._scoparium*_ATCC_38227	-CATGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG
*Cy._scoparium*_ATCC_46300	-CATGTAGGC	TTCTGGCAAC	AAGTTCCGTC	CTTG-TCTGT	CGTCGT-GAT	CTTGAGCCCG
*Cy._scoparium*_STE-U_1720	-CATGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG
*Cy._scoparium*_STE-U_1722	-CATGTAGGC	TTCTGGCAAC	AAGTTCGTTC	CTCGCGCTGT	CCTCGTCGAT	CTCGAGCCCG

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                                                                                                                    638
F._subglutinans_NRRL_22061          GTACCATGGA CGCCGTCCGA GCTGGTCCCT TCGGTCAGCT CTTCCGTCCC GACAACTT
Cy._candelabrum_STE-U_1674          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._candelabrum_STE-U_1677          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._candelabrum_STE-U_1951          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TNGGTCAGNT CTTTCGCCCC GACAACTT
Cy._insulare_STE-U_616              GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTTCGCCCC GACAACTT
Cy._insulare_STE-U_768              GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTNCGCCCC GACAACTT
Cy._insulare_STE-U_954              GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._mexicanum_STE-U_927             GTACCATGGA TGCCGTCCGT GCTGGTCCCT TCGGTCAGCT CTTCCGTCCC GACAACTT
Cy._mexicanum_STE-U_941             GTACCATGGA TGCCGTCCGT GCTGGTCCCT TCGGTCAGCT CTTCCGTCCC GACAACTT
Cy._multiseptatum_STE-U_1589        GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTTCGCCCC GACAACTT
Cy._multiseptatum_STE-U_1602        GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._ovatum_STE-U_2232               GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._ovatum_UFV_90                   GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._pauciramosum_STE-U_416          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._pauciramosum_STE-U_925          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._pauciramosum_STE-U_972          GTACCATGGA CGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._scoparium_ATCC_38227            GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._scoparium_ATCC_46300            GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._scoparium_STE-U_1720            GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
Cy._scoparium_STE-U_1722            GTACCATGGA TGCCGTCCGT GCCGGTCCTT TCGGTCAGCT CTTCCGCCCC GACAACTT
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Alignment 3. Part 3. Partial *MAT-2* HMG box DNA sequence alignment of selected *Cylindrocladium* species

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                                                                                                                    60
Cy._multiseptatum_STE-U_1602      CCGAAATCAC GAACAGTGAG ATTTGTAAGT ACCCATCGCC TTATTATAGT TTCCATGTTA
Cy._multiseptatum_STE-U_1589      CGGAAATCAC GAACAGTGAG ATTTGTAAGT ACCCATCGCC TTATTATAGT TTCCATGTTA
Cy._pauciramosum_STE-U_925        CCGAAATCAC GAACAGTGAG ATTTGTAAGT ACCTACCACC TTGGCACAAT TTCTGTGCTG
Cy._pauciramosum_STE-U_972        CCGAAATCAC GAACAGTGAG ATTTGTAAGT ACCTACCACC TTGGCACAAT TTCTGTGCTG
Cy._candelabrum_STE-U_1674        CCGAAATCAC GAACAGTGAG ATTTGTAAGT ACCTACCACC TTAGCACAAT TTCTGTACTA
Cy._candelabrum_STE-U_1677        CCGAAAACAC GAACAGTGAG ATTTGTAAGT ACCTACCACC TTAGCACAAT TTCTGTACTA
Cy._ovatum_STE-U_2232             XXXXXXXXXX XXXXAGTGAG ATCTGTAAGT ACCCGCTACC CTAGCACAGT TTCTGTACTA
Cy._insulare_STE-U_616            CAGAAATTAC CAACAGTGAG ATTTGTAGGT ACTCACCACC TTGGTACAGT TTCTGTACTA
Cy._insulare_STE-U_768            CAGAAATCAC CAACAGTGAG ATTTGTAAGT ACTCACCACC TTGGTACAGT TTCTGTACTA
Cy._scoparium_STE-U_1720          XXXXXXXXXX XAACAGTGAG ATTTGTAAGT ACTCACCAAC TTGGTACAGT TTCTGTACTG
Cy._scoparium_ATCC_38227          XXXXXXXXAC CAACAGTGAG ATTTGTAAGT ACTCACCACC TTGGTACAGT TTCTATACTA

                                                                                                                   120
Cy._multiseptatum_STE-U_1602      ACACTTTTCA GCCATGGTTC TTGGTCGCGC CTGGAACATG GAGACTCCGG AGACGCGCAA
Cy._multiseptatum_STE-U_1589      ACACTTTTCA GCCATGGTTC TTGGTCGCGC CTGGAACATG GAGACTCCGG AGACGCGCAA
Cy._pauciramosum_STE-U_925        ACATTTTTCA GCCATGGTTC TTGGCCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._pauciramosum_STE-U_972        ACATTCTTCA GCCATGGTTC TTGGCCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._candelabrum_STE-U_1674        AAAGTTTTCA GCCATGGTCC TTGGCCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._candelabrum_STE-U_1677        AAAGTTTTCA GCCATGGTCC TTGGCCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._ovatum_STE-U_2232             ACATTTCTCA GCTATGGTTC TGGGTCGTGC CTGGAACATG GAAACTCCAG AAACGCGAAA
Cy._insulare_STE-U_616            ACATTTTTCA GCCATGGTTC TTGGTCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._insulare_STE-U_768            ACATTTTTCA GCCATGGTTC TTGGTCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._scoparium_STE-U_1720          ACATTTTTTA GCCATGGTTC TTGGTCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA
Cy._scoparium_ATCC_38227          ACATTTTTCA GCCATGGTTC TTGGTCGTGC CTGGAACATG GAGACTCCAG AGACGCGAAA

                                                                                                             171
Cy._multiseptatum_STE-U_1602      GAAGTATAAG CTCATGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._multiseptatum_STE-U_1589      GAAGTATAAG CTCATGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._pauciramosum_STE-U_925        GAAGTACAAG CTCAAGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._pauciramosum_STE-U_972        GAAGTACAAG CTCAAGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._candelabrum_STE-U_1674        GAAGTACAAG CTCAAGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._candelabrum_STE-U_1677        GAAGTACAAG CTCAAGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._ovatum_STE-U_2232             GAAGTACAAA CTCATGGCAG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._insulare_STE-U_616            GAAGTACAAG CTCATGGCGG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._insulare_STE-U_768            GAAGTACAAG CTCATGGCGG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._scoparium_STE-U_1720          GAAGTACAAG CTCATGGCGG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
Cy._scoparium_ATCC_38227          GAAGTACAAG CTCATGGCGG ATGAGATCAA GGCTGAGCTC ATCAAGAAGC A
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Alignment 4. Part 4. 5' end of β-tubulin gene DNA sequence alignment of *Cylindrocladium pauciramosum*

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                                                                                                                    60
F._subglutinans_NRRL_22061          GCGTTGAGTT TATGG-T-XX XXXGCCCCTG ATTCTACCCC GCTGGGC-GG TGGC-AGCTC
Cy._candelabrum_STE-U_1674          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCATCGC
Cy._candelabrum_STE-U_1677          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCATCGC
Cy._candelabrum_STE-U_1951          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCATCGC
Cy._candelabrum_UFV_89              GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCATCGC
Cy._mexicanum_STE-U_927             GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG GTTCTACCCC GCCGTCCCGG TTTCCACCGC
Cy._mexicanum_STE-U_941             GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGTCCCGG TTTCCACCGC
Cy._multiseptatum_STE-U_1589        GAG-TGCCTT TGTTGCTTT- CTGGCCCCTG ATTCTACCCC GCGGCCCCGG TTTCCACCGC
Cy._multiseptatum_STE-U_1602        GAG-TGCCTT TGTTGCTTTG CT-GCCCCTG ATTCTACCCC GCGGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_127         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_128         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_192         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_196         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_2           GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_26          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_6           GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_60          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_62          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_DISTEF_84          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_1160         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_143          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_1691         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_1692         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_1990         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_2030         GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_344          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_416          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_913          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_925          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_951          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_971          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_STE-U_972          GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_UFV_25             GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC
Cy._pauciramosum_UFV_27             GCG-TGCCTT TGTTGCT-XX XXXGCCCCTG ATTCTACCCC GCCGCCCCGG TTTCCACCGC

                                                                                                                   120
F._subglutinans_NRRL_22061          AACGACAATG -CACGATAGC -TAGCAGCTT TAAATACC-T TCTGTCAAGA TGAAGAA-GC
Cy._candelabrum_STE-U_1674          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._candelabrum_STE-U_1677          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._candelabrum_STE-U_1951          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._candelabrum_UFV_89              TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._mexicanum_STE-U_927             TACAACGACA ACAAAGCCGC AGCCTCGACA ACATGAGCAA GATATCA-GG ATATGATGGC
Cy._mexicanum_STE-U_941             TACAACGACA ACAAAGCCGC AGCCTCGACA ACATGAGCAA GATATCA-GG ATATGATGGC
Cy._multiseptatum_STE-U_1589        TCCGACGAAA ACAAAGCCGC AACCTCACGA ATGTGA-CGA GATATCA-GA ACAAGATTGC
Cy._multiseptatum_STE-U_1602        TCCGACGAAA ACAAAGCCGC AACCTCACGA ATGTGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_127         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_128         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_192         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_196         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_2           TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_26          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_6           TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_60          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_62          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_DISTEF_84          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1160         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_143          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1670         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1671         TTCGACGACA ACAAGGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1691         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1692         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_1990         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_2030         TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_344          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_416          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_913          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_925          TTGGACGACA ACAAAGCCGC AGGCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_951          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATGA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_971          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
Cy._pauciramosum_STE-U_972          TTCGACGACA ACAAAGCCGC AGCCTCACGA TCATAA-CGA GATATCA-GA ACAAGATTGC
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                                                                                                     180
F._subglutinans_NRRL_22061        TAATCA-GAT CTTTTCTCT- XGCGATAGGT TCACCTCCAG ACCGGTCAGT GCGTAAGTGC
Cy._mexicanum_STE-U_927           TAACCGTGTG TTTCTTCCTC AATTCTAGGT TCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._mexicanum_STE-U_941           TAACCGTGTG TTTCTTCCTC AATTCTAGGT TCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._multiseptatum_STE-U_1602      TAACCTTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGCCAGT GCGTAAGTGC
Cy._multiseptatum_STE-U_1589      TAACCTTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGCCAGT GCGTAAGTGC
Cy._candelabrum_STE-U_1951        TAACCGTGTG CTTCTTTTTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._candelabrum_STE-U_1674        TAACCGTGTG CTTCTTTTTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._candelabrum_UFV_89            TAACCGTGTG CTTCTTTTTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._candelabrum_STE-U_1677        TAACCGTGTG CTTCTTTTTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1671       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1670       TAACCGTGTG CTTCTTTTTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_416        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_972        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_143        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_2         TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_127       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_128       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_84        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_2030       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_925        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_913        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1160       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_951        TAACCGTGTG CTTCTTTCTC GACTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1990       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1692       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_344        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_971        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_STE-U_1691       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_60        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_62        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_6         TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_26        TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_196       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
Cy._pauciramosum_DISTEF_192       TAACCGTGTG CTTCTTTCTC GATTATAGGT CCACCTCCAG ACCGGTCAGT GCGTAAGTAC
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                                                                                                     240
F._subglutinans_NRRL_22061        TCATCGCTTC CTC-GACGTC GCATGTGGGG G-ATGCTCAC- GAT-GTT-X -TATCAGGGT
Cy._mexicanum_STE-U_927           TCCTTGCAA- CTCCAACAAC TTTCTCACGG CCATGATCGCT GACAGACGT CGAT-AGGGT
Cy._mexicanum_STE-U_941           TCCTTGCAA- CTCCAACAAC TTTCTCACGG CCATGATCTCT GACAGACGT CGAT-AGGGT
Cy._multiseptatum_STE-U_1602      TCCTCTCGA- CTCCAACGAT ATTCTTATGA CAAGATTCACT GACAGTTTT CGAT-AGGGT
Cy._multiseptatum_STE-U_1589      TCCTCTCGA- CTCCAACGAT ATTCTTATGA CAAGATTCACT GACAGTTTT CGAT-AGGGT
Cy._candelabrum_STE-U_1951        CCTTCTCAA- CTCCGACCAA ATTCTCACGA CGAGATTCACT GACAGTTGT CCAT-AGGGT
Cy._candelabrum_STE-U_1674        CCTTCTCAA- CTCCGACCAA ATTCTCACGA CGAGATTCACT GACAGTTGT CCAT-AGGGT
Cy._candelabrum_UFV_89            CCTTCTCAA- CTCCGACCAA ATTCTCACGA CGAGATTCACT GACAGTTGT CCAT-AGGGT
Cy._candelabrum_STE-U_1677        CCTTCTCAA- CTCCGACCAA ATTCTCACGA CGAGATTCACT GACAGTTGT CCAT-AGGGT
Cy._pauciramosum_STE-U_1671       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATGCACT GACAGCTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_1670       CCTTCTCAA- CTCCGACCAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_416        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_972        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_143        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_2         TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_127       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_128       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_84        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_2030       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_925        TCTTCTCAA- CTCCAACCAA ATTCTCACGA CGAGGTTCGCT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_913        TCTTCTCAA- CTCCAACCAA ATTCTCACGA CGAGGTTCGCT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_1160       TCTTCTCAA- CTCCAACCAA ATTCTCACGA CAAGATTCGCT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_951        TCTTCTCAA- CTCCAACCAA ATTCTCACGA CAAGATTCGCT GACGGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_1990       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_1692       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_344        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_971        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_STE-U_1691       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_60        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_62        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_6         TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_26        TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_196       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
Cy._pauciramosum_DISTEF_192       TCTTCTCAA- CTCCAACAAA ATTCTCACGA CGAGATTCACT GACAGTTGT CGAT-AGGGT
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F._subglutinans_NRRL_22061         AACCAAATTG GTGCTGCTTT CTGGCAAACC ATCTCTGGCG AGCACGGCCT CGACAGCAAT
Cy._mexicanum_STE-U_927            AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._mexicanum_STE-U_941            AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._multiseptatum_STE-U_1602       AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._multiseptatum_STE-U_1589       AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CKACAGCAAT
Cy._candelabrum_STE-U_1951         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._candelabrum_STE-U_1674         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._candelabrum_UFV_89             AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._candelabrum_STE-U_1677         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1671        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1670        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATCTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_416         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_972         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_143         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_2          AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_127        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_128        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_84         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_2030        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_925         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_913         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1160        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_951         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1990        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1692        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_344         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_971         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_STE-U_1691        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_60         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_62         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_6          AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_26         AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_196        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
Cy._pauciramosum_DISTEF_192        AACCAAATTG GTGCTGCTTT CTGGCAGACC ATTTCTGGCG AGCACGGTCT CGACAGCAAT
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                                                                                         360
F._subglutinans_NRRL_22061         GGTGTCTACA ACGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAGTGTCTA CTTCAACGAG
Cy._mexicanum_STE-U_927            GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._mexicanum_STE-U_941            GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._multiseptatum_STE-U_1602       GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._multiseptatum_STE-U_1589       GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._candelabrum_STE-U_1951         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._candelabrum_STE-U_1674         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._candelabrum_UFV_89             GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._candelabrum_STE-U_1677         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1671        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1670        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_416         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_972         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_143         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_2          GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_127        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_128        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_84         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_2030        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_925         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_913         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1160        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_951         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1990        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1692        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_344         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_971         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_STE-U_1691        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_60         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
Cy._pauciramosum_DISTEF_62         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTTTA CTTCAACGAG
Cy._pauciramosum_DISTEF_6          GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTTTA CTTCAACGAG
Cy._pauciramosum_DISTEF_26         GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTTTA CTTCAACGAG
Cy._pauciramosum_DISTEF_196        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTTTA CTTCAACGAG
Cy._pauciramosum_DISTEF_192        GGTGTCTACG CCGGTACCTC CGAGCTCCAG CTCGAGCGTA TGAACGTCTA CTTCAACGAG
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F._subglutinans_NRRL_22061      GTATGCTTTA A-CAGTCAAT GCCAAGAATT -XXXXXXXXX CCCAAG-XXX CTCACACAAC
Cy._mexicanum_STE-U_927         GTATGTAAAA ACCGCTCCAA GAAATTTCTT TGTCGGGACG CCCAAACAAA CTCACA-XXX
Cy._mexicanum_STE-U_941         GTATGTAAAA ACCGCTCCAA GAAATTTCTT TGTCGGGACG CCCAAACAAA CTCACACA-C
Cy._multiseptatum_STE-U_1602    GTATGCGAAA AATCATGAGT GCGCTCGCTT TGTGGAGAAA CATAGTCAAA CTGACACACC
Cy._multiseptatum_STE-U_1589    GTATGCGAAA AATCATGAGT GCGCTCGCTT TGTGGAGAAA CATAGTCAAA CTGACACACC
Cy._candelabrum_STE-U_1951      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAATCCGA CTCACAC-XC
Cy._candelabrum_STE-U_1674      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAATCCGA CTCACAC-XC
Cy._candelabrum_UFV_89          GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAATCCGA CTCACAC-XC
Cy._candelabrum_STE-U_1677      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAATCCGA CTCACAC-XC
Cy._pauciramosum_STE-U_1671     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XA
Cy._pauciramosum_STE-U_1670     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAATCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_416      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_972      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_143      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_2       GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_127     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_128     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_84      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_2030     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_925      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XA
Cy._pauciramosum_STE-U_913      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XA
Cy._pauciramosum_STE-U_1160     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAAAAG CACAAGCCAA CTCACAC-XA
Cy._pauciramosum_STE-U_951      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAT-XA
Cy._pauciramosum_STE-U_1990     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_1692     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_344      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_971      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_STE-U_1691     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_60      GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
Cy._pauciramosum_DISTEF_62      GTATGTGAAA ACCACTCGAA GCACTCGCTT GACTGAGAAG CACAAGCCAA CTGACAC-XC
Cy._pauciramosum_DISTEF_6       GTATGTGAAA ACCACTCGAA GCACTCGCTT GACTGAGAAG CACAAGCCAA CTGACAC-XC
Cy._pauciramosum_DISTEF_26      GTATGTGAAA ACCACTCGAA GCACTCGCTT GACTGAGAAG CACAAGCCAA CTGACAC-XC
Cy._pauciramosum_DISTEF_196     GTATGTGAAA ACCACTCGAA GCACTCGCTT GACTGAGAAG CACAAGCCAA CTGACAC-XC
Cy._pauciramosum_DISTEF_192     GTATGTGAAA ACCACTCGAA GCACTCCCTT GACCGAGAAG CACAAGCCAA CTCACAC-XC
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F._subglutinans_NRRL_22061      -XXXXXTAGG CCTCTGGCAA CAAGTATGTT CCCCGAGCCG TCCTCGTCGA TCTTGAGCCT
Cy._mexicanum_STE-U_927         -TCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._mexicanum_STE-U_941         GTCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._multiseptatum_STE-U_1602    AT-GTGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTTGA TCTTGAGCCC
Cy._multiseptatum_STE-U_1589    AT-GTGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTTGA TCTTGAGCCC
Cy._candelabrum_STE-U_1951      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._candelabrum_STE-U_1674      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._candelabrum_UFV_89          ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._candelabrum_STE-U_1677      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1671     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1670     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_416      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_972      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_143      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_2       ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_127     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_128     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_84      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_2030     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_925      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_913      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1160     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_951      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1990     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1692     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_344      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_971      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_STE-U_1691     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_60      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_62      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_6       ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_26      ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_196     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
Cy._pauciramosum_DISTEF_192     ATCATGTAGG CTTCCGGCAA CAAGTTCGTT CCTCGCGCTG TCCTCGTCGA TCTTGAGCCC
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F._subglutinans_NRRL_22061        GGTACCATGG ACGCCGTCCG AGCTGGTCCC TTCGGTCAGC T
Cy._mexicanum_STE-U_927           GGTACCATGG ATGCCGTCCG TGCTGGTCCC TTCGGTCAGC T
Cy._mexicanum_STE-U_941           GGTACCATGG ATGCCGTCCG TGCTGGTCCC TTCGGTCAGC T
Cy._multiseptatum_STE-U_1602      GGTACCATGG ATGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._multiseptatum_STE-U_1589      GGTACCATGG ATGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._candelabrum_STE-U_1951        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._candelabrum_STE-U_1674        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._candelabrum_UFV_89            GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._candelabrum_STE-U_1677        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1671       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1670       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_416        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_972        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_143        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_2         GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_127       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_128       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_84        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_2030       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_925        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_913        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1160       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_951        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1990       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1692       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_344        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_971        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_STE-U_1691       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_60        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_62        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_6         GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_26        GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_196       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
Cy._pauciramosum_DISTEF_192       GGTACCATGG ACGCCGTCCG TGCCGGTCCT TTCGGTCAGC T
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Alignment 5. Part 5. 5' end of β-tubulin gene DNA sequence alignment from *Cylindrocladium* species

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                                                                                                      60
F._subglutinans_NRRL_22061          GCGTT-GAGT TTATG-XXXX XGT-GCCCCT GATTCTACCC CGCTGGGC-G -XXXXGTGG-
Cy._avesiculatum_ATCC_38226         GCGTGCC-TT TGTTG-XXXX XCC-GCCCCT GATTCTACCC CGCCGTCCCG -XXXXGTTTC
Cy._candelabrum_STE-U_1674          GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._candelabrum_STE-U_1677          GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._candelabrum_STE-U_1951          GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._candelabrum_UFV_89              GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._citri_CBS_186.36                GCGTGCC-TT TGTTGTTGTT GCT-GCCCCT GATCCTACCC CGCCGCCCCA TGGGTGTTTC
Cy._colhounii_STE-U_1237            GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._colhounii_STE-U_1339            GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._colhounii_STE-U_681             GCGTGCC-TT TGTTG-XXXX XCT-GACCCT GATTCTACCC CGACGACCCG -XXXXGTTTC
Cy._colhounii_STE-U_705             GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._curvisporum_STE-U_763           GCGTGCC-TT TGTT-XXXXX -CT-GCCCCT GATTCTACCC CCCCGCCCCG -XXXXGTTTC
Cy._curvisporum_STE-U_765           GCGTGCC-TT TGTT-XXXXX -CT-GCCCCT GAGCGTACCC CCCCGCCCCG -XXXXGTTTC
Cy._flexuosum_STE-U_2536            GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._floridanum_ATCC_18834           GCGTGCC-TT TGTTA-XXXX XCT-GCCCCT GAGCGTACCC CGCCGACCCG -XXXXGTTTC
Cy._floridanum_ATCC_18882           GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGACCCG -XXXXGTTTC
Cy._floridanum_CBS_413.67           XXXXGCC-TT TGTTG-XXTT GCT-GCCCCT GATTGTACCC CGCCGCCCCG -XXXXGTTTC
Cy._floridanum_IMI_35428            XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGCCCCG -XXXXGTTTC
Cy._floridanum_IMI_35429            XXXXGCC-TT GGTTG-XXXX XCT-GCCCCA GAACGTACCA CGCCGCCCTG -XXXXGTTAC
Cy._floridanum_STE-U_2350           GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGACCCG -XXXXGTTTC
Cy._floridanum_STE-U_682            XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGACCCG -XXXXGTTTC
Cy._floridanum_UFV_76               XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGCCCCG -XXXXGTTTC
Cy._gracile_ATCC_22833              GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._gracile_IMI_167580              GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._gracile_PC_551197               GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._gracile_STE-U_1586              GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._gracile_STE-U_623               GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._graciloideum_STE-U_1153         ACGTGCC-TT GGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGTCCCG -XXXXGTTTC
Cy._hawksworthii_MUCL_30866         GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._heptaseptatum_FTCC_1002         GCGGGCN-TT TGTTG-XXXX XTT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._heptaseptatum_FTCC_1003         GCGTGCC-TT TGCTG-XXXX XCT-GCCCCT GATACTACCC CGCCGCCCCG -XXXXGTTTC
Cy._heptaseptatum_STE-U 2344        XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._insulare_STE-U_616              GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._insulare_STE-U_768              ACGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._insulare_STE-U_954              GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._leucothoes_ATCC_64824           XXXXXXXXXX XXXXXXXXXX XCT-GCCCCT GATCCTACCC CGCCGCCTCG GGGG-ATTTC
Cy._leucothoes_P97.2605             GCGAGCC-TT TGTTGTTGTT GCT-GCCCCT GATCCTACCC CGCCGCCTCG GGGG-ATTTC
Cy._macroconidiale_STE-U_307        GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._macroconidiale_STE-U_413        GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._mexicanum_STE-U_927             GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GGTTCTACCC CGCCGTCCCG -XXXXGTTTC
Cy._mexicanum_STE-U_941             GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGTCCCG -XXXXGTTTC
Cy._multiseptatum_STE-U_1589        GAGTGCC-TT TGTTGCT-TT -CTGGCCCCT GATTCTACCC CGCGGCCCCG -XXXXGTTTC
Cy._multiseptatum_STE-U_1602        GAGTGCC-TT TGTTGCT-TT GCT-GCCCCT GATTCTACCC CGCGGCCCCG -XXXXGTTTC
Cy._naviculatum_STE-U_627           GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXAATTC
Cy._naviculatum_STE-U_628           XXXXGCC-TT TGTTG-XXXX XTT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXAATTC
Cy._ovatum_UFV_90                   GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._parasiticum_ATCC_46133          GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGCCCYG -XXXXGTTTC
Cy._parasiticum_CBS_190.50          GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGCCCCG -XXXXGTTTC
Cy._parasiticum_STE-U_723           GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GAGCGTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pauciramosum_STE-U_416          GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pauciramosum_STE-U_925          GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pauciramosum_STE-U_972          GCGTGCC-TT TGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._penicilloides_CBS_174.55        GCGTGCCTTT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pseudogracile_AR_2677           GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pseudogracile_STE-U_1588        GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pteridiS_STE-U_2869             GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pteridis_STE-U_2190             GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._pteridis_UFV_43                 GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._quinqueseptatum_ATCC_16550      GCGTGCC-TT GGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._quinqueseptatum_STE-U_516       GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._quinqueseptatum_STE-U_759       GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._rumohrae_STE-U_1603             XXXXXCC-TT TGTTG-XXXX XCTTGCCCCT AATTCAACCC CGCCGCCCCG -XXXXGTTTC
Cy._rumohrae_UFV_215                GCGTGCCCTT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._rumohrae_UFV_218                GCGTGCCCTT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._scoparium_ATCC_38227            GGGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._scoparium_ATCC_46300            GCGTGCC-TT GGTTG-XXXX XCTTGCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._scoparium_STE-U_1720            GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._scoparium_STE-U_1722            GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._sp._STE-U_599                   XXXXXXC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCYCG -XXXXGTTTC
Cy._sp._STE-U_1150                  GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._sp._STE-U_1484                  GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._sp._STE-U_2321                  GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._sp._STE-U_2322                  GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGACCCG -XXXXGTTTC
Cy._sp._STE-U_2347                  GCGTGCC-TT TGTTG-XXXX XTT-GCCCCT GATTCTACCC CGCCGATCCG -XXXXGTTTC
Cy._sp._STE-U_2712                  GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathiphylli_ATCC_44730         GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathiphylli_STE-U_1624         XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathiphylli_STE-U_1641         XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathiphylli_STE-U_2186         XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathiphylli_STE-U_2188         XXXXGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathulatum_AR_1844             GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._spathulatum_ATCC_62616          GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._theae_ATCC_48895                GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTCC
Cy._theae_UFV_16A                   GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTCC
Cy._variabile_AR_2675               GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
Cy._variabile_UFV_28                GCGTGCC-TT TGTTG-XXXX XCT-GCCCCT GATTCTACCC CGCCGCCCCG -XXXXGTTTC
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						120
F._subglutinans_NRRL_22061	CA-XXGCTC-	XAACGACAAT	G-CACGATAG	CT-AGCAGC-	TTTAA-AT-X	ACCTTCTG-X
Cy._avesiculatum_ATCC_38226	CACC-GCTTC	-AACGACAA-	XXCAAAGCCG	CA-XGCCTCG	AGGAACAT-X	GGCGAGATA-
Cy._candelabrum_STE-U_1674	CATC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._candelabrum_STE-U_1677	CATC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._candelabrum_STE-U_1951	CATC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._candelabrum_UFV_89	CATC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._citri_CBS_186.36	CACC-GCTTC	GAACGACAA-	XXCAAAGCCG	CA-XGCCTCG	A-GAACAT-X	GGCGAGATAA
Cy._colhounii_STE-U_1237	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	GACGAGATA-
Cy._colhounii_STE-U_1339	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	GACGAGATA-
Cy._colhounii_STE-U_681	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	GACGAGATA-
Cy._colhounii_STE-U_705	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	GACGAGATA-
Cy._curvisporum_STE-U_763	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._curvisporum_STE-U_765	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._flexuosum_STE-U_2536	CACC-GCTCC	GA-CGACAA-	XXCAAAGCCG	TA-XGCCTC-	ACGAATAT-X	GGCGAGATA-
Cy._floridanum_ATCC_18834	CACC-GTTTC	GA-CAACAA-	XXCAAAGCTC	GATGGCTTC-	AAG-XCAC-X	AATGCGATA-
Cy._floridanum_ATCC_18882	CACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GATGGCTTC-	AAG-XCAC-X	AATGCGATA-
Cy._floridanum_CBS_413.67	AACC-GCCTC	GA-CAACAA-	XXCAAAGCTC	GACGGGGTCC	AAGAAC-XXX	TATGTGATA-
Cy._floridanum_IMI_35428	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._floridanum_IMI_35429	GACC-GCTTC	TA-CAACAA-	XXCAAAACTG	GACAACCCC-	AAG-XCAC-X	CATGTGATA-
Cy._floridanum_STE-U_2350	CACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GATGGCTTC-	AAG-XCAC-X	AATGCGATA-
Cy._floridanum_STE-U_682	CACC-GCTTC	GA-CAACAA-	XXCAAAGCTC	GATGGCTTG-	AAG-XCAC-X	AATGCGATA-
Cy._floridanum_UFV_76	GACC-GCTTC	GA-CGACAAC	AACAAAGCTC	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._gracile_ATCC_22833	CACC-GCTCC	GA-CGACAA-	XXCAAAGCCA	CA-XGCCTC-	ACGAACAT-X	GGCGAGATA-
Cy._gracile_IMI_167580	CACC-GCTCC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GGCGAGATA-
Cy._gracile_PC_551197	CACC-GCTCC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	GGCGAGATA-
Cy._gracile_STE-U_1586	CACC-GCTCC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GGCGAGATA-
Cy._gracile_STE-U_623	CACC-GCTCC	GA-CGACAA-	XXXAAAGCCA	CW-XTTCTC-	ACGAACAT-X	GGCGAGATA-
Cy._graciloideum_STE-U_1153	CACC-GCTTC	GA-CGAAAA-	XXCAAGGCCG	CA-XGCCTC-	AAGAACAT-X	GACGAGATA-
Cy._hawksworthii_MUCL_30866	CACC-ACCTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._heptaseptatum_FTCC_1002	CACC-GCTTC	GA-CGACAG-	XXCAAAGCCG	CG-XTCCTC-	ATGAACAT-X	GGCGAGATA-
Cy._heptaseptatum_FTCC_1003	CACC-GCTTC	GA-CGACAG-	XXCAAAGCCG	CG-XTCCTC-	ATGAACGT-X	GGCGAGATA-
Cy._heptaseptatum_STE-U 2344	CACC-GNTTT	GA-CGACAG-	XXCAAARCCG	CG-XTCCTC-	ATGAACAT-X	GGCGAGATA-
Cy._insulare_STE-U_616	CACC-ACCTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._insulare_STE-U_768	CACC-ACCTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._insulare_STE-U_954	CACC-ACCTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._leucothoes_ATCC_64824	CACC-GCTTC	AAACGACAA-	XXCAAAGCCG	CA-XGCCTCG	A-GAACAT-X	GGCGAGATAA
Cy._leucothoes_P97.2605	CACC-GCTTC	AAACGACAA-	XXCAAAGCCG	CA-XGCCTCG	A-GAACAT-X	GGCGAGATAA
Cy._macroconidiale_STE-U_307	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XTCCTC-	ACGAACAT-X	GGCGAGATA-
Cy._macroconidiale_STE-U_413	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XTCCTC-	ACGAACAT-X	GGCGAGATA-
Cy._mexicanum_STE-U_927	CACC-GCTAC	-AACGACAA-	XXCAAAGCCG	CA-XGCCTCG	AC-AACAT-G	AGCAAGATA-
Cy._mexicanum_STE-U_941	CACC-GCTAC	-AACGACAA-	XXCAAAGCCG	CA-XGCCTCG	AC-AACAT-G	AGCAAGATA-
Cy._multiseptatum_STE-U_1589	CACC-GCTCC	GA-CGAAAA-	XXCAAAGCCG	CA-XACCTC-	ACGAATGT-X	GACGAGATA-
Cy._multiseptatum_STE-U_1602	CACC-GCTCC	GA-CGAAAA-	XXCAAAGCCG	CA-XACCTC-	ACGAATGT-X	GACGAGATA-
Cy._naviculatum_STE-U_627	TGCC-GCCTC	GA-CAACAA-	XXCAAAGCCC	GACAACCTC-	GAG-XCGT-X	GATGTGACA-
Cy._naviculatum_STE-U_628	TTGCCGCNTC	GA-CAACAA-	XXCAAAGCCG	-ACAACCTC-	GAG-XCGT-X	GATGTGACA-
Cy._ovatum_UFV_90	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGACTC-	ACGAACAT-X	GACGAGATA-
Cy._parasiticum_ATCC_46133	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTG	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._parasiticum_CBS_190.50	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTG	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._parasiticum_STE-U_723	GACC-GCTTC	GA-CAACAA-	XXCAAAGCTG	GACGACCCC-	AAG-XCAC-X	GATGTGATA-
Cy._pauciramosum_STE-U_416	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	AACGAGATA-
Cy._pauciramosum_STE-U_925	CACC-GCTTG	GA-CGACAA-	XXCAAAGCCG	CA-XGGCTC-	ACGATCAT-X	GACGAGATA-
Cy._pauciramosum_STE-U_972	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	AACGAGATA-
Cy._penicilloides_CBS_174.55	GACC-GCC-C	GA-CGACAG-	XXAACAGCTC	GGCGGCTTC-	AGG-XCAT-X	GATGTGATGG
Cy._pseudogracile_AR_2677	CACC-GCTTC	GA-CAACAA-	XXCAAAGCCG	CT-XGCCTC-	ACGAACAT-X	GGCAAGATA-
Cy._pseudogracile_STE-U_1588	CACC-GCTTC	GA-CAACAA-	XXCAAAGCCG	CT-XGCCTC-	ACGAACAT-X	GGCAAGATA-
Cy._pteridiS_STE-U_2869	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GACGAGATA-
Cy._pteridis_STE-U_2190	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GACGAGATA-
Cy._pteridis_UFV_43	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GACGAGATA-
Cy._quinqueseptatum_ATCC_16550	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XXCCTCG	-TGAACAT-X	GACGAGATA-
Cy._quinqueseptatum_STE-U_516	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XACATC-	ATGAACAA-X	GACGAGATA-
Cy._quinqueseptatum_STE-U_759	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XXCATC-	ATGAACAA-X	GACGAGATA-
Cy._rumohrae_STE-U_1603	CACC-GCTTC	GA-CAACAG-	XXCAAAGTCG	CA-XCCCTC-	TTGAACAT-X	GATGATATA-
Cy._rumohrae_UFV_215	CACC-GCTTY	GA-CAACAG-	XXCAAAGCCG	CA-XCCCTC-	TTGAACAT-X	GACGATATA-
Cy._rumohrae_UFV_218	CACC-GCTTC	GA-CAACAG-	XXCAAAGCCG	CA-XCCCTC-	TTGAACAT-X	GACGATATA-
Cy._scoparium_ATCC_38227	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._scoparium_ATCC_46300	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._scoparium_STE-U_1720	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._scoparium_STE-U_1722	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._sp._STE-U_599	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._sp._STE-U_1150	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._sp._STE-U_1484	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._sp._STE-U_2321	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GACGAGATA-
Cy._sp._STE-U_2322	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACGT-X	GACGAGATA-
Cy._sp._STE-U_2347	CACC-GNTTC	GA-CGACAG-	XXCGAAACCG	CG-XTTCTC-	ATGAACAT-X	GACGAGATA-
Cy._sp._STE-U_2712	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._spathiphylli_ATCC_44730	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._spathiphylli_STE-U_1624	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	CATGAGATA-
Cy._spathiphylli_STE-U_1641	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	CATGAGATA-
Cy._spathiphylli_STE-U_2186	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	CATGAGATA-
Cy._spathiphylli_STE-U_2188	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAGCAT-X	CATGAGATA-
Cy._spathulatum_AR_1844	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._spathulatum_ATCC_62616	CACC-GCTTC	GA-CGACAA-	XXCAAAGCCG	CA-XGCCTC-	ACGATCAT-X	GACGAGATA-
Cy._theae_ATCC_48895	CACC-GCCTC	GA-TGGCAG-	XXCGAAGCCG	CA-XTCCTC-	ATGAACAAAA	GACGAGGCA-
Cy._theae_UFV_16A	CACC-GCCTC	GA-TGGCAG-	XXCGAAGCCG	CA-XTCCTC-	ATGAACAAAA	GACGAGGCA-
Cy._variabile_AR_2675	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-
Cy._variabile_UFV_28	CACC-ACATC	GA-CGAAAA-	XXCAAAGCCG	CA-XGCCTC-	ACGAACAT-X	GATGTGATA-

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*F.*_*subglutinans*_NRRL_22061	TCAAG-XATG	AAG-AAGCTA	ATCAGAT-CT	TTTCTCT-GC	GAT-XXAGGT	TCACCTCCAG
*Cy.*_*avesiculatum*_ATCC_38226	TCAAG-XATG	CAAT-GGCTA	ACCGTGTGTT	TCTTTCT-XC	AATTATAGGT	TCACCTTCAG
*Cy.*_*candelabrum*_STE-U_1674	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTTT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*candelabrum*_STE-U_1677	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTTT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*candelabrum*_STE-U_1951	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTTT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*candelabrum*_UFV_89	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTTT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*citri*_CBS_186.36	TCGGG-XATA	TGATT-GCTA	ACCGTCTGTT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*colhounii*_STE-U_1237	TCGAA-XACA	AGATTTGCTG	ACCATGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*colhounii*_STE-U_1339	TCGAA-XACA	AGATTTGCTG	ACCATGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*colhounii*_STE-U_681	TCGAA-XACA	AGATTTGGTG	ACCATGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*colhounii*_STE-U_705	TCGAA-XACA	AGATTTGCTG	ACCATGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*curvisporum*_STE-U_763	TCGGAGGACA	AGGTT-GCTG	ACTAT-XATT	TCTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*curvisporum*_STE-U_765	TCGGAGGACA	AGGTT-GCTG	ACTAT-XATT	TCTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*flexuosum*_STE-U_2536	CCAGA-XACA	AGATT-GCTA	ACCATGTGCT	TATTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*floridanum*_ATCC_18834	TTGGAGGACA	AGGTT-GCTA	ACTAT-CGTT	TTTCTCTCTC	AATTATAGGT	CCACCTCCAG
*Cy.*_*floridanum*_ATCC_18882	TTGGAGGACA	AGGTT-GCTA	ACTAT-CGTT	TTTCTCTCTC	AATTATAGGT	CCACCTCCAG
*Cy.*_*floridanum*_CBS_413.67	TCGGAGGACA	AGATT-GCTA	ACGA-XCGGT	TT-CTTCC-C	AATTCTAGGT	CCACCTCCAG
*Cy.*_*floridanum*_IMI_35428	TCGAAGGACA	AGGTT-GCTG	ACTAT-TATT	TCTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*floridanum*_IMI_35429	TCGAAGGACA	AGGTT-GCTG	ACTAT-TATA	AATTGGT-XC	AATTCTAGGT	TCACCTACAG
*Cy.*_*floridanum*_STE-U_2350	TTGGAGGACA	AGGTT-GCTA	ACTAT-CGTT	TTTCTCTCTC	AATTATAGGT	CCACCTCCAG
*Cy.*_*floridanum*_STE-U_682	TTGGAGGACA	AGGTT-GCTA	ACTAT-CGTT	TTTCTCTCTC	AATTATAGGT	CCACCTCCAG
*Cy.*_*floridanum*_UFV_76	TCGGAGGACA	AGGGC-GCTG	ACTAT-TATT	TGTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*gracile*_ATCC_22833	TCAGA-XACA	AGATT-GCTA	ACCATGTCCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*gracile*_IMI_167580	TCAGA-XACA	AGATT-GCTA	ACCATGTCCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*gracile*_PC_551197	TCAGA-XACA	AGATT-GCTA	ACCATGTCCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*gracile*_STE-U_1586	TCAGA-XACA	AGATT-GCTA	ACCATGTCCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*gracile*_STE-U_623	TCAGA-XACA	AGATAA-CNA	ACCATGTCCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*graciloideum*_STE-U_1153	TCAGA-XACA	AGATT-GCTG	ACCATGTGCT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*hawksworthii*_MUCL_30866	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*heptaseptatum*_FTCC_1002	TCAGA-XACA	AGATT-GCTG	ACTATGTGCT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*heptaseptatum*_FTCC_1003	TCACA-XACA	AGATT-GCTG	ACTATGTGCT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*heptaseptatum*_STE-U 2344	TCAGA-XACA	AGATN-GCTG	ACTATGTGCT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*insulare*_STE-U_616	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCC	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*insulare*_STE-U_768	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*insulare*_STE-U_954	TCAGA-XACA	AGATT-GCTA	ACCGTCTGCT	TCTTTCT-XC	GACTATAGGT	CCACCTCCAG
*Cy.*_*leucothoes*_ATCC_64824	TCGGG-XATA	TGAT-GGCTA	ACCGTGT-XT	TCTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*leucothoes*_P97.2605	TCGGG-XATA	TGAT-GGCTA	ACCGTGT-XT	TCTTTCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*macroconidiale*_STE-U_307	TCGGA-XACA	AGATTTGCTG	ACCATGTGCT	TCTTTCT-XC	AACTATAGGT	CCACCTCCAG
*Cy.*_*macroconidiale*_STE-U_413	TCGGA-XACA	AGATTTGCTG	ACCATGTGCT	TCTTTCT-XC	AACTATAGGT	CCACCTCCAG
*Cy.*_*mexicanum*_STE-U_927	TCAGG-XATA	TGAT-GGCTA	ACCGTGTGTT	TCTTCCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*mexicanum*_STE-U_941	TCAGG-XATA	TGAT-GGCTA	ACCGTGTGTT	TCTTCCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*multiseptatum*_STE-U_1589	TCAGA-XACA	AGATT-GCTA	ACCTTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*multiseptatum*_STE-U_1602	TCAGA-XACA	AGATT-GCTA	ACCTTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*naviculatum*_STE-U_627	TAGGGGAACA	AGTTT-GCTG	ACCATGTGCT	TTTT-XXXXC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*naviculatum*_STE-U_628	TAGGGGAACA	AGTTT-GCTG	ACCATGTGCT	TTTT-XXXXC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*ovatum*_UFV_90	TCAGA-XACG	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*parasiticum*_ATCC_46133	TCGGAGGACA	AGGTT-GCTG	ACTAT-XXXT	TCTTTCT-XC	AATTCTAGGT	CCACCTCCAG
*Cy.*_*parasiticum*_CBS_190.50	TCGGAGGACA	AGGTT-GCTG	ACTAT-XXXT	TCTTTCT-XC	AATTCTAGGT	CCACCTCCAG
*Cy.*_*parasiticum*_STE-U_723	TCGGAGGACA	AGGTT-GCTG	ACTAT-TATT	TCTTCCT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*pauciramosum*_STE-U_416	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*pauciramosum*_STE-U_925	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*pauciramosum*_STE-U_972	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*penicilloides*_CBS_174.55	ACG-AGGACA	AGATT-GCTG	ACCAAGT-XT	TCTT-CT-XC	AATTCTAGGT	TCACCTCCAG
*Cy.*_*pseudogracile*_AR_2677	TCAGA-XACA	AGATT-GCTA	ACCGTTTGCT	TCTTTTT-XC	GATCATAGGT	CCACCTCCAG
*Cy.*_*pseudogracile*_STE-U_1588	TCAGA-XACA	AGATT-GCTA	ACCGTTTGCT	TCTTTTT-XC	GATCATAGGT	CCACCTCCAG
*Cy.*_*pteridiS*_STE-U_2869	TCAGA-XACG	AGATC-GCTA	ACCGTGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*pteridis*_STE-U_2190	TCAGA-XACG	AGATC-GCTA	ACCGTGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*pteridis*_UFV_43	TCAGA-XACG	AGATC-GCTA	ACCGTGTGCT	TCTTTTT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_*quinqueseptatum*_ATCC_16550	TCGGA-XACA	AGATT-GCTA	ACCATGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*quinqueseptatum*_STE-U_516	TCGGA-XACA	AGATT-GCTA	ACCATGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*quinqueseptatum*_STE-U_759	TCGGA-XACA	AGATT-GCTA	ACCATGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*rumohrae*_STE-U_1603	TTGGA-XATC	AGATT-GCTG	ACCGTGTGCT	TCTTTCT-XC	AATAATAGGT	CCACCTCCAG
*Cy.*_*rumohrae*_UFV_215	TTGGA-XATC	AAATT-GCTG	ACCATGTGCT	TCTTTCT-XC	AATTATAGGT	CTACCTCCAG
*Cy.*_*rumohrae*_UFV_218	TTGGA-XATC	AAATT-GCTG	ACCATGTGCT	TCTTTCT-XC	AATTATAGGT	CTACCTCCAG
*Cy.*_*scoparium*_ATCC_38227	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*scoparium*_ATCC_46300	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*scoparium*_STE-U_1720	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*scoparium*_STE-U_1722	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_599	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_1150	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_1484	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_2321	TCGGA-XACA	AGATT-GCTG	ACCATGTGCT	TCTTTCT-XC	AACTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_2322	TCGGA-XACA	AGATT-GCTG	ACCATGTGCT	TCTTTCT-XC	AACTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_2347	TCAGA-XACA	AGATT-GCTA	ACCATGTGCT	TCCTTCT-XC	AATTATAGGT	CCACCTCCAG
*Cy.*_sp._STE-U_2712	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*spathiphylli*_ATCC_44730	TCGGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	CATTATAGGT	CCACCTCCAG
*Cy.*_*spathiphylli*_STE-U_1624	TCGGA-XACA	AGATT-GCTA	ACCGTGTGTT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*spathiphylli*_STE-U_1641	TCGGA-XACA	AGATT-GCTA	ACCGTGTGTT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*spathiphylli*_STE-U_2186	TCGGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	CATTATAGGT	CCACCTCCAG
*Cy.*_*spathiphylli*_STE-U_2188	TCGGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	CATTATAGGT	CCACCTCCAG
*Cy.*_*spathulatum*_AR_1844	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*spathulatum*_ATCC_62616	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*theae*_ATCC_48895	TCAGA-XACC	AGATT-GCTG	ACCATGTCCT	TTTCTCT-XG	AATTATAGGT	CCACCTCCAG
*Cy.*_*theae*_UFV_16A	TCAGA-XACC	AGATT-GCTG	ACCATGTCCT	TTTCTCT-XG	AATTATAGGT	CCACCTCCAG
*Cy.*_*variabile*_AR_2675	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG
*Cy.*_*variabile*_UFV_28	TCAGA-XACA	AGATT-GCTA	ACCGTGTGCT	TCTTTCT-XC	GATTATAGGT	CCACCTCCAG

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F._subglutinans_NRRL_22061	ACCGGTCAGT	GCGTAAGTGC	TCATCG-CTT	CC-TCGAC-X	-XXGTCGCAT	-XGTGGGG-G
Cy._avesiculatum_ATCC_38226	ACCGGTCAGT	GCGTAAGTGC	TCTCAT-CAA	CC-CCGAAAA	AAAACTTTCT	-CGAGGCCAT
Cy._candelabrum_STE-U_1674	ACCGGTCAGT	GCGTAAGTAC	CCTTCT-CAA	CT-CCGACCA	AA-XXXTTCT	-CACGACGAG
Cy._candelabrum_STE-U_1677	ACCGGTCAGT	GCGTAAGTAC	CCTTCT-CAA	CT-CCGACCA	AA-XXXTTCT	-CACGACGAG
Cy._candelabrum_STE-U_1951	ACCGGTCAGT	GCGTAAGTAC	CCTTCT-CAA	CT-CCGACCA	AA-XXXTTCT	-CACGACGAG
Cy._candelabrum_UFV_89	ACCGGTCAGT	GCGTAAGTAC	CCTTCT-CAA	CT-CCGACCA	AA-XXXTTCT	-CACGACGAG
Cy._citri_CBS_186.36	ACCGGTCAGT	GCGTAAGTCA	CCATCTTCAA	CT-CCGAAAA	AA-XCTTTCT	-CACGGCCAT
Cy._colhounii_STE-U_1237	ACCGGCCAGT	GCGTAAGTGC	TCTTGT-CAA	CT-CCAACAA	TA-XXXTTAT	-CAC-XXGAG
Cy._colhounii_STE-U_1339	ACCGGTCAAT	GCGTAAGTGC	TCTTGT-CAA	CT-CCAACAA	TA-XXXTTAT	-CAC-XXGAG
Cy._colhounii_STE-U_681	ACCGGTCAGT	GCGTAAGTGC	TCTTGT-TAA	CT-CCAACAA	TA-XXXTTAT	-CAC-XXGAG
Cy._colhounii_STE-U_705	ACCGGCCAGT	GCGTAAGTGC	TCTTGT-CAA	CT-CCAACAA	TA-XXXTTAT	-CAC-XXGAG
Cy._curvisporum_STE-U_763	ACCGGTCAGT	GCGTAAGTGA	TCATTC-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCCTGAGG
Cy._curvisporum_STE-U_765	ACCGGTCAGT	GCGTAAGTGA	TCATTC-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCCTGAGG
Cy._flexuosum_STE-U_2536	ACCGGCCAGT	GCGTAAGTAC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CATGACGAG
Cy._floridanum_ATCC_18834	ACCGGTCAGT	GCGTAAGTGA	TAGTTCCCAA	CTT-CAAAAA	AAAAA-XTCT	-ACCGTGAAG
Cy._floridanum_ATCC_18882	ACCGGTCAGT	GCGTAAGTGA	TAGTTCCCAA	CTT-CAAAAA	AAAAA-XTCT	-ACCGTGAAG
Cy._floridanum_CBS_413.67	ACCGGTCAGT	GCGTAAGTGT	TCATTCCGAA	-T-CCAAAG-	XXXXXXXTCT	-GCCCCGAGT
Cy._floridanum_IMI_35428	ACCGGTCAGT	GCGTAAGTGA	TCATT-CCAG	CTTCCAA-AA	A-XXXXXXCT	-CCCCTGAGG
Cy._floridanum_IMI_35429	ACCGGTCAAC	GCGTAAGTGA	TAATTT-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCCTGAGG
Cy._floridanum_STE-U_2350	ACCGGTCAGT	GCGTAAGTGA	TAGTTCCCAA	CTTCAAAAAA	AAAA-XXTCT	-ACCGTGAAG
Cy._floridanum_STE-U_682	ACCGGTCAGT	GCGTAAGTGA	TAGTTCCCAA	CTTCAAAAAA	AAAA-XXTCT	-ACCGNGAAG
Cy._floridanum_UFV_76	ACCGGTCAGT	GCGTAAGTGA	TTATT-CCAG	CTTCCAA-AA	A-XXXXXXCT	-GCCTTGGGG
Cy._gracile_ATCC_22833	ACCGGTCAGT	GCGTAAGTGA	TATTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGATGAG
Cy._gracile_IMI_167580	ACCGGTCAGT	GCGTAAGTGA	TATTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._gracile_PC_551197	ACCGGTCAGT	GCGTAAGTGA	TATTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._gracile_STE-U_1586	ACCGGTCAGT	GCGTAAGTGA	TATTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._gracile_STE-U_623	ACCGGTCAGT	GCGTAAGTGA	TATTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGATGAG
Cy._graciloideum_STE-U_1153	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CGCGGCCA-
Cy._hawksworthii_MUCL_30866	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCAG
Cy._heptaseptatum_FTCC_1002	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CCCGGCGAG
Cy._heptaseptatum_FTCC_1003	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-ACAACAA	AA-XXXTTCT	-CGCGGCAAG
Cy._heptaseptatum_STE-U 2344	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CCCGGCGAG
Cy._insulare_STE-U_616	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACGG	AA-XXXTTCT	-CACGACCAG
Cy._insulare_STE-U_768	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCAG
Cy._insulare_STE-U_954	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CTAACAA	AA-XXXTTCT	-CACGACCAG
Cy._leucothoes_ATCC_64824	ACCGGTCAGT	GCGTAAGTGA	TCCTATTCAA	CCCCCAA-AA	A-XXCTTTCT	-CGCCGCCAT
Cy._leucothoes_P97.2605	ACCGGTCAGT	GCGTAAGTGA	TCCTATTCAA	CCCCCAA-AA	A-XXCTTTCT	-CGCCGCCAT
Cy._macroconidiale_STE-U_307	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCGACAA	TA-XXXTTAT	-CACGGCGAG
Cy._macroconidiale_STE-U_413	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCGACAA	TA-XXXTTAT	-CACGGCGAG
Cy._mexicanum_STE-U_927	ACCGGTCAGT	GCGTAAGTAC	TCCTTG-CAA	CT-CCAACAA	-XXXCTTTCT	-CACGGCCAT
Cy._mexicanum_STE-U_941	ACCGGTCAGT	GCGTAAGTAC	TCCTTG-CAA	CT-CCAACAA	-XXXCTTTCT	-CACGGCCAT
Cy._multiseptatum_STE-U_1589	ACCGGCCAGT	GCGTAAGTGC	TCCTCT-CGA	CT-CCAACGA	TA-XXXTTCT	-TATGACAAG
Cy._multiseptatum_STE-U_1602	ACCGGCCAGT	GCGTAAGTGC	TCCTCT-CGA	CT-CCAACGA	TA-XXXTTCT	-TATGACAAG
Cy._naviculatum_STE-U_627	ACCGGTCAGT	GCGTAAGT-A	TTTAATCCGA	CT-CCAG-AA	-XXXXXTTCG	TCGTGATGAG
Cy._naviculatum_STE-U_628	ACCGGTCAGT	GCGTAAGT-A	TTTAATCCGA	CT-CCAG-AA	-XXXXXTTCG	TCGTGATGAG
Cy._ovatum_UFV_90	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CAA	CT-CCAACAA	GA-XXXTTCT	-CACGACGAG
Cy._parasiticum_ATCC_46133	ACCGGTCAGT	GCGTAAGTGA	TCATTC-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCCTGGGG
Cy._parasiticum_CBS_190.50	ACCGGTCAGT	GCGTAAGTGA	TCATTC-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCCTGGGG
Cy._parasiticum_STE-U_723	ACCGGTCAGT	GCGTAAGTGA	TCATTC-CAG	CTTCCAA-AA	A-XXXXXXCT	-GCCTTGAGG
Cy._pauciramosum_STE-U_416	ACCGGTCAGT	GCGTAAGTAC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._pauciramosum_STE-U_925	ACCGGTCAGT	GCGTAAGTAC	TCTTCT-CAA	CT-CCAACCA	AA-XXXTTCT	-CACGACGAG
Cy._pauciramosum_STE-U_972	ACCGGTCAGT	GCGTAAGTAC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._penicilloides_CBS_174.55	ACCGGTCAGT	GCGTAAGTCT	TCAC-XXCAA	CGCCCAA-XX	XXXXTTCTCT	-CCCAAGGAG
Cy._pseudogracile_AR_2677	ACCGGTCAGT	GCGTAAGTGA	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACAAG
Cy._pseudogracile_STE-U_1588	ACCGGTCAGT	GCGTAAGTGA	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACAAG
Cy._pteridiS_STE-U_2869	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CGA	CT-CCAGCAA	GA-XXXTTTT	-CACGACGAG
Cy._pteridis_STE-U_2190	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CGA	CT-CCAGCAA	GA-XXXTTTT	-CACGACGAG
Cy._pteridis_UFV_43	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CGA	CT-CCAGCAA	GA-XXXTTTT	-CACGACGAG
Cy._quinqueseptatum_ATCC_16550	ACCGGTCAGT	GCGTAAGTGC	TCCTC-XXXG	CT-CCGAAAA	TG-XXXTTCT	-CATGACAAC
Cy._quinqueseptatum_STE-U_516	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CGA	-TTCCAAATA	TG-XXXTTCT	-CATGACAAG
Cy._quinqueseptatum_STE-U_759	ACCGGTCAGT	GCGTAAGTGC	TCCTCT-CGA	-TTCCAAATA	TG-XXXTTCT	-CATGACAAG
Cy._rumohrae_STE-U_1603	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAGCAA	AA-XXXTTCT	-CGCAGCGAG
Cy._rumohrae_UFV_215	ACCGGTCAGT	GCGTAAGTAC	ATTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CGCAGCGAG
Cy._rumohrae_UFV_218	ACCGGTCAGT	GCGTAAGTAC	ATTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CGCAGCGAG
Cy._scoparium_ATCC_38227	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._scoparium_ATCC_46300	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._scoparium_STE-U_1720	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._scoparium_STE-U_1722	ACCGGTCAGT	GCGTAAGTGC	TCTT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._sp._STE-U_599	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._sp._STE-U_1150	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._sp._STE-U_1484	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._sp._STE-U_2321	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAA-XX	GA-XXXTTCT	-CACCACGGG
Cy._sp._STE-U_2322	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-TCGA-XX	TA-XXXTTCT	-CACGACGAG
Cy._sp._STE-U_2347	ACCGGTCAGT	GCGTAAGTGC	TCTTCC-CAA	CT-CGAACAA	AA-XXXTTCT	-CGCGGCGAG
Cy._sp._STE-U_2712	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._spathiphylli_ATCC_44730	ACCGGTCAGT	GCGTAAGTGC	TCCT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._spathiphylli_STE-U_1624	ACCGGTCAGT	GCGTAAGTGC	TACT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCAG
Cy._spathiphylli_STE-U_1641	ACCGGTCAGT	GCGTAAGTGC	TACT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCAG
Cy._spathiphylli_STE-U_2186	ACCGGTCAGT	GCGTAAGTGC	TCCT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._spathiphylli_STE-U_2188	ACCGGTCAGT	GCGTAAGTGC	TCCT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._spathulatum_AR_1844	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._spathulatum_ATCC_62616	ACCGGTCAGT	GCGTAAGTAC	TTTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGAG
Cy._theae_ATCC_48895	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGGG
Cy._theae_UFV_16A	ACCGGTCAGT	GCGTAAGTGC	TCTTCT-CAA	CT-CCAACAA	AA-XXXTTCT	-CACGACGGG
Cy._variabile_AR_2675	ACCGGTCAGT	GCGTAAGTGC	TCAT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGG
Cy._variabile_UFV_28	ACCGGTCAGT	GCGTAAGTGC	TCAT-XXCAA	CT-CCAACAA	AA-XXXTTCT	-CACGACCGT

						300
*F._subglutinans*_NRRL_22061	A-XXXTGCTC	AC-XGAGTTT	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAAACCAT
*Cy._avesiculatum*_ATCC_38226	ATT-XCACTG	ACAGGAGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._candelabrum*_STE-U_1674	ATT-XCACTG	ACAGTTGTCC	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._candelabrum*_STE-U_1677	ATT-XCACTG	ACAGTTGTCC	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._candelabrum*_STE-U_1951	ATT-XCACTG	ACAGTTGTCC	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._candelabrum*_UFV_89	ATT-XCACTG	ACAGTTGTCC	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._citri*_CBS_186.36	GTT-XCTCTA	ACTCTCGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._colhounii*_STE-U_1237	ATT-XTACTG	ACATATGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._colhounii*_STE-U_1339	ATT-XTACTG	ACACATGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._colhounii*_STE-U_681	ATT-XTACTG	ACATATGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._colhounii*_STE-U_705	ATT-XTACTG	ACATATGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._curvisporum*_STE-U_763	ATT-XCACTA	ACA-TTCGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._curvisporum*_STE-U_765	ATT-XCACTA	ACA-TTCGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._flexuosum*_STE-U_2536	ATT-XTACTG	ACGGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._floridanum*_ATCC_18834	ATT-XGACTG	ACACTTATGG	CT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._floridanum*_ATCC_18882	ATT-XGACTG	ACACTTATGG	CT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._floridanum*_CBS_413.67	ATT-XCACTG	ACATTCGTGG	TT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCANACCAT
*Cy._floridanum*_IMI_35428	ATT-XCACTA	ACA-TTCGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._floridanum*_IMI_35429	ATT-XCACTA	ACA-TTCGGG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAAACCAT
*Cy._floridanum*_STE-U_2350	ATT-XGACTG	ACACTTATGG	CT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCACACCAT
*Cy._floridanum*_STE-U_682	ATT-XGACTG	ACACTTATGG	CT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._floridanum*_UFV_76	ATT-XCACTA	ACA-TTCGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._gracile*_ATCC_22833	ATT-XCACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._gracile*_IMI_167580	ATT-XCACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._gracile*_PC_551197	ATT-XCACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._gracile*_STE-U_1586	ATT-XCACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._gracile*_STE-U_623	ATT-XCACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._graciloideum*_STE-U_1153	GATT-CGCTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._hawksworthii*_MUCL_30866	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._heptaseptatum*_FTCC_1002	ATT-XTACTG	ACATGTTTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._heptaseptatum*_FTCC_1003	ATT-XTACTG	ACATGTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._heptaseptatum*_STE-U 2344	ATT-XTACTG	ACATGTTTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._insulare*_STE-U_616	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._insulare*_STE-U_768	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._insulare*_STE-U_954	ATT-XCACTG	ACAATTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._leucothoes*_ATCC_64824	GTT-XCACTG	ACAGTCGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._leucothoes*_P97.2605	GTT-XCACTG	ACAGTCGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._macroconidiale*_STE-U_307	GTT-XTACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._macroconidiale*_STE-U_413	GTT-XTACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._mexicanum*_STE-U_927	GAT-XCGCTG	ACAGACGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._mexicanum*_STE-U_941	GAT-XCTCTG	ACAGACGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._multiseptatum*_STE-U_1589	ATT-XCACTG	ACAGTTTTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._multiseptatum*_STE-U_1602	ATT-XCACTG	ACAGTTTTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._naviculatum*_STE-U_627	ATT-XTGCTG	AC-CTTGGTG	GACAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._naviculatum*_STE-U_628	ATT-XTGCTG	AC-CTTGGTG	GACAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._ovatum*_UFV_90	ATT-XCGCTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._parasiticum*_ATCC_46133	ATT-XCACTA	ACA-TTSGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._parasiticum*_CBS_190.50	ATT-XCACTA	ACA-TTGGCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._parasiticum*_STE-U_723	ATT-XCACTA	ACA-TTCRCG	ATCAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pauciramosum*_STE-U_416	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pauciramosum*_STE-U_925	GTT-XCGCTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pauciramosum*_STE-U_972	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._penicilloides*_CBS_174.55	ATT-XCGCTC	ACAAT-CACA	AACAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAAACCAT
*Cy._pseudogracile*_AR_2677	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pseudogracile*_STE-U_1588	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pteridiS*_STE-U_2869	ATT-XCGCTG	ACAGTTGTCA	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pteridis*_STE-U_2190	ATT-XCGCTG	ACAGTTGTCA	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._pteridis*_UFV_43	ATT-XCGCTG	ACAGTTGTCA	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._quinqueseptatum*_ATCC_16550	GTT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._quinqueseptatum*_STE-U_516	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTTT	GGCAGACCAT
*Cy._quinqueseptatum*_STE-U_759	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._rumohrae*_STE-U_1603	ATG-XAACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._rumohrae*_UFV_215	ATA-XAACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._rumohrae*_UFV_218	ATA-XAACTG	ACATTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._scoparium*_ATCC_38227	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._scoparium*_ATCC_46300	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._scoparium*_STE-U_1720	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._scoparium*_STE-U_1722	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_599	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_1150	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_1484	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_2321	ATT-XTACTG	ACAGCTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_2322	ATT-XTACTG	ACAGCTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_2347	ATT-XTACTG	ACATTTGTCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._sp.*_STE-U_2712	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathiphylli*_ATCC_44730	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathiphylli*_STE-U_1624	ATT-XTACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathiphylli*_STE-U_1641	ATT-XTACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathiphylli*_STE-U_2186	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathiphylli*_STE-U_2188	ATT-XCACTG	ACAGTTATCG	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathulatum*_AR_1844	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._spathulatum*_ATCC_62616	ATT-XCACTG	ACAGTTGTCG	AT-AGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._theae*_ATCC_48895	ATT-XCGCTG	ACACTCGCGG	AT-AGGGTAA	CCAAATCGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._theae*_UFV_16A	ATT-XCGCTG	ACACTCGCGG	AT-AGGGTAA	CCAAATCGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._variabile*_AR_2675	ATT-XCACTG	ACAGTTATCA	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT
*Cy._variabile*_UFV_28	ATT-XCACTG	ACAGTTATCA	A-CAGGGTAA	CCAAATTGGT	GCTGCTTTCT	GGCAGACCAT

						360
F._subglutinans_NRRL_22061	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	AGCTCCAGCT
Cy._avesiculatum_ATCC_38226	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._candelabrum_STE-U_1674	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._candelabrum_STE-U_1677	CTSTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._candelabrum_STE-U_1951	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._candelabrum_UFV_89	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._citri_CBS_186.36	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._colhounii_STE-U_1237	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._colhounii_STE-U_1339	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._colhounii_STE-U_681	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._colhounii_STE-U_705	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._curvisporum_STE-U_763	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._curvisporum_STE-U_765	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._flexuosum_STE-U_2536	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._floridanum_ATCC_18834	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_ATCC_18882	TTTTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_CBS_413.67	CTTTGGCGAG	CACGGCCTTG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_IMI_35428	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTTTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_IMI_35429	CTTTGGCGAG	CACGGTCTCG	ACAGCGGTGG	TGTCTACAAC	GGAACCTCCG	ACCTGCAGTT
Cy._floridanum_STE-U_2350	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_STE-U_682	CTTTGGCGAG	CACGGCCTCT	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._floridanum_UFV_76	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTTCG	ACCTCCAGTT
Cy._gracile_ATCC_22833	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._gracile_IMI_167580	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._gracile_PC_551197	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._gracile_STE-U_1586	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._gracile_STE-U_623	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._graciloideum_STE-U_1153	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._hawksworthii_MUCL_30866	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._heptaseptatum_FTCC_1002	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTNTACGCC	GGTACCTCCG	AGCTTCAGCT
Cy._heptaseptatum_FTCC_1003	TTCTGGCGAG	CACGGTCTCA	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTTCAGCT
Cy._heptaseptatum_STE-U 2344	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTTTACGCC	GGTACCTCCG	AGCTTCAGCT
Cy._insulare_STE-U_616	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._insulare_STE-U_768	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._insulare_STE-U_954	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._leucothoes_ATCC_64824	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCTG	AGCTCCAGCT
Cy._leucothoes_P97.2605	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCTG	AGCTCCAGCT
Cy._macroconidiale_STE-U_307	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._macroconidiale_STE-U_413	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._mexicanum_STE-U_927	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._mexicanum_STE-U_941	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._multiseptatum_STE-U_1589	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._multiseptatum_STE-U_1602	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._naviculatum_STE-U_627	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGCACCTCTG	AGCTCCAGCT
Cy._naviculatum_STE-U_628	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTYTACAAC	GGCACCTCTG	AGCTCCAGCT
Cy._ovatum_UFV_90	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._parasiticum_ATCC_46133	CTCTGGMGAG	CACGGCCTTK	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._parasiticum_CBS_190.50	CTCTGGCGAG	CACGGCCTTG	ACAGCAATGG	TGTCTACAAC	GGTACCTCCG	ACCTCCAGTT
Cy._parasiticum_STE-U_723	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACAAC	GGTACCTCTG	ACCTCCAGTT
Cy._pauciramosum_STE-U_416	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._pauciramosum_STE-U_925	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._pauciramosum_STE-U_972	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._penicilloides_CBS_174.55	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	ATCTCCAGCT
Cy._pseudogracile_AR_2677	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AACTCCAGCT
Cy._pseudogracile_STE-U_1588	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AACTCCAGCT
Cy._pteridiS_STE-U_2869	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._pteridis_STE-U_2190	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._pteridis_UFV_43	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._quinqueseptatum_ATCC_16550	CTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	TGTCTACGCT	GGTACTTCCG	AGCTCCAGCT
Cy._quinqueseptatum_STE-U_516	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._quinqueseptatum_STE-U_759	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._rumohrae_STE-U_1603	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._rumohrae_UFV_215	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._rumohrae_UFV_218	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._scoparium_ATCC_38227	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._scoparium_ATCC_46300	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._scoparium_STE-U_1720	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._scoparium_STE-U_1722	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._sp._STE-U_599	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._sp._STE-U_1150	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._sp._STE-U_1484	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._sp._STE-U_2321	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._sp._STE-U_2322	TTCTGGCGAG	CACGGCCTAG	ACAGCAATGG	TGTCTACGCT	GGTACCTCTG	AGCTCCAGCT
Cy._sp._STE-U_2347	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCTG	AGCTCCAGCT
Cy._sp._STE-U_2712	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._spathiphylli_ATCC_44730	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._spathiphylli_STE-U_1624	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._spathiphylli_STE-U_1641	CTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._spathiphylli_STE-U_2186	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._spathiphylli_STE-U_2188	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._spathulatum_AR_1844	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._spathulatum_ATCC_62616	TTCTGGCGAG	CACGGCCTCG	ACAGCAATGG	CGTCTACGCC	GGTACCTCCG	AGCTCCAGCT
Cy._theae_ATCC_48895	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACTTCCG	AGCTCCAGCT
Cy._theae_UFV_16A	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACTTCCG	AGCTCCAGCT
Cy._variabile_AR_2675	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT
Cy._variabile_UFV_28	TTCTGGCGAG	CACGGTCTCG	ACAGCAATGG	TGTCTACGCT	GGTACCTCCG	AGCTCCAGCT

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*F.*_*subglutinans*_NRRL_22061	CGAGCGTATG AGTGTCTACT	TCAACGAGGT	ATGC-TTTAA	-XCA-G-TCA	ATGCCAA-GA
*Cy.*_*avesiculatum*_ATCC_38226	CGAGCGTATG AACGTCTACT	TTAACGAGGT	GTGTA-XAAA	ACCGCGCCGA	-GAACTTTC-
*Cy.*_*candelabrum*_STE-U_1674	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*candelabrum*_STE-U_1677	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*candelabrum*_STE-U_1951	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*candelabrum*_UFV_89	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*citri*_CBS_186.36	CGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCGCGCCGA	-GAACTCTC-
*Cy.*_*colhounii*_STE-U_1237	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	GCTGC-TTGG	TGT-XCCCC-
*Cy.*_*colhounii*_STE-U_1339	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	GCTGC-TTGG	TGTA-CCCC-
*Cy.*_*colhounii*_STE-U_681	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	GCTGC-TTGG	TGTA-CCCT-
*Cy.*_*colhounii*_STE-U_705	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	GCTGC-TTGG	TGTA-CCCC-
*Cy.*_*curvisporum*_STE-U_763	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AATA-XXAAA	CG-XCTCGCC
*Cy.*_*curvisporum*_STE-U_765	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AATA-XXAAA	CG-XCTCGCC
*Cy.*_*flexuosum*_STE-U_2536	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*floridanum*_ATCC_18834	GGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGGTCAA	ATT-XGC-AA	CA-XXTCGC-
*Cy.*_*floridanum*_ATCC_18882	GGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGGTCAA	ATTGC-XXAA	CA-XXTCGC-
*Cy.*_*floridanum*_CBS_413.67	GGAGCGCATG AACGTTTACT	TCAACGAGGT	ATGTAGCGAA	AGAGCGCGCA	TACGCGCTCA
*Cy.*_*floridanum*_IMI_35428	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGNTAA	AATA-XXAAA	CG-XCTCGCC
*Cy.*_*floridanum*_IMI_35429	GGAGCGCATG AACGTCTACT	TAAACAAGGG	ATGTGGGTAA	AATA-XXAAA	CGCTCTC-C-
*Cy.*_*floridanum*_STE-U_2350	GGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGGTCAA	ATT-XGC-AA	CA-XXTCGC-
*Cy.*_*floridanum*_STE-U_682	GGAGCGTATG AACGTTTACT	TTAACGAGGT	TTGTGGTCAA	ATT-XGC-AA	CA-XXTCGC-
*Cy.*_*floridanum*_UFV_76	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AATA-XXAAA	CG-XCTCGCC
*Cy.*_*gracile*_ATCC_22833	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*gracile*_IMI_167580	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*gracile*_PC_551197	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*gracile*_STE-U_1586	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*gracile*_STE-U_623	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*graciloideum*_STE-U_1153	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACA-XGA	-GTAC-TTCG
*Cy.*_*hawksworthii*_MUCL_30866	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCAC-
*Cy.*_*heptaseptatum*_FTCC_1002	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTT-CAAA	-CCACAC-GA	CCTACTCCC-
*Cy.*_*heptaseptatum*_FTCC_1003	CGAGCGTATG AACGTCTACT	TCAACGAGGT	TTGTA-XAAA	ACCACAC-GA	ACTACTTCC-
*y.*_*heptaseptatum*_STE-U 2344	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTT-CAAA	-CCACAC-GA	CCTACTCCC-
._*insulare*_STE-U_616	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ATCACGC-GG	TGTACTCACA
*insulare*_STE-U_768	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCGCGC-GG	TGTACCCACA
*insulare*_STE-U_954	CGAGCGTATG AACGTCTACT	TCAACGAGGT	GTGTG-XAAA	ACCGCGC-GG	TGTACTCACA
*leucothoes*_ATCC_64824	CGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGT-GAAAA	-TCACGCTGA	T-AACACTC-
*eucothoes*_P97.2605	CGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGT-GA-AA	ATCACGCTGA	T-AACACTC-
*croconidiale*_STE-U_307	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	CCCAT-CTGA	TCTGACCCC-
*croconidiale*_STE-U_413	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	CCCAT-CTGA	TCTGACCCC-
*xicanum*_STE-U_927	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTA-XAAA	ACCGCTCCAA	-GAAATTTC-
*xicanum*_STE-U_941	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTA-XAAA	ACCGCTCCAA	-GAAATTTC-
*ltiseptatum*_STE-U_1589	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGCGA-AAA	ATCATG-XAG	TGCGCTCGC-
*ultiseptatum*_STE-U_1602	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGCG-AAAA	ATCATG-XAG	TGCGCTCGC-
_*naviculatum*_STE-U_627	CGAGCGCATG AACGTCTACT	TCAACGAGGT	AGGTAGT-GG	GCTA-GC-XA	CA-XXXCCCA
*y.*_*naviculatum*_STE-U_628	CGAGCGCATG AACGTCTACT	TCAACGAGGT	AGGTAGT-GG	GCTA-GC-XA	CA-XXXCCCA
*Cy.*_*ovatum*_UFV_90	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAG	ACCACGC-GG	TGCACCCCT-
*Cy.*_*parasiticum*_ATCC_46133	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AACA-XXAAA	CG-XCTCGCC
*Cy.*_*parasiticum*_CBS_190.50	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AACA-XXAAA	CG-XCTCGCC
*Cy.*_*parasiticum*_STE-U_723	GGAGCGCATG AACGTCTACT	TCAACGAGGT	ATGTGGTTAA	AATA-XXAAA	CG-XCTCGCC
*Cy.*_*pauciramosum*_STE-U_416	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*pauciramosum*_STE-U_925	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*pauciramosum*_STE-U_972	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*penicilloides*_CBS_174.55	GGAGCGCATG AGCGTCTACT	TCAACGAGGT	ATGTAGAGAA	GCCCCATTGG	-GAAAAC-XX
*Cy.*_*pseudogracile*_AR_2677	GGAGCGTATG AACGTCTACT	TCAACGAGGT	ACGTG-XAAA	ACCACAC-GG	AGTACTCCCG
*Cy.*_*pseudogracile*_STE-U_1588	GGAGCGTATG AACGTCTACT	TCAACGAGGT	ACGTG-XAAA	ACCACAC-GG	AGTACTCCCG
*Cy.*_*pteridiS*_STE-U_2869	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*pteridis*_STE-U_2190	CGAGMGWATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*pteridis*_UFV_43	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	AGCACTCCC-
*Cy.*_*quinqueseptatum*_ATCC_16550	CGAGCGTATG AACGTCTACT	TCAACGAGGT	AT-CAA-AAA	AC-ATGC-XG	TGCGCTCAC-
*Cy.*_*quinqueseptatum*_STE-U_516	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGCG-AAAA	ACCATGCC-X	TGCGCTCGC-
*Cy.*_*quinqueseptatum*_STE-U_759	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGCG-AAAA	ACCATGCC-X	TGCGCTCGC-
*Cy.*_*rumohrae*_STE-U_1603	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTTACAA-	XCCGCGC-GG	CGTAT-CGCC
*Cy.*_*rumohrae*_UFV_215	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTTGCAA-	XCCGCGC-GG	CGTAT-CGCC
*Cy.*_*rumohrae*_UFV_218	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTTGCAA-	XCCGCGC-GG	CGTATCGCC-
*Cy.*_*scoparium*_ATCC_38227	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCACA
*Cy.*_*scoparium*_ATCC_46300	CGAGCGTATG AACGTCTACT	TCCACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTTCTCACA
*Cy.*_*scoparium*_STE-U_1720	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCACA
*Cy.*_*scoparium*_STE-U_1722	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCACA
*Cy.*_sp._STE-U_599	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_sp._STE-U_1150	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_sp._STE-U_1484	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACT-XGA	AGCACTCCC-
*Cy.*_sp._STE-U_2321	CGAGCGTNTG AACGTNTACT	TCAACGAGGT	ATGTGG-A-G	GCTAC-CTGG	TGCACCCCC-
*Cy.*_sp._STE-U_2322	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGG-AAA	-CTGC-CTGG	TGCATCCCC-
*Cy.*_sp._STE-U_2347	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTTGCAA-	XCCGCAC-GG	CGTATTCCCT
*Cy.*_sp._STE-U_2712	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*spathiphylli*_ATCC_44730	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTTCTCGC-
*Cy.*_*spathiphylli*_STE-U_1624	CGAGCGTATG AACGTTTACT	TCAACGAGGT	ATGTG-XAAT	GCCACGC-GG	TGTTCTCCC-
*Cy.*_*spathiphylli*_STE-U_1641	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	GCCACGC-GG	TGTTCTCCC-
*Cy.*_*spathiphylli*_STE-U_2186	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTTCTCGC-
*Cy.*_*spathiphylli*_STE-U_2188	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTTCTCGC-
*Cy.*_*spathulatum*_AR_1844	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*spathulatum*_ATCC_62616	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACTC-GA	AGCACTCCC-
*Cy.*_*theae*_ATCC_48895	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGA-AAA	AA-GCAC-XX	XGCAC-AGT-
*Cy.*_*theae*_UFV_16A	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTGA-AAA	AA-GCAC-XX	XGCAC-AGT-
*Cy.*_*variabile*_AR_2675	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCACA
*Cy.*_*variabile*_UFV_28	CGAGCGTATG AACGTCTACT	TCAACGAGGT	ATGTG-XAAA	ACCACGC-GG	TGTACTCACA

						480
*F._subglutinans*_NRRL_22061	ATT-XCC-XX	XXXXXXXCAA	-G-XXXXCTC	ACACA-XXXX	XXXAC-TAGG	CCTCTGGCAA
*Cy._avesiculatum*_ATCC_38226	TGTG-TCGAG	G-XXCATAAA	CCCAA-XCTC	ACAC-XXXXX	GTCATGTAGG	CTTCCGGCAA
*Cy._candelabrum*_STE-U_1674	TT-GACCGAG	AAG-CACAA-	TCCGA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._candelabrum*_STE-U_1677	TT-GACCGAG	AAG-CACAA-	TCCGA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._candelabrum*_STE-U_1951	TT-GACCGAG	AAG-CACAA-	TCCGA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._candelabrum*_UFV_89	TT-GACCGAG	AAG-CACAA-	TCCGA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._citri*_CBS_186.36	TGTG-TCGAG	ACAACACA-X	GTAAA-XCTC	ACACAC-XXX	G-CATGTAGG	CTTCTGGCAA
*Cy._colhounii*_STE-U_1237	TATG-TCGAG	AGA-CGCAA-	CTAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CCTTCGGCAA
*Cy._colhounii*_STE-U_1339	TATG-TCGAG	AGA-CGCAA-	GCAAA-XCTG	ACGC-XXXXX	-XCATGTAGG	CTTCCGGCAA
*Cy._colhounii*_STE-U_681	TATG-TCGAG	AGA-CGCAA-	GTAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CCTTCGGCAA
*Cy._colhounii*_STE-U_705	TATG-TCGAG	AGA-CGCAA-	CTAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CCTCCGGCAA
*Cy._curvisporum*_STE-U_763	-XTGGTCGA-	AAAACTTGTG	CACAAA-CTC	ACAC-XXXXX	-XGATACAGG	CTTCCGGCAA
*Cy._curvisporum*_STE-U_765	-XTGGTCGA-	AAAACTTGTG	CACAAA-CTC	ACAC-XXXXX	-XGATACAGG	CTTCCGGCAA
*Cy._flexuosum*_STE-U_2536	TT-GATCGAG	AAA-CATAAA	-CAAA-XCTC	ACAC-XXXXX	-XCATGTAGG	CTTCCGGCAA
*Cy._floridanum*_ATCC_18834	TTTGG-CGAG	AA-XTATAGA	GCCAGCACTC	ACAC-XXXXX	-XCATCTAGG	CTTCCGGCAA
*Cy._floridanum*_ATCC_18882	TTTGG-CGAG	AA-XTATAGA	GCCAGCACTC	ACAC-XXXXX	-XCATCTAGG	CTTCCGGCAA
*Cy._floridanum*_CBS_413.67	CCCTG-CGAG	AAA-CAT-GA	ATAAAAACTC	ACAC-XXXXX	-XTATCAAGG	CCTNCGGCAA
*Cy._floridanum*_IMI_35428	-XTGGTCGA-	AAAACTTGTG	CACAAA-CTC	ACAT-XXXXX	-XGATACAGG	CTTNCGGCAA
*Cy._floridanum*_IMI_35429	-XTGGTCGA-	AAAACTTGTG	CACAAA-CTC	ACAT-XXXXX	-XGATACAGG	CTTGCGGCAA
*Cy._floridanum*_STE-U_2350	TTTGG-CGAG	AA-XTATAGA	GCCAGCACTC	ACAC-XXXXX	-XCATNTAGG	CTTCCGGCAA
*Cy._floridanum*_STE-U_682	TTTGGG-GAG	AA-XTTTAGA	GCCAGCACTC	ACAC-XXXXX	-XCATTTAGG	CTTTCGGCAA
*Cy._floridanum*_UFV_76	-XTGGTCGA-	AAAACTTGTG	CACAAAACTC	ACAC-XXXXX	-XGATACAGG	CTTCCGGCAA
*Cy._gracile*_ATCC_22833	TT-GATCGAG	AAG-CACAA-	GCAAA-XCTC	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._gracile*_IMI_167580	TT-GATCGAG	AAG-CACAA-	GCAAA-XCTC	ACACAC-XXX	-XCACGTAGG	CTTCCGGCAA
*Cy._gracile*_PC_551197	TT-GATCGAG	AAG-CACAA-	GCAAA-XCTC	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._gracile*_STE-U_1586	TT-GATCGAG	AAG-CACAA-	GCAAA-XCTC	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._gracile*_STE-U_623	TT-GATCGAG	AAG-CACAA-	GCAAA-XCTC	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._graciloideum*_STE-U_1153	TTTG-TCGGG	AAGAT-CAA-	GCGAA-XCTC	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._hawksworthii*_MUCL_30866	-XXXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XTATGTAGG	CTTCTGGCAA
*Cy._heptaseptatum*_FTCC_1002	TCATACCAGC	AG-XTAT-GA	GAAAA-XCTC	A-XXXXXXXX	XXCATGTAGG	CCTCTGGCAA
*Cy._heptaseptatum*_FTCC_1003	TTATACCAGC	AG-XTAT-GA	GAAAA-XCTC	AC-XXXXXXX	-XXXTGTGGG	CCTCTGGCAA
*Cy._heptaseptatum*_STE-U 2344	TCATACCAG-	CAG-TAT-GA	GAAAA-XCTC	A-XXXXXXXX	XXCATGTAGG	CCTCTGGCAA
*Cy._insulare*_STE-U_616	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._insulare*_STE-U_768	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XC-TGTAGG	CTTCTGGCAA
*Cy._insulare*_STE-U_954	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._leucothoes*_ATCC_64824	TTTG-TTG-X	AGACA-ACAA	AGCGAA-CTC	ACACAC-XXX	GTCATGTAGG	CTTNCGGCAA
*Cy._leucothoes*_P97.2605	TTTG-TTGAG	ACAACAAAGC	G-AA-XXCTC	ACACAC-XXX	GTCATGTAGG	CTTCCGGCAA
*Cy._macroconidiale*_STE-U_307	TTCG-TCGAT	AGG-CACAAA	GTAAA-XCTG	ACAC-XXXXX	GCTATGTAGG	CTTCCGGCAA
*Cy._macroconidiale*_STE-U_413	TTCG-TCGAT	AGG-CACAA-	GTAAA-XCTG	ACAC-XXXXX	GCTATGTAGG	CTTCCGGCAA
*Cy._mexicanum*_STE-U_927	TTTG-TCGGG	ACG-CCCAAA	-CAAA-XCTC	ACA-XXXXXX	XTCATGTAGG	CTTCCGGCAA
*Cy._mexicanum*_STE-U_941	TTTG-TCGGG	ACG-CCCAAA	-CAAA-XCTC	ACACAC-XXX	GTCATGTAGG	CTTCCGGCAA
*Cy._multiseptatum*_STE-U_1589	TTTG-TGGAG	AAA-CATAG-	TCAAA-XCTG	ACACAC-XXC	AT-GTGTAGG	CTTCCGGCAA
*Cy._multiseptatum*_STE-U_1602	TTTG-TGGAG	AAA-CATAG-	TCAAA-XCTG	ACACAC-XXC	AT-GTGTAGG	CTTCCGGCAA
*Cy._naviculatum*_STE-U_627	TTTG-TCAAG	AAA-CATTGA	ACAAA-XCTG	ACAGACCGCA	ACCGCACAGG	CTTCCGGCAA
*Cy._naviculatum*_STE-U_628	TTTG-TCAA-	XGAAACATTG	AACAAA-CTG	ACAGACCGCA	ACCGCACAGG	CTTCCGGCAA
*Cy._ovatum*_UFV_90	TTT-GCCGAG	AAG-CACAA-	GCAAA-XCTG	ACACA-XXXX	XCCATGTAGG	CTTCCGGCAA
*Cy._parasiticum*_ATCC_46133	-XTGGTCGAA	AAA-CTTGT-	GCACAAACTC	ACAC-XXXXX	-XGATACAGG	CTTCCGGCAA
*Cy._parasiticum*_CBS_190.50	-XTGGTCGAA-AAA-CTTGT-		GCACAAACTC	ACAC-XXXXX	-XGATACAGG	CTTCCGGCAA
*Cy._parasiticum*_STE-U_723	-XTGGTCGAG	AAA-CTTGT-	GCCCCAACTC	ACAC-XXXXX	-XAATACAGG	CTTTCGGCAA
*Cy._pauciramosum*_STE-U_416	TT-GACCGAG	AAG-CACAA-	GCCAA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._pauciramosum*_STE-U_925	TT-GACCGAG	AAG-CACAA-	GCCAA-XCTC	ACACA-XXXX	ATCATGTAGG	CTTCCGGCAA
*Cy._pauciramosum*_STE-U_972	TT-GACCGAG	AAG-CACAA-	GCCAA-XCTC	ACAC-XXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._penicilloides*_CBS_174.55	-XTGAT-GA-	XAAT-CTCAC	ACACG-XCT-	XXXXXXXXXX	-XXACTCAGG	CTTCCGGCAA
*Cy._pseudogracile*_AR_2677	TT-G-CCCAG	AAG-CACAA-	GCAAA-XCTC	ACA-XXXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._pseudogracile*_STE-U_1588	TT-G-CCCAG	AAG-CACAA-	GCAAA-XCTC	ACA-XXXXXC	ATCATGTAGG	CTTCCGGCAA
*Cy._pteridiS*_STE-U_2869	TTT-ACCGGG	AAG-CACAA-	GCAAA-XCTG	ACACGC-XXX	-XCGTGCAGG	CTTCTGGCAA
*Cy._pteridis*_STE-U_2190	TTT-ACCGGG	AAG-CACAA-	GCAAA-XCTG	ACACGC-XXX	-XCGTGCAGG	CTTCTGGCAA
*Cy._pteridis*_UFV_43	TTT-ACCGGG	AAG-CACAA-	GCAAA-XCTG	ACACG-XXXX	XCCGTGCAGG	CTTCTGGCAA
*Cy._quinqueseptatum*_ATCC_16550	TTTGA-CGAG	AAA-TACAG-	GCAAA-XCTG	ACACAC-XXC	AT-GTGTAGG	CTTCCGGCAA
*Cy._quinqueseptatum*_STE-U_516	TTTG-TCGAA	AAAGCACAA-	GCAAA-XCTG	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._quinqueseptatum*_STE-U_759	TTTG-TCGAA	AAAGCACAA-	GCAAA-XCTG	ACNCAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._rumohrae*_STE-U_1603	TTTAACCAGC	AG-XTGCAA-	GAAAA-XCTC	A-XXXXXXXX	XXCATGTAGG	CCTCTGGCAA
*Cy._rumohrae*_UFV_215	TTTAACCGGC	AG-XTGCAA-	GAAAA-XCTC	A-XXXXXXXX	XXCATGTAGG	CCTCTGGCAA
*Cy._rumohrae*_UFV_218	TTTAACCGGC	AG-XTGCAA-	GAAAA-XCTC	A-XXXXXXXX	XXCATGTAGG	CCTCTGGCAA
*Cy._scoparium*_ATCC_38227	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._scoparium*_ATCC_46300	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._scoparium*_STE-U_1720	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._scoparium*_STE-U_1722	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._sp.*_STE-U_599	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._sp.*_STE-U_1150	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._sp.*_STE-U_1484	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._sp.*_STE-U_2321	TTTG-CCGAG	AGG-CACAAA	-CAAA-XCTG	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._sp.*_STE-U_2322	TTGG-CCGAG	AGG-CACAAA	-CAAA-XCTG	ACACAC-XXX	-XCATGTAGG	CTTCCGGCAA
*Cy._sp.*_STE-U_2347	TCA-GCCAAC	CG-XTGCAAG	GAAA-XXCTC	A-XXXXXXXX	XXCATGTAGG	CTTCTGGCAA
*Cy._sp.*_STE-U_2712	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._spathiphylli*_ATCC_44730	-XXXXTCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._spathiphylli*_STE-U_1624	-XXXXTCGAG	AGG-CACAG-	GAAAA-XCTG	ACAC-XXXXX	-XCATGTNGG	CTTTTGGCAA
*Cy._spathiphylli*_STE-U_1641	-XXXXTCGAG	AGG-CACAG-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._spathiphylli*_STE-U_2186	-XXXXTCGAG	AGG-CACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._spathiphylli*_STE-U_2188	-XXXXTCGAG	AGG-XACAA-	GCAAA-XCTG	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._spathulatum*_AR_1844	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._spathulatum*_ATCC_62616	TT-GGCCGAG	AAG-CACAA-	GCCAA-XCTC	ACACAC-XXX	-TCATGTAGG	CTTCCGGCAA
*Cy._theae*_ATCC_48895	TGTGAACGCG	AAGG-ACAG-	CCAA-XXCTC	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._theae*_UFV_16A	TGTGAACGCG	AAGG-ACAG-	CCAA-XXCTC	ACAC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._variabile*_AR_2675	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACGC-XXXXX	-XCATGTAGG	CTTCTGGCAA
*Cy._variabile*_UFV_28	C-XXGCCGAG	AGG-CACAA-	GCAAA-XCTG	ACGC-XXXXX	-XCATGTAGG	CTTCTGGCAA

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*F.*_*subglutinans*_NRRL_22061	CAAGTATGTT	CCCCGAGCCG	TCCTCGTCGA	TCTTGAGCCT	GGTACCATGG	ACGCCGTCCG
*Cy.*_*avesiculatum*_ATCC_38226	CAAGTTCGTT	CCTCGCGCTG	TCCTTGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*candelabrum*_STE-U_1674	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*candelabrum*_STE-U_1677	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*candelabrum*_STE-U_1951	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*candelabrum*_UFV_89	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*citri*_CBS_186.36	CAAGTTCGTT	CCTCGTGCCG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*colhounii*_STE-U_1237	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*colhounii*_STE-U_1339	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTNGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*colhounii*_STE-U_681	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTTCA	TCTTGAGCCC	CGTACCATGG	ATGCCGTCCG
*Cy.*_*colhounii*_STE-U_705	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*curvisporum*_STE-U_763	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*curvisporum*_STE-U_765	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*flexuosum*_STE-U_2536	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*floridanum*_ATCC_18834	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*floridanum*_ATCC_18882	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TNTTGAGCCC	GGTNCCATGG	ATGCCGTCCG
*Cy.*_*floridanum*_CBS_413.67	CAAGTTTGTC	CCTTGCGCTG	TCCTCGTTGA	TNTTNAGCCC	GGTCCCATGG	ATGXXXXXXX
*Cy.*_*floridanum*_IMI_35428	CAAGTATGTC	CCTTGCGCTG	TCCTTGTNGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCC
*Cy.*_*floridanum*_IMI_35429	CAAGTATGTC	CCTCGCGCTG	NCCTCGTTTA	TCTTGAGCCC	GGTACCATGG	ATGCCGXXXX
*Cy.*_*floridanum*_STE-U_2350	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*floridanum*_STE-U_682	CAAGTATGTC	CCTCCGGCTG	TCCTCGTCGA	TTTTGAGCCC	GGTACCNTGG	ATGCCGTCCG
*Cy.*_*floridanum*_UFV_76	CAAGTATGTG	CCTTGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*gracile*_ATCC_22833	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*gracile*_IMI_167580	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*gracile*_PC_551197	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*gracile*_STE-U_1586	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*gracile*_STE-U_623	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*graciloideum*_STE-U_1153	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*hawksworthii*_MUCL_30866	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*heptaseptatum*_FTCC_1002	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGC	ATGCCGTCCG
*Cy.*_*heptaseptatum*_FTCC_1003	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*heptaseptatum*_STE-U 2344	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*insulare*_STE-U_616	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*insulare*_STE-U_768	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*insulare*_STE-U_954	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*leucothoes*_ATCC_64824	CAAGTTCGKT	CCCCGTGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGNCCG
*Cy.*_*leucothoes*_P97.2605	CAAGTTCGTT	CCCCGTGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*macroconidiale*_STE-U_307	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*macroconidiale*_STE-U_413	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*mexicanum*_STE-U_927	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*mexicanum*_STE-U_941	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*multiseptatum*_STE-U_1589	CAAGTTCGTT	CCTCGCGCTG	CCCTCGTTGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*multiseptatum*_STE-U_1602	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTTGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*naviculatum*_STE-U_627	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*naviculatum*_STE-U_628	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*ovatum*_UFV_90	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*parasiticum*_ATCC_46133	CAAGTATGTC	CCTCGAGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*parasiticum*_CBS_190.50	CAAGTATGTC	CCTCGAGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*parasiticum*_STE-U_723	CAACTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCT	GGTACCATGG	ATGCCGTCCG
*Cy.*_*pauciramosum*_STE-U_416	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*pauciramosum*_STE-U_925	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*pauciramosum*_STE-U_972	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*penicilloides*_CBS_174.55	CAAGTATGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*pseudogracile*_AR_2677	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*pseudogracile*_STE-U_1588	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*pteridiS*_STE-U_2869	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*pteridis*_STE-U_2190	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*pteridis*_UFV_43	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*quinqueseptatum*_ATCC_16550	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*quinqueseptatum*_STE-U_516	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*quinqueseptatum*_STE-U_759	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*rumohrae*_STE-U_1603	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*rumohrae*_UFV_215	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*rumohrae*_UFV_218	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*scoparium*_ATCC_38227	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*scoparium*_ATCC_46300	CAAGTTCCGT	CCTTGTGCTG	TCGTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*scoparium*_STE-U_1720	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*scoparium*_STE-U_1722	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_sp._STE-U_599	CAAGTTCGTT	CCTCGCGCTG	NCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_sp._STE-U_1150	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_sp._STE-U_1484	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_sp._STE-U_2321	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_sp._STE-U_2322	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTNGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_sp._STE-U_2347	CAAGTTCGTC	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_sp._STE-U_2712	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*spathiphylli*_ATCC_44730	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*spathiphylli*_STE-U_1624	CAAGTNCGTT	CCTTCCGCTG	TCCTCGTCGA	TTTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*spathiphylli*_STE-U_1641	CAAGTTCGTT	TCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTNCG
*Cy.*_*spathiphylli*_STE-U_2186	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*spathiphylli*_STE-U_2188	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	NTTTGANCCC	CGTACCATGG	ATGCCGTCCG
*Cy.*_*spathulatum*_AR_1844	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*spathulatum*_ATCC_62616	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ACGCCGTCCG
*Cy.*_*theae*_ATCC_48895	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*theae*_UFV_16A	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTTGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*variabile*_AR_2675	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG
*Cy.*_*variabile*_UFV_28	CAAGTTCGTT	CCTCGCGCTG	TCCTCGTCGA	TCTCGAGCCC	GGTACCATGG	ATGCCGTCCG

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*F.*_*subglutinans*_NRRL_22061	AGCTGGTCCC TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*avesiculatum*_ATCC_38226	CGCTGGTCCC TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*candelabrum*_STE-U_1674	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*candelabrum*_STE-U_1677	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC NGACAACTT
*Cy.*_*candelabrum*_STE-U_1951	NGCCGGTCCT TTNGGTCAGN TCTTTCGCCC CGACAACTT
*Cy.*_*candelabrum*_UFV_89	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*citri*_CBS_186.36	TGCCGGTCCC TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*colhounii*_STE-U_1237	TGCCGGTCCT TTCTGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*colhounii*_STE-U_1339	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*colhounii*_STE-U_681	TGCCGGTCCT TTTTGTTAGC TCTTCCGCCC CGACAACTT
*Cy.*_*colhounii*_STE-U_705	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*curvisporum*_STE-U_763	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGAXXXXXX
*Cy.*_*curvisporum*_STE-U_765	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGAXXXXXX
*Cy.*_*flexuosum*_STE-U_2536	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*floridanum*_ATCC_18834	TGCCGGTCCC TTCGGTCAGT TCTTCCGCCC CGACAACTT
*Cy.*_*floridanum*_ATCC_18882	TGCCGGCCCT TTNGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*floridanum*_CBS_413.67	XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*floridanum*_IMI_35428	GGCCCXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*floridanum*_IMI_35429	XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*floridanum*_STE-U_2350	TGCCGGTCCC TTCGGTCAGC TCTTNCGCCC CGACAACTT
*Cy.*_*floridanum*_STE-U_682	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*floridanum*_UFV_76	TGCCXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*gracile*_ATCC_22833	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACXX
*Cy.*_*gracile*_IMI_167580	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*gracile*_PC_551197	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*gracile*_STE-U_1586	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*gracile*_STE-U_623	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*graciloideum*_STE-U_1153	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*hawksworthii*_MUCL_30866	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*heptaseptatum*_FTCC_1002	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*heptaseptatum*_FTCC_1003	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*heptaseptatum*_STE-U 2344	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGXXXXXXX
*Cy.*_*insulare*_STE-U_616	TGCCGGTCCT TTCGGTCAGC TCTTTCGCCC CGACAACTT
*Cy.*_*insulare*_STE-U_768	TGCCGGTCCT TTCGGTCAGC TCTTNCGCCC NGACAACTT
*Cy.*_*insulare*_STE-U_954	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*leucothoes*_ATCC_64824	TGCCGGCCCT TNCGGNCAGC TCTXXXXXXX XXXXXXXXX
*Cy.*_*leucothoes*_P97.2605	TGCCGGTCCC TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_*macroconidiale*_STE-U_307	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*macroconidiale*_STE-U_413	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*mexicanum*_STE-U_927	TGCTGGTCCC TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*mexicanum*_STE-U_941	TGCTGGTCCC TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*multiseptatum*_STE-U_1589	TGCCGGTCCT TTCGGTCAGC TCTTTCGCCC CGACAACTT
*Cy.*_*multiseptatum*_STE-U_1602	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*naviculatum*_STE-U_627	TGCCGGTCCC TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_*naviculatum*_STE-U_628	TGCCGGTCCC TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_*ovatum*_UFV_90	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*parasiticum*_ATCC_46133	TGCCGGTCCT TTCGGTCAAC TCTTCCGTCC CGACAACTT
*Cy.*_*parasiticum*_CBS_190.50	TGCCGGTCCT TTCGGTCAAC TCTTCCGTCC CGACAACTT
*Cy.*_*parasiticum*_STE-U_723	TGCCGGTCCT TTCCGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*pauciramosum*_STE-U_416	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC NGACAACTT
*Cy.*_*pauciramosum*_STE-U_925	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*pauciramosum*_STE-U_972	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*penicilloides*_CBS_174.55	TGCCGGTCCC TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*pseudogracile*_AR_2677	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*pseudogracile*_STE-U_1588	TGCCGGTCCT TTCGGTCAGC TCTTCCGTCC CGACAACTT
*Cy.*_*pteridiS*_STE-U_2869	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC GGACAACTT
*Cy.*_*pteridis*_STE-U_2190	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*pteridis*_UFV_43	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*quinqueseptatum*_ATCC_16550	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*quinqueseptatum*_STE-U_516	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*quinqueseptatum*_STE-U_759	TGCCGGTCCT TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_*rumohrae*_STE-U_1603	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*rumohrae*_UFV_215	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*rumohrae*_UFV_218	TGCCGGTCCT TTCGGGCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*scoparium*_ATCC_38227	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*scoparium*_ATCC_46300	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*scoparium*_STE-U_1720	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*scoparium*_STE-U_1722	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_sp._STE-U_599	TGCCGGTCCT TTCGGTCAGC TCTXXXXXXX XXXXXXXXX
*Cy.*_sp._STE-U_1150	TGCCGGTCCT TTCGGTCAGC TCTTTCGCCC CGACAACTT
*Cy.*_sp._STE-U_1484	TGCCGGTCCT TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_sp._STE-U_2321	TGCCGGTCCT TTCGGTCAGM TCTTCCGNCC CGACAACTT
*Cy.*_sp._STE-U_2322	TGCCGGTCCT TTCGGTCAGC TCTTCNGNCC CGACAACTT
*Cy.*_sp._STE-U_2347	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGNCAACXX
*Cy.*_sp._STE-U_2712	TGCCGGTCCT TTCGGTCAGC TCTTXXXXXX XXXXXXXXX
*Cy.*_*spathiphylli*_ATCC_44730	TGCCGGTCCT TTCGGCCAGC TCTTTCGACC CGACAACTT
*Cy.*_*spathiphylli*_STE-U_1624	TGCCGGTCTT TTXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*spathiphylli*_STE-U_1641	TGCCGGCCTT TTXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*spathiphylli*_STE-U_2186	TGCCGGTCCT TTCGGCCAGC TCTTCCGXXX XXXXXXXXX
*Cy.*_*spathiphylli*_STE-U_2188	TGCCXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXX
*Cy.*_*spathulatum*_AR_1844	TGCCGGTCCT TTNGGTCAGC TCTTCCGNCC CGACAACTT
*Cy.*_*spathulatum*_ATCC_62616	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*theae*_ATCC_48895	TGCCGGTCCT TTCGGTCAGC TTTTCCGTCC CGACAACTT
*Cy.*_*theae*_UFV_16A	TGCCGGTCCT TTCGGTCAGC TTTTCCGTCC CGACAACTT
*Cy.*_*variabile*_AR_2675	TGCCGGTCCT TTCGGTCAGC TCTTCCGCCC CGACAACTT
*Cy.*_*variabile*_UFV_28	TGCCGGTCCT TTCGGTCAGC TCTTCCGNCC CGACAACTT

Alignment 6. Part 6. ITS1 5.8S ITS2 rDNA sequence alignment from selected isolates of Hypocrelaean species with nectriaceous teleomorphs and anamorphs with cylindrical macroconidia

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                                                                                                 60
Ce._camelliae_STE-U_234                 CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._camelliae_STE-U_277                 CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._elegans_STE-U_518                   XXXXACATAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCATGT-XC GTTGCCTCGG
Ce._infestans_ATCC_44816                CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-GT-XC GTTGCCTCGG
Ce._infestans_IMI_299376                XXXXXXAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-GT-XC GTTGCCTCGG
Ce._infestans_STE-U_2319                CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-GT-XC GTTGCCTCGG
Ce._infestans_STE-U_708                 CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-GT-XC GTTGCCTCGG
Ce._lageniformis_UFV_115                CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-GT-XC GTTGCCTCGG
Ce._microcylindrica_ATCC_38571          CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._microcylindrica_STE-U_683           CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._microcylindrica_STE-U_918           XXXXACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._novae-zelandiae_ATCC_44815          CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCATGT-XC GTTGCCTCGG
Ce._parva_ATCC_28272                    CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._parva_STE-U_373                     XXXXXXXXAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._peruviana_IMUR_1843                 CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Ce._peruviana_STE-U_395                 CATTACAGAG TTTACAACTC CCAAACCCC- TGTGAACT-T ACCATGT-XC GTTGCCTCGG
Co._destructans_AR_2553                 CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCAT-ATT- GTTGCCTCGG
Co._destructans_CTR_71-322              CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCAT-ATT- GTTGCCTCGG
Co._destructans_var_coprosmae_CTR_73-152 CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCAT-ATT- GTTGCCTCGG
Co._destructans_var_coprosmae_GJS_85-182 CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCAT-TATC GTTGCCTCGG
Co._macroconidialis_GJS_83-162          CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCATGT-XC GTTGCCTCGG
Cu._cigneum_STE-U_1595                  CATTACCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TCAAAC GTTCCCTCGG
Cy._candelabrum_STE-U_1674              XXXXXCCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._candelabrum_STE-U_1675              XXXXXCCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._floridanum_ATCC_18834               CATTACCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._floridanum_ATCC_18882               CATTACCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._multiseptatum_STE-U_1589            CATTACCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._multiseptatum_STE-U_1602            CATTACCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._scoparium_ATCC_38227                XXXXXXXXXX XXXXXXXCTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
Cy._scoparium_ATCC_46300                XXXXXCCGAG TTTACAACTC CCAAACCCCA TGTGAAC-AT ACC-TGTTTC GTTCCCTCGG
F._subglutinans_NRRL_22061              CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAAC-AT ACCA-XATT- GTTGCCTCGG
Ge._bulbilium_GJS_92-7                  CATTACCGAG TTTACAACTC CCAAACCCA- TGTGAA-TTT ACC-XTTTAC GTTCCCTCGG
Gl._irregularis_STE-U_718               CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAACTAT ACC-XTTTAC GTTGCCTCGG
Gl._sumatrensis_STE-U_1351              CATTACCGAG TTTACAACTC CCAAACCCC- TGTGAACTAT ACC-XTTTAC GTTGCCTCGG
X._serpens_STE-U_1144                   CATTACCGAG TTTACAACTC CCAAACCCAA TGTGAACTAT ACC-TGTT-C GTTCCCTCGG
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F._subglutinans_NRRL_22061              CGG-ATCAGC CCGC-XTCCC GGTAAAACGG GACGGCCCGC CAGAGGACCC C-TAAACTCT
Ce._camelliae_STE-U_277                 CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._camelliae_STE-U_234                 CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._elegans_STE-U_518                   CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._infestans_ATCC_44816                CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._infestans_IMI_299376                CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._infestans_STE-U_2319                CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._infestans_STE-U_708                 CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._lageniformis_UFV_115                CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._microcylindrica_ATCC_38571          CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._microcylindrica_STE-U_683           CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._microcylindrica_STE-U_918           CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._novae-zelandiae_ATCC_44815          CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._parva_ATCC_28272                    CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._parva_STE-U_373                     CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._peruviana_IMUR_1843                 CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Ce._peruviana_STE-U_395                 CGGTGT-XXC TTGC-TTC-X GGC-XXXXXX GA-XGCCCGC CAGAGGACCC AACAAACTCT
Co._destructans_AR_2553                 CGGTG-XXXC CCG-TTTC-X GGC-XXXXXX XXXGGCCCGC CAGAGGACCC AA-ACCCT-X
Co._destructans_CTR_71-322              CGGTGT-XXC -TG-TTTC-X GGCA-XXXXX -XXXGCCCGC CAGAGGACCC AA-ACCCTA-
Co._destructans_var_coprosmae_CTR_73-152 CGGTGT-XXC -TG-TTTC-X GGCA-XXXXX -XXXGCCCGC CAGAGGACCC AA-ACCCTA-
Co._destructans_var_coprosmae_GJS_85-182 CGGTG-XXXC CCGC-TTC-X GGC-XXXXXX XXXGGCCCGC CAGAGGACTG AA-ACCCTT-
Co._macroconidialis_GJS_83-162          CGGTG-XXXC CCGC-XTCC- GGCGG-XXXX XXXXTCCCGC CAGAGGACCC C-CAAACCCT
Cu._cigneum_STE-U_1595                  CGGTGT-XXC CCGCGCTCC- GGCAA-XXXX XXGGGCCCGC CAGAGGACCC AACAAACTCT
Cy._candelabrum_STE-U_1674              CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._candelabrum_STE-U_1675              CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._floridanum_ATCC_18834               CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._floridanum_ATCC_18882               CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._multiseptatum_STE-U_1589            CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._multiseptatum_STE-U_1602            CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._scoparium_ATCC_38227                CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Cy._scoparium_ATCC_46300                CGGTGT-XXX -XXXXXXCC- GGCAA-XXXX XXCGGCCCGC CAGAGGACCC AACAAACTCT
Ge._bulbilium_GJS_92-7                  CGGCGTTC-C CC-XXXTC-X GG-GG-XXXX XXXTTCCCGC CAGAGGACCA AACAAACCCT
Gl._irregularis_STE-U_718               CGGCGT-XXX CCGC-TTC-X GGC-XXXXXX XXXGGCCCGC CAGAGGACCC AA-XXACTCT
Gl._sumatrensis_STE-U_1351              CGGCGT-XXX CCGC-TTC-X GGC-XXXXXX XXXGGCCCGC CAGAGGACCC AA-XXACTCT
X._serpens_STE-U_1144                   CGGTGTTCGC -TGC-TTC-X GGCA-XXXXX GA-GGCCCGC CAGAGGACCC AACAAACTCT
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F._subglutinans_NRRL_22061                     -XXG-XTTTC -XXXTATATG TA-XA-CTTC TGAGTAAAAC CA-XXTAAAT -AAATCAAAA
Ce._camelliae_STE-U_277                        T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._camelliae_STE-U_234                        T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._elegans_STE-U_518                          T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTA-XAC AAGTTT-AAT -AAATCAAAA
Ce._infestans_ATCC_44816                       T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
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Ce._infestans_STE-U_2319                       T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._infestans_STE-U_708                        T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._lageniformis_UFV_115                       T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._microcylindrica_ATCC_38571                 T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._microcylindrica_STE-U_683                  T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._microcylindrica_STE-U_918                  T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
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Ce._peruviana_IMUR_1843                        T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Ce._peruviana_STE-U_395                        T-XG-XTTTT T-XXTT-A-G TATTATCT-X -GAGTG-XAC AAGTTT-AAT -AAATCAAAA
Co._destructans_AR_2553                        -XXGTATTA- XXXXXXAA-G TAT-XTCTTC TGAGT-AAAT -XGATTAAAT CAA-TCAAAA
Co._destructans_CTR_71-322                     -XXGA-TTAC -XXATTAAAG CATT-T-TTN TGAGT-XXCA ATGATTAAAT CAA-TCAAAA
Co._destructans_var_coprosmae_CTR_73-152       -XXG-ATTA- CA-XTTAAAG CATT-T-TTC TGAGT-CAAT -XGATTAAAT CAA-TCAAAA
Co._destructans_var_coprosmae_GJS_85-182       -XXGAATTTT T-XXXTACAG -XTTATCTTC TGAGTACA-T -XGATTAAAT CAA-TCAAAA
Co._macroconidialis_GJS_83-162                 T-XG-ATCTA -XXXTTACTG TAT-ATCTTC TGAGTAAACG ATGA-XAAAT CAAATCAAAA
Cu._cigneum_STE-U_1595                         TT-GTATTT- CAA-TCTA-G TA-XXTCTTC TGAGTGAAAA CAAA-C-AAT -AAATAAAAA
Cy._candelabrum_STE-U_1674                     TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGT-AAAA AA-XXCAAAT -AAATCAAAA
Cy._candelabrum_STE-U_1675                     TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGT-AAAA AA-XXCAAAT -AAATCAAAA
Cy._floridanum_ATCC_18834                      TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGTGAAAA AAA-XC-AAT -AAATCAAAA
Cy._floridanum_ATCC_18882                      TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGTGAAAA AAA-XC-AAT -AAATCAAAA
Cy._multiseptatum_STE-U_1589                   TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGTGAAAA AAAAAC-AAT -AAATAAAAA
Cy._multiseptatum_STE-U_1602                   TTTGAATTTT T-XXXXCA-G TA-XXTCTTC TGAGTGAAAA AAAAAC-AAT -AAATAAAAA
Cy._scoparium_ATCC_38227                       TTTGAATTTT TC-XXXXA-G TA-XXTCTTC TGAGT-AAAA AAAAAC-AAT -AAATCAAAA
Cy._scoparium_ATCC_46300                       TTTGAATTTT TC-XXXXA-G TA-XXTCTTC TGAGT-AAAA AAAAAC-AAT -AAATCAAAA
Ge._bulbilium_GJS_92-7                         TT-GCATTT- XXXATT-A-G TATTAT-XTC TGAGTGATTT AAT-XC-AAT -AAATCAAAA
Gl._irregularis_STE-U_718                      T-XGTATTT- GAA-TTGA-G TAT-XTC-TC TGAGTGATAC AAG-XC-AAT -AAATTAAAA
Gl._sumatrensis_STE-U_1351                     T-XGTATTT- XGAATTGA-G TAT-XTC-TC TGAGTGATAC AAG-XC-AAT -AAATTAAAA
X._serpens_STE-U_1144                          TTTGAATCTT T-XXXXXA-G TA-XXTCTTC TGAGTGAAAA AAA-XC-AAT -AAATCAAAA
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F._subglutinans_NRRL_22061                     CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCAAA ATGCGATAAG
Ce._camelliae_STE-U_277                        CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._camelliae_STE-U_234                        CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._elegans_STE-U_518                          CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._infestans_ATCC_44816                       CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Ce._infestans_STE-U_708                        CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._lageniformis_UFV_115                       CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._microcylindrica_ATCC_38571                 CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Ce._microcylindrica_STE-U_918                  CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Ce._parva_ATCC_28272                           CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Ce._peruviana_IMUR_1843                        CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ce._peruviana_STE-U_395                        CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Co._destructans_AR_2553                        CTTTCAACAA CGGATCTCTT GGCTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Co._destructans_CTR_71-322                     CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Co._destructans_var_coprosmae_CTR_73-152       CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Co._destructans_var_coprosmae_GJS_85-182       CTTTCAACAA CGGATCTCTT GGCTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Co._macroconidialis_GJS_83-162                 CTTTCAACAA CGGATCTCTT GGCTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Cu._cigneum_STE-U_1595                         CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Cy._floridanum_ATCC_18834                      CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Cy._floridanum_ATCC_18882                      CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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Cy._multiseptatum_STE-U_1602                   CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Cy._scoparium_ATCC_38227                       CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Cy._scoparium_ATCC_46300                       CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Ge._bulbilium_GJS_92-7                         CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Gl._irregularis_STE-U_718                      CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
Gl._sumatrensis_STE-U_1351                     CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
X._serpens_STE-U_1144                          CTTTCAACAA CGGATCTCTT GGTTCTGGCA TCGATGAAGA ACGCAGCGAA ATGCGATAAG
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F._subglutinans_NRRL_22061                 TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._camelliae_STE-U_277                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._camelliae_STE-U_234                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._elegans_STE-U_518                      TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._infestans_ATCC_44816                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._infestans_IMI_299376                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._infestans_STE-U_2319                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._infestans_STE-U_708                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._lageniformis_UFV_115                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._microcylindrica_ATCC_38571             TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._microcylindrica_STE-U_683              TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._microcylindrica_STE-U_918              TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._novae-zelandiae_ATCC_44815             TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCTA
Ce._parva_ATCC_28272                       TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._parva_STE-U_373                        TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._peruviana_IMUR_1843                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ce._peruviana_STE-U_395                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Co._destructans_AR_2553                    TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Co._destructans_CTR_71-322                 TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Co._destructans_var_coprosmae_CTR_73-152   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Co._destructans_var_coprosmae_GJS_85-182   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Co._macroconidialis_GJS_83-162             TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCGA
Cu._cigneum_STE-U_1595                     TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._candelabrum_STE-U_1674                 TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
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Cy._floridanum_ATCC_18834                  TAATGTGAAT TGCAGAATTC AGNGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._floridanum_ATCC_18882                  TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._multiseptatum_STE-U_1589               TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._multiseptatum_STE-U_1602               TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._scoparium_ATCC_38227                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Cy._scoparium_ATCC_46300                   TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Ge._bulbilium_GJS_92-7                     TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Gl._irregularis_STE-U_718                  TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
Gl._sumatrensis_STE-U_1351                 TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA
X._serpens_STE-U_1144                      TAATGTGAAT TGCAGAATTC AGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCGCCA


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F._subglutinans_NRRL_22061                 GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCCCA -XXXXXXXG
Ce._camelliae_STE-U_277                    GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._camelliae_STE-U_234                    GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._elegans_STE-U_518                      GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
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Ce._infestans_STE-U_2319                   GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._infestans_STE-U_708                    GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._lageniformis_UFV_115                   GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._microcylindrica_ATCC_38571             GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._microcylindrica_STE-U_683              GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._microcylindrica_STE-U_918              GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._novae-zelandiae_ATCC_44815             GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._parva_ATCC_28272                       GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAAACCC CGG-XXXXXT
Ce._parva_STE-U_373                        GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAAACCC CGG-XXXXXT
Ce._peruviana_IMUR_1843                    GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Ce._peruviana_STE-U_395                    GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAACCCC CGG-XXXXXG
Co._destructans_AR_2553                    GTATTCTGGC GGGCATGCCT GTCCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
Co._destructans_CTR_71-322                 GTATTCTGGC GGGCATGCCT GTCCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
Co._destructans_var_coprosmae_CTR_73-152   GTATTCTGGC GGGCATGCCT GTCCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
Co._destructans_var_coprosmae_GJS_85-182   GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
Co._macroconidialis_GJS_83-162             GTATTCTCGC GGGCATGCCT GTCCGAGCGT CATTTCAACC CTCGAGCCCC CGG-XXXXXG
Cu._cigneum_STE-U_1595                     GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGC-CT CTTCTG-XXG
Cy._candelabrum_STE-U_1674                 GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCTCA -XXXXXXXG
Cy._candelabrum_STE-U_1675                 GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCTCA -XXXXXXXG
Cy._floridanum_ATCC_18834                  GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCAC- CTTC-GGGAG
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Cy._scoparium_ATCC_46300                   GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCTCT -XXXXXXXG
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Gl._irregularis_STE-U_718                  GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
Gl._sumatrensis_STE-U_1351                 GTATTCTGGC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAAGCCCC CGG-XXXXXG
X._serpens_STE-U_1144                      GTATTCTGAC GGGCATGCCT GTTCGAGCGT CATTTCAACC CTCAATTCCT CTTTTGGGA-
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F._subglutinans_NRRL_22061                    CTTGGTGTTG GGACTCG-C- XXXGA-XXGT -XXXXC-AAA T-CGC-XXXG TTCCCCAAAT
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Ce._camelliae_STE-U_234                       TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
Ce._elegans_STE-U_518                         TTTGGTGTTG GAGATCGACA -XTGA-XXGT CCCTTC-GGG GGCGACGTCG TCTCCCAAAT
Ce._infestans_ATCC_44816                      TTTGGTGTTG GAGATCGGCA -XTGA-XXGT -CCTTC-GGG -GCGACGCCG TCTCCCAAAT
Ce._infestans_IMI_299376                      TTTGGTGTTG GAGATCGGCA -XTGA-XXGT -CCTTC-GGG -GCGACGCCG TCTCCCAAAT
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Ce._infestans_STE-U_708                       TTTGGTGTTG GAGATCGGCA -XTGAG-XXT -CCTTC-GGG -GCGACGCCG TCTCCCAAAT
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Ce._microcylindrica_ATCC_38571                TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
Ce._microcylindrica_STE-U_683                 TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
Ce._microcylindrica_STE-U_918                 TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
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Ce._parva_ATCC_28272                          TTTGGTGTTG GAGATCGGCA -XTGA-XXGT -CCTTC-GGG -GCGACGCCG TCTCCCAAAT
Ce._parva_STE-U_373                           TTTGGTGTTG GAGATCGGCA -XTGA-XXGT -CCTTC-GGG -GCGACGCCG TCTCCCAAAT
Ce._peruviana_IMUR_1843                       TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
Ce._peruviana_STE-U_395                       TTTGGTGTTG GAGATCGACA -XTGAA-XG- CCCTTCTGGG TGTGAAGTCG TCTCCCAAAT
Co._destructans_AR_2553                       CTTGGTGTTG GAGATCGGC- XXXGA-XXG- CCCTCC-GGG G-CAC-GCCG TCTCCCAAAT
Co._destructans_CTR_71-322                    CTTGGTGTTG GAGATCGGC- XXXGA-XXG- CCCT-CCGGG G-CGC-GCCG TCTCCCAAAT
Co._destructans_var_coprosmae_CTR_73-152      CTTGGTGTTG GAGATCGGC- XXXGA-XXG- CCCTCC-GGG G-CGC-GCCG TCTCCCAAAT
Co._macroconidialis_GJS_83-162                CTCGGTGTTG GAGACCGGC- XXXGAGG-XX CCCXXXXXXX XXXXXXXXXX XXXXXXXXXX
Co._destructans_var_coprosmae_GJS_85-182      CTTGGTGTTG GAGATCGGC- XXXXXGG-G- CCCTCC-GGG G-CGC-GCCG CCTCCCAAAT
Cu._cigneum_STE-U_1595                        CTTGGTGTTG GGGATCGGCA -C-G-GGCG- CCCTCA-GGG G-CGCTGCCG TCCCCCAAAT
Cy._candelabrum_STE-U_1674                    CTTGGTGTTG GGGATCGGCA -XXXAGGCG- GCCTCC-GGG T-CGC-GCCG TCCCCCAAAT
Cy._candelabrum_STE-U_1675                    CTTGGTGTTG GGGATCGGCA -XXXAGGCG- GCCTCC-GGG T-CGC-GCCG TCCCCCAAAT
Cy._floridanum_ATCC_18834                     CTTGGTGTTG GGGATCGGCA -XXG-GGCGT -CCTTC-GGG T-CGC-GCCG TCCCCCAAAT
Cy._floridanum_ATCC_18882                     CTTGGTGTTG GGGATCGGCA -XXG-GGCGT -CCTTC-GGG T-CGC-GCCG TCCCCCAAAT
Cy._multiseptatum_STE-U_1589                  CTTGGTGTTG GGGATCGGCA -XXXAGGCGT -CCTCC-GGG T-CGC-GCCG TCCCCCAAAT
Cy._multiseptatum_STE-U_1602                  CTTGGTGTTG GGGATCGGCA -XXXAGGCGT -CCTCC-GGG T-CGC-GCCG TCCCCCAAAT
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Cy._scoparium_ATCC_46300                      CTTGGTGTTG GGGATCGGCA -XXXAGGCGT -CCTCC-GGG T-CGC-GCCG TCCCCCAAAT
Ge._bulbilium_GJS_92-7                        CTTGGTGTTG GAGATCGGCA -C-XAAGCGT -CCTCC-GGG T-CGCCGCCG TCTCCCAAAT
Gl._irregularis_STE-U_718                     CTTGGTGTTG GAGATCGGCA ACT-XXXXGC CCCTTGCGGG -XTGC-GCCG TCTCCCAAAT
Gl._sumatrensis_STE-U_1351                    CTTGGTGTTG GAGATCGGCA ACT-XXXXGC CCCTTGCGGG -XTGC-GCCG TCTCCCAAAT
X._serpens_STE-U_1144                         -TTGGTGTTG GGGATCGGCA -XXXAGGCG- ACCTTC-GGG -CCGC-GCCG TCCCCTAAAT


                                                                                                  480
F._subglutinans_NRRL_22061                    TGATTGGCGG TCACGTCG-A GCTTCCATAG C-GTAGTAGT AAAACCCTCG TTACTGGTAA
Ce._camelliae_STE-U_277                       ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._camelliae_STE-U_234                       ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._elegans_STE-U_518                         ATAGTGGCGG TCTCGCTGTA GCTTCNTATG CCGTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._infestans_ATCC_44816                      ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
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Ce._infestans_STE-U_708                       ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._lageniformis_UFV_115                      ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._microcylindrica_ATCC_38571                ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._microcylindrica_STE-U_683                 ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._microcylindrica_STE-U_918                 ATAGTGGCGG NCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._novae-zelandiae_ATCC_44815                ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._parva_ATCC_28272                          ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._parva_STE-U_373                           ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._peruviana_IMUR_1843                       ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Ce._peruviana_STE-U_395                       ATAGTGGCGG TCTCGCTGTA GCTTCCTATG C-GTAGTAGC ACA-XCCTCG C-ACTGG-AA
Co._destructans_AR_2553                       TTAGTGGCGG TCCCGCTGTA GCTTCCTCTG C-GTAGTAGC ACA-XCCTCG C-ACTGGGAA
Co._destructans_CTR_71-322                    ATAGTGGCGG TCCCGCTGTA GCTTCCTCTG C-GTAGTAGC ACA-XCCTCG C-ACTGGGAA
Co._destructans_var_coprosmae_CTR_73-152      ATAGTGGCGG TCCCGCTGTA GCTTCCTCTG C-GTAGTAGC ACA-XCCTCG C-ACTGGGAA
Co._destructans_var_coprosmae_GJS_85-182      ATAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAGC ACA-XCCTCG C-ACTGGGAA
Co._macroconidialis_GJS_83-162                XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
Cu._cigneum_STE-U_1595                        CTAGTGGCGG TCTCGCTGTA GCCAACTCTG C-GTAGTAAT ACA-XCCTCG C-ACTGG-AA
Cy._candelabrum_STE-U_1674                    ATAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Cy._candelabrum_STE-U_1675                    ATAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Cy._floridanum_ATCC_18834                     TTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Cy._floridanum_ATCC_18882                     TTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Cy._multiseptatum_STE-U_1589                  TTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
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Cy._scoparium_ATCC_38227                      ATAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Cy._scoparium_ATCC_46300                      ATAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AG
Ge._bulbilium_GJS_92-7                        CTAGTGGCGG TCTCGCTGTA GCCTCCTCTG C-GTAGTAAC TCA-XCCTCG C-ACTGG-AA
Gl._irregularis_STE-U_718                     CTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT TCA-XCCTCG C-TCTGG-AA
Gl._sumatrensis_STE-U_1351                    CTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT TCA-XCCTCG C-TCTGG-AA
X._serpens_STE-U_1144                         CTAGTGGCGG TCTCGCTGTA GCTTCCTCTG C-GTAGTAAT ACA-XCCTCG C-TCTGG-AA
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						540
F._subglutinans_NRRL_22061	-XTCGTCGCG	GCCACGCCGT	TAAACCCC-A	ACTT-XXXXC	TGAATG-TT-	GACCTCGGAT
Ce._camelliae_STE-U_277	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._camelliae_STE-U_234	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGACT
Ce._elegans_STE-U_518	AA-CAGCGTG	CCCACGCCGT	TAAACCCCCA	ACTTT-XXXC	TGAA-XGTTT	GNCCTCGAAT
Ce._infestans_ATCC_44816	A-GCAGCGCG	GCCACGCCGT	TAAACCCCCA	ACTTTT-XXC	TGA-XXGTTT	GACCTCGAAT
Ce._infestans_IMI_299376	A-GCAGCGCG	GC-ACGCCGT	TAAACCCCCA	ACTTTT-XXC	TGA-XXGTTT	GACCTCGAAT
Ce._infestans_STE-U_2319	A-GCAGCGCG	GC-ACGCCGT	TAAACCCCCA	ACTTTT-XXC	TGA-XXGTTT	GACCTCGAAT
Ce._infestans_STE-U_708	A-GCAGCGCG	GCCACGCCGT	TAAACCCCCA	ACTTTT-XXA	KKA-XXGTTT	KACCTCGAAT
Ce._lageniformis_UFV_115	A-GCAGCGCG	GCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._microcylindrica_ATCC_38571	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._microcylindrica_STE-U_683	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._microcylindrica_STE-U_918	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._novae-zelandiae_ATCC_44815	AA-CAGCTTG	CCCACGCCGT	TAAACCCCCA	ACTTT-XXXC	TGAA-XGTTT	GACCTCGAAT
Ce._parva_ATCC_28272	AA-CAGCGTG	CCCACGCCGT	TAAACCCCCA	ACTTT-XXXC	TGAA-XGTTT	GACCTTGAAT
Ce._parva_STE-U_373	AA-CAGCGTG	CCCACGCCGT	TAAACCCCCA	ACTTT-XXXC	TGAA-XGTTT	GACCTCGAAT
Ce._peruviana_IMUR_1843	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Ce._peruviana_STE-U_395	A-GCAGCAAG	CCCACGCCGT	TAAACCCCCC	ACTTT-XXXC	TGA-XXGTTT	GACCTCGAAT
Co._destructans_AR_2553	A-XCAGCGTG	ACCACGCCGT	AAAACCCCCC	ACTT-XXXXC	TGAAAGGTT-	GACCTCGGAT
Co._destructans_CTR_71-322	A-XCAGCGTG	GCCACGCCGT	AAAACCCCCC	ACTT-XXXXC	TGAAAGGTT-	GACCTCGGAT
Co._destructans_var_coprosmae_CTR_73-152	A-XCAGCGTG	GCCACGCCGT	AAAACCCCCC	ACTT-XXXXC	TGAAAGGTT-	GACCTCGGAT
Co._destructans_var_coprosmae_GJS_85-182	A-XCAGCGCG	GCCACGCCGT	TAAACCCCCC	ACTT-XXXXC	TGAAAGGTT-	GACCTCGGAT
Co._macroconidialis_GJS_83-162	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
Cu._cigneum_STE-U_1595	GCTCGGCGCG	GCCAAGCCGT	TAAACCCCCA	ACTTTTTTTX	XXXXXXXXXX	XXXXXXXXXX
Cy._candelabrum_STE-U_1674	TCTCGGTGCG	ACCACGCCGT	AAAACCCCCA	ACTTTTT-XC	TG-XXXGXXX	XXXXXXXXXX
Cy._candelabrum_STE-U_1675	TCTCGGTGCG	ACCACGCCGT	AAAACCCCCA	ACTTTTT-XC	TG-XXXGXXX	XXXXXXXXXX
Cy._floridanum_ATCC_18834	TCTCGGTGCG	ACCACGCCGT	AAAACCCCCA	ACTTTTT-XC	TG-XXXGTT-	GACCTCGAAT
Cy._floridanum_ATCC_18882	TCTCGGTGCG	ACCACGCCGT	AAAACCCCCA	ACTTTTT-XC	TG-XXXGTT-	GACCTCGAAT
Cy._multiseptatum_STE-U_1589	TCTCGGTGCG	GCCACGCCGT	AAAAACCCCA	ACTTTTTT-C	TG-XXXGTT-	GACCTCGAAT
Cy._multiseptatum_STE-U_1602	TCTCGGTGCG	GCCACGCCGT	AAAAACCCCA	ACTTTTTT-C	TG-XXXGTT-	GACCTCGAAT
Cy._scoparium_ATCC_38227	TCTCGGTGCG	GCCACGCCGT	AAAACCCCCA	ACTTTTTT-C	TG-XXXXXXX	XXXXXXXXXX
Cy._scoparium_ATCC_46300	TCTCGGTGCG	GCCACGCCGT	AAAACCCCCA	ACTTTTTT-C	TG-XXXXXXX	XXXXXXXXXX
Ge._bulbilium_GJS_92-7	-CGCGGCGCG	GCCAAGCCGT	TAAACCCCCA	ACTT-XXXXC	TGAA-XGTTT	GACCTCGGAT
Gl._irregularis_STE-U_718	-CGCGGCGCG	GCCACGCCGT	TAAACCCCCC	ACTT-XXXXC	TGAA-GGTT-	GACCTCGGAT
Gl._sumatrensis_STE-U_1351	-CGCGGCGCG	GCCACGCCGT	TAAACCCCCC	ACTT-XXXXC	TGAA-GGTT-	GACCTCGGAT
X._serpens_STE-U_1144	ACGCGGCGCG	GCCAAGCCGT	TAAACCCCCA	ACTTTTTTTT	TG-XXXXTTT	GACCTCGAAT

			564
F._subglutinans_NRRL_22061	CAGGTAGGAA	TACCCGCTGA	ACXX
Ce._camelliae_STE-U_277	CAGGTAGGAT	TACCCGCXXX	XXXX
Ce._camelliae_STE-U_234	CXXXXXXXXX	XXXXXXXXXX	XXXX
Ce._elegans_STE-U_518	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._infestans_ATCC_44816	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._infestans_IMI_299376	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._infestans_STE-U_2319	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._infestans_STE-U_708	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._lageniformis_UFV_115	CAGGTAGGAT	TAXXXXXXXX	XXXX
Ce._microcylindrica_ATCC_38571	CAGGTAGGAT	TACCCGCTGX	XXXX
Ce._microcylindrica_STE-U_683	CAGGTAGGAT	TACCCGCTGA	AXXX
Ce._microcylindrica_STE-U_918	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._novae-zelandiae_ATCC_44815	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._parva_ATCC_28272	CAXXXXXXXX	XXXXXXXXXX	XXXX
Ce._parva_STE-U_373	CAGGTAGGAT	TACCCGCTGA	ACTT
Ce._peruviana_IMUR_1843	CAGGTAGGAT	TAXXXXXXXX	XXXX
Ce._peruviana_STE-U_395	CAGGTAGGAT	TACCXXXXXX	XXXX
Co._destructans_AR_2553	CANGTAGGAA	TACCCGCTGA	ACTT
Co._destructans_CTR_71-322	CAGGTAGGAA	TACCCGCTGA	ACTT
Co._destructans_var_coprosmae_CTR_73-152	CAGGTAGGAA	TACCCGCTGA	ACTT
Co._destructans_var_coprosmae_GJS_85-182	CAGGTAGGAA	TACCCGCTGA	ACTT
Co._macroconidialis_GJS_83-162	XXXXXXXXXX	XXXXXXXXXX	XXXX
Cu._cigneum_STE-U_1595	XXXXXXXXXX	XXXXXXXXXX	XXXX
Cy._candelabrum_STE-U_1674	XXXXXXXXXX	XXXXXXXXXX	XXXX
Cy._candelabrum_STE-U_1675	XXXXXXXXXX	XXXXXXXXXX	XXXX
Cy._floridanum_ATCC_18834	CAGGTXXXXX	XXXXXXXXXX	XXXX
Cy._floridanum_ATCC_18882	CAGGTAGGAC	TACCCGCTXX	XXXX
Cy._multiseptatum_STE-U_1589	CAGGTAGGAC	TACCCGCTGA	ACTT
Cy._multiseptatum_STE-U_1602	CAGGTAGGAC	TACCCGCTGA	ACTT
Cy._scoparium_ATCC_38227	XXXXXXXXXX	XXXXXXXXXX	XXXX
Cy._scoparium_ATCC_46300	XXXXXXXXXX	XXXXXXXXXX	XXXX
Ge._bulbilium_GJS_92-7	CAGGTAGGAC	TACCCGCTGA	ACTT
Gl._irregularis_STE-U_718	CAGGTAGGAC	TACCCGCTGA	ACTT
Gl._sumatrensis_STE-U_1351	CAGGTAGGAC	TACCXXXXXX	XXXX
X._serpens_STE-U_1144	CAGGTAGGAC	TACCCGCTGA	ACTT

Alignment 7. Part 6. ITS1 5.8S ITS2 rDNA sequence alignment from isolates of selected *Cylindrocladiella* species

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                                                                                                                    60
F._subglutinans_NRRL_22061                CATTACCGAG TTTACAACTC CCAAACCCCT GTGAACATAC CAATT-GTTG CCTCGGCGG-
Ce._camelliae_STE-U_234                   CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._camelliae_STE-U_277                   CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._elegans_STE-U_518                     MTCNACATAG TTTACAACTC CCAAACCCCT GTGAACATAC CATGTCGTTG CCTCGGCGGT
Ce._infestans_ATCC_44816                  CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CA-GTCGTTG CCTCGGCGGT
Ce._infestans_IMI_299376                  XXXXXXAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CA-GTCGTTG CCTCGGCGGT
Ce._infestans_STE-U_2319                  CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CA-GTCGTTG CCTCGGCGGT
Ce._infestans_STE-U_708                   CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CA-GTCGTTG CCTCGGCGGT
Ce._lageniformis_UFV_115                  CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CA-GTCGTTG CCTCGGCGGT
Ce._microcylindrica_ATCC_38571            CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._microcylindrica_STE-U_683             CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._microcylindrica_STE-U_918             XXXXACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._novae-zelandiae_ATCC_44815            CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACATAC CATGTCGTTG CCTCGGCGGT
Ce._parva_ATCC_28272                      CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._parva_STE-U_373                       XXXXXXXXAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._peruviana_IMUR_1843                   CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT
Ce._peruviana_STE-U_395                   CATTACAGAG TTTACAACTC CCAAACCCCT GTGAACTTAC CATGTCGTTG CCTCGGCGGT

                                                                                                                   120
F._subglutinans_NRRL_22061                ATCAGCCCGC TCCCGGTAAA ACGGGACGGC CCGCCAGAGG ACCCC-TAAA CTCT-GTTTC
Ce._camelliae_STE-U_234                   GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._camelliae_STE-U_277                   GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._elegans_STE-U_518                     GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._infestans_ATCC_44816                  GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._infestans_IMI_299376                  GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._infestans_STE-U_2319                  GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._infestans_STE-U_708                   GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._lageniformis_UFV_115                  GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._microcylindrica_ATCC_38571            GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._microcylindrica_STE-U_683             GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._microcylindrica_STE-U_918             GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._novae-zelandiae_ATCC_44815            GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._parva_ATCC_28272                      GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._parva_STE-U_373                       GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._peruviana_IMUR_1843                   GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT
Ce._peruviana_STE-U_395                   GT-XXCTTGC TTCGGC-XXX -XXXGA-XGC CCGCCAGAGG ACCCAACAAA CTCTTGTTTT

                                                                                                                   180
F._subglutinans_NRRL_22061                -XXTATATGT AACTTCTGAG TAA-AACCAT AAATAAATCA AAACTTTCAA CAACGGATCT
Ce._camelliae_STE-U_234                   TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._camelliae_STE-U_277                   TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._elegans_STE-U_518                     TTT-AGTATT ATCT-XXGAG TAACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._infestans_ATCC_44816                  TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._infestans_IMI_299376                  TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._infestans_STE-U_2319                  TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._infestans_STE-U_708                   TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._lageniformis_UFV_115                  TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._microcylindrica_ATCC_38571            TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._microcylindrica_STE-U_683             TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._microcylindrica_STE-U_918             TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._novae-zelandiae_ATCC_44815            TTTTAGTATT ATCT-XXGAG TAACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._parva_ATCC_28272                      TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._parva_STE-U_373                       TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._peruviana_IMUR_1843                   TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT
Ce._peruviana_STE-U_395                   TTT-AGTATT ATCT-XXGAG TGACAAGTTT -AATAAATCA AAACTTTCAA CAACGGATCT

                                                                                                                   240
F._subglutinans_NRRL_22061                CTTGGTTCTG GCATCGATGA AGAACGCAGC AAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._camelliae_STE-U_234                   CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._camelliae_STE-U_277                   CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._elegans_STE-U_518                     CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._infestans_ATCC_44816                  CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._infestans_IMI_299376                  CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._infestans_STE-U_2319                  CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._infestans_STE-U_708                   CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._lageniformis_UFV_115                  CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._microcylindrica_ATCC_38571            CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._microcylindrica_STE-U_683             CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._microcylindrica_STE-U_918             CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._novae-zelandiae_ATCC_44815            CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._parva_ATCC_28272                      CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._parva_STE-U_373                       CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._peruviana_IMUR_1843                   CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
Ce._peruviana_STE-U_395                   CTTGGTTCTG GCATCGATGA AGAACGCAGC GAAATGCGAT AAGTAATGTG AATTGCAGAA
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                                                                                                  300
F._subglutinans_NRRL_22061            TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._camelliae_STE-U_234               TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._camelliae_STE-U_277               TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._elegans_STE-U_518                 TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._infestans_ATCC_44816              TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._infestans_IMI_299376              TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._infestans_STE-U_2319              TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._infestans_STE-U_708               TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._lageniformis_UFV_115              TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._microcylindrica_ATCC_38571        TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._microcylindrica_STE-U_683         TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._microcylindrica_STE-U_918         TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._novae-zelandiae_ATCC_44815        TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CTAGTATTCT GGCGGGCATG
Ce._parva_ATCC_28272                  TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._parva_STE-U_373                   TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._peruviana_IMUR_1843               TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
Ce._peruviana_STE-U_395               TTCAGTGAAT CATCGAATCT TTGAACGCAC ATTGCGCCCG CCAGTATTCT GGCGGGCATG
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                                                                                                  360
F._subglutinans_NRRL_22061            CCTGTTCGAG CGTCATTTCA ACCCTCAAGC CCA-XXGCTT GGTGTTGGGA CTCG-XXXCG
Ce._camelliae_STE-U_234               CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._camelliae_STE-U_277               CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._elegans_STE-U_518                 CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._infestans_ATCC_44816              CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGGCA-TG
Ce._infestans_IMI_299376              CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGGCA-TG
Ce._infestans_STE-U_2319              CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGGCA-TG
Ce._infestans_STE-U_708               CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGGCA-TG
Ce._lageniformis_UFV_115              CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGGCAATG
Ce._microcylindrica_ATCC_38571        CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._microcylindrica_STE-U_683         CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._microcylindrica_STE-U_918         CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._novae-zelandiae_ATCC_44815        CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._parva_ATCC_28272                  CCTGTTCGAG CGTCATTTCA ACCCTCAAAA CCCCGGTTTT GGTGTTGGAG ATCGGCA-TG
Ce._parva_STE-U_373                   CCTGTTCGAG CGTCATTTCA ACCCTCAAAA CCCCGGTTTT GGTGTTGGAG ATCGGCA-TG
Ce._peruviana_IMUR_1843               CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
Ce._peruviana_STE-U_395               CCTGTTCGAG CGTCATTTCA ACCCTCAAAC CCCCGGGTTT GGTGTTGGAG ATCGACA-TG
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                                                                                                  420
F._subglutinans_NRRL_22061            A-GTCAAATC GC-XXXXXXX -XXGTTCCCC AAATTGATTG GCGGTCACGT CG-AGCTTCC
Ce._camelliae_STE-U_234               AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._camelliae_STE-U_277               AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._elegans_STE-U_518                 A-GTCCCTTC -GGGGGCGAC GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCN
Ce._infestans_ATCC_44816              A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._infestans_IMI_299376              A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGNCTCGC TGTANCTTCC
Ce._infestans_STE-U_2319              A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGNCTCGC TGTAGCTTCC
Ce._infestans_STE-U_708               A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._lageniformis_UFV_115              A-G-CCCTCC GGGGCGAAAC GCCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._microcylindrica_ATCC_38571        AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._microcylindrica_STE-U_683         AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._microcylindrica_STE-U_918         AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGNCTCGC TGTAGCTTCC
Ce._novae-zelandiae_ATCC_44815        A-GTCCCTTC GGGGG-CGAC GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._parva_ATCC_28272                  A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._parva_STE-U_373                   A-GT-CCTTC -GGG-GCGAC GCCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._peruviana_IMUR_1843               AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
Ce._peruviana_STE-U_395               AAG-CCCTTC TGGGTGTGAA GTCGTCTCCC AAATATAGTG GCGGTCTCGC TGTAGCTTCC
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                                                                                                  480
F._subglutinans_NRRL_22061            ATAGC-GTAG TAGTAAAACC CTCGTTACTG GTAATCGTCG CGGCCACGCC GTTAAACCCC
Ce._camelliae_STE-U_234               TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._camelliae_STE-U_277               TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._elegans_STE-U_518                 TATGCCGTAG TAGCACA-XC CTCGC-ACTG GAAAACAGCG TGCCCACGCC GTTAAACCCC
Ce._infestans_ATCC_44816              TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCG CGGCCACGCC GTTAAACCCC
Ce._infestans_IMI_299376              TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCG CGGC-ACGCC GTTAAACCCC
Ce._infestans_STE-U_2319              TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCG CGGC-ACGCC GTTAAACCCC
Ce._infestans_STE-U_708               TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCG CGGCCACGCC GTTAAACCCC
Ce._lageniformis_UFV_115              TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCG CGGCCACGCC GTTAAACCCC
Ce._microcylindrica_ATCC_38571        TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._microcylindrica_STE-U_683         TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._microcylindrica_STE-U_918         TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._novae-zelandiae_ATCC_44815        TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAACAGCT TGCCCACGCC GTTAAACCCC
Ce._parva_ATCC_28272                  TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAACAGCG TGCCCACGCC GTTAAACCCC
Ce._parva_STE-U_373                   TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAACAGCG TGCCCACGCC GTTAAACCCC
Ce._peruviana_IMUR_1843               TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
Ce._peruviana_STE-U_395               TATGC-GTAG TAGCACA-XC CTCGC-ACTG GAAAGCAGCA AGCCCACGCC GTTAAACCCC
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                                                                                                                                  532
F._subglutinans_NRRL_22061                -AACTT-XCT GAATGTT-GA CCTCGGATCA GGTAGGAATA CCCGCTGAAC XX
Ce._camelliae_STE-U_234                   CCACTTT-CT GA-XGTTTGA CCTCGACTCX XXXXXXXXXX XXXXXXXXXX XX
Ce._camelliae_STE-U_277                   CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCXXXXX XX
Ce._elegans_STE-U_518                     CAACTTT-CT GAA-GTTTGN CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._infestans_ATCC_44816                  CAACTTTTCT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._infestans_IMI_299376                  CAACTTTTCT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._infestans_STE-U_2319                  CAACTTTTCT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._infestans_STE-U_708                   CAACTTTTAK KA-XGTTTKA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._lageniformis_UFV_115                  CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA XXXXXXXXXX XX
Ce._microcylindrica_ATCC_38571            CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGXXX XX
Ce._microcylindrica_STE-U_683             CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAX XX
Ce._microcylindrica_STE-U_918             CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._novae-zelandiae_ATCC_44815            CAACTTT-CT GAA-GTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._parva_ATCC_28272                      CAACTTT-CT GAA-GTTTGA CCTTGAATCA XXXXXXXXXX XXXXXXXXXX XX
Ce._parva_STE-U_373                       CAACTTT-CT GAA-GTTTGA CCTCGAATCA GGTAGGATTA CCCGCTGAAC TT
Ce._peruviana_IMUR_1843                   CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA XXXXXXXXXX XX
Ce._peruviana_STE-U_395                   CCACTTT-CT GA-XGTTTGA CCTCGAATCA GGTAGGATTA CCXXXXXXXX XX
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Alignment 8. Part 6. 5' end of β-tubulin gene DNA sequence alignment of *Cylindrocladiella* species

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                                                                                                60
F._subglutinans_NRRL_22061           GCGTTGAGTT TATGGTGCCC CTGATTCTAC CCCGCTGGGC GGTGG-XCA- XXXXXGC-TC
Ce._camelliae_STE-U_234              GCGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC
Ce._camelliae_STE-U_277              GCGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC
Ce._elegans_STE-U_518                GCGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CGTTTTCCAC C-XXXGCCTC
Ce._infestans_ATCC_44816             XXXXXXXXXX -XXGCTGCCC CTSATTCTAT CCMGCCGAAT CGTTTCCCAC CCACCGCCTC
Ce._infestans_IMI_299376             GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC CCACCGCCTC
Ce._infestans_STE-U_2319             GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC CCACCGCCTC
Ce._infestans_STE-U_708              GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC CCACCGCCTC
Ce._lageniformis_UFV_115             GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC C-XXXGCCTC
Ce._microcylindrica_ATCC_38571       XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXAC CATTTTCCAC C-XXXGCYTC
Ce._microcylindrica_STE-U_683        GCGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC
Ce._microcylindrica_STE-U_918        GCGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC
Ce._novae-zelandiae_ATCC_44815       XXXXXXXXXX XXXXCTGCCC CTGATTCTAC CCCGCCGAAY CCTTTTCCAC C-XXXGCCTC
Ce._parva_ATCC_28272                 GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC C-XXXGCTTC
Ce._parva_STE-U_373                  GCGTT-XGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAT CGTTTCCCAC C-XXXGCTTC
Ce._peruviana_IMUR_1843              GCGTT-TGTT -XXGNTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC
Ce._peruviana_STE-U_395              ACGTT-TGTT -XXGCTGCCC CTGATTCTAC CCCGCCGAAC CATTTTCCAC C-XXXGCCTC

                                                                                               120
F._subglutinans_NRRL_22061           AACGACAATG CACGATAGCT AGCA-GCTTT A-XAATACCT TCTGTCAAG- ATGAAGAAGC
Ce._camelliae_STE-U_234              GACAACAA-C AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATGTCTTGA ATGAGATTGC
Ce._camelliae_STE-U_277              GACAACAA-C AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATGTCTTGA ATGAGATTGC
Ce._elegans_STE-U_518                GACAACAA-C AAAGCTCGCG ATTATGCCCA C-XXXGTCGT GATA-GTTGG ATCAGATTGC
Ce._infestans_ATCC_44816             GACAACAA-C AAAGCTCGCG AT-XXGCCCA CCCACATCGT GATATCT-GA AGACAATGGC
Ce._infestans_IMI_299376             GACAACAA-C AAAGCTCGCG AT-XXGCCCA CCCACATCGT GATATCT-GA AGACAATGGC
Ce._infestans_STE-U_2319             GACAACAA-C AAAGCTCGCG AT-XXGTCCA CCCACATCGT GATATCT-GA AGACAATGGC
Ce._infestans_STE-U_708              GACAACAA-C AAAGCTCGCG AT-XXGTCCA CCCACATCGT GATATCT-GA AGACAATGGC
Ce._lageniformis_UFV_115             GACAACAA-C AAAGCTCGCG AT-XXGCCCA CCCACACCAT GATATCT-GA ACATAATGGC
Ce._microcylindrica_ATCC_38571       GGCAACAAAC AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATATCTTGA ATGAGATTGC
Ce._microcylindrica_STE-U_683        GACAACAA-C AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATATCTTGA ATCAGATTGC
Ce._microcylindrica_STE-U_918        GACAACAA-C AAAGCTCGCA ATAATGCCCA C-XXXGTCGT GATATCTTGA ATCAGATTGC
Ce._novae-zelandiae_ATCC_44815       GACAACAA-C AAAACTCGCG ATTATGCCCA C-XXXGTCGT GATA-CTTGG ATCAGATTGC
Ce._parva_ATCC_28272                 GACAACAA-C AAAGCTCGCG ATGATACCCA C-CAC-XCGT AATATCT-GG ATACAATGGC
Ce._parva_STE-U_373                  GACAACAA-C AAAGCTCGCG ATGATACCCA C-CAC-XCGT GATATCT-GG ATACAATGGC
Ce._peruviana_IMUR_1843              GACAA-XXXC AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATATCTTGA ATCAGATTGC
Ce._peruviana_STE-U_395              GACAA-XXXC AAAGCTCGCG ATAATGCCCA C-XXXGTCGT GATATCTTGA ATCAGATTGC

                                                                                               180
F._subglutinans_NRRL_22061           TAATCAGAT- CTTTTCTCT- GCGATAGGTT CACCTCCAGA CCGGTCAGTG CGTAAGTGCT
Ce._camelliae_STE-U_234              TAATT-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA
Ce._camelliae_STE-U_277              TAATT-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA
Ce._elegans_STE-U_518                TAATT-XATG TGTTTCTG-A AATATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTACA
Ce._infestans_ATCC_44816             TAATTTTGTG TGTTTCTGCG AATATAGGTC CACCTCCAGA CCGGTCAGTG CGTAAGTACA
Ce._infestans_IMI_299376             TAATTTTGTG TGTTTCTGCG AATATAGGTC CACCTCCAGA CCGGTCAGTG CGTAAGTACA
Ce._infestans_STE-U_2319             TAATTTTGTG TGTTTCTGCG AATATAGGTC CACCTCCAGA CCGGTCAGTG CGTAAGTACA
Ce._infestans_STE-U_708              TAATTTTGTG TGTTTCTGCG AATATAGGTC CACCTCCAGA CCGGTCAGTG CGTAAGTACA
Ce._lageniformis_UFV_115             TAATTTTGCG TGTTTCTGCG AATATAGGTC CACCTCCAGA CCGGTCAGTG CGTAAGTGCA
Ce._microcylindrica_ATCC_38571       TAATT-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG NGTAAGTTTA
Ce._microcylindrica_STE-U_683        TAATC-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA
Ce._microcylindrica_STE-U_918        TAATC-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA
Ce._novae-zelandiae_ATCC_44815       TAATT-XATG TGTTTCCG-A AATATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTACA
Ce._parva_ATCC_28272                 TAATT-XCTC TGTTTCTCAA AATATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTACA
Ce._parva_STE-U_373                  TAATT-XCTC TGTTTCTCAA AATATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTACA
Ce._peruviana_IMUR_1843              TAATC-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA
Ce._peruviana_STE-U_395              TAATC-XATG TGTTTCTG-A ACTATAGGTC CACCTCCAGA CCGGCCAGTG CGTAAGTTTA

                                                                                               240
F._subglutinans_NRRL_22061           CATCGCTTCC TCG-ACGTCG CATGTGGGGG ATGCTCACGA TG-TTTATCA GGGTAACCAA
Ce._camelliae_STE-U_234              CACCTCACCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
Ce._camelliae_STE-U_277              CACCTCACCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
Ce._elegans_STE-U_518                TCCCGAACCT CGACGAGCCT T-GCGGGCAT TTGCTAACGG TGCCATAATA GGGTAACCAA
Ce._infestans_ATCC_44816             TTCCTCACCT CGACAAGCTT C-GTCAACGG CTGCTAACGG TGTCTCGATA GGGTAACCAA
Ce._infestans_IMI_299376             TTCCTCACCT CGACAAGCTT C-GTCAACGG CTGCTAACGC TGTCTCGATA GGGTAACCAA
Ce._infestans_STE-U_2319             TTCCTCACCT CGACAAGCTT C-GTCAACGG CTGCTAACGG TGTCTCGATA GGGTAACCAA
Ce._infestans_STE-U_708              TTCCTCACCT CGACAAGCTT C-GTCAACGG CTGCTAACGG TGTCTCGATA GGGTAACCAA
Ce._lageniformis_UFV_115             TTCCTCACCT CGACAAGCCT C-GTCAACGG CTGCTAACGG TGTCTTGATA GGGTAACCAA
Ce._microcylindrica_ATCC_38571       CACCTCACCT TCACGAGTCT C-TGCGGCGT TTGCTCNCGA TT-CATAACA GGGTAACCAA
Ce._microcylindrica_STE-U_683        CACCTCGCCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
Ce._microcylindrica_STE-U_918        CACCTCGCCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
Ce._novae-zelandiae_ATCC_44815       TTC-GAACCT CGACGAACCT T-GCGGGCAT TTGCTAACGG TGGCATAATA GGGTAACCAA
Ce._parva_ATCC_28272                 TTCCTCACCT CGATAGGCCT C-AACGGCGG GTGCTAACGG TTTCTCAATA GGGTAACCAA
Ce._parva_STE-U_373                  TTCCTCACCT CGATAGGCCT C-AACGGCGG GTGCTAACGG TTTCTCAATA GGGTAACCAA
Ce._peruviana_IMUR_1843              CACCTCGCCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
Ce._peruviana_STE-U_395              CACCTCGCCT TCACGAGTCT C-TGCGGCGT TTGCTCACGA TA-CATAACA GGGTAACCAA
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                                                                                                  300
F._subglutinans_NRRL_22061          ATTGGTGCTG CTTTCTGGCA AACCATCTCT GGCGAGCACG GCCTCGACAG CAATGGTGTC
Ce._camelliae_STE-U_234             ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._camelliae_STE-U_277             ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._elegans_STE-U_518               ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._infestans_ATCC_44816            ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTN
Ce._infestans_IMI_299376            ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._infestans_STE-U_2319            ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._infestans_STE-U_708             ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._lageniformis_UFV_115            ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTT
Ce._microcylindrica_ATCC_38571      ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._microcylindrica_STE-U_683       ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._microcylindrica_STE-U_918       ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._novae-zelandiae_ATCC_44815      ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._parva_ATCC_28272                ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTTGACAG CAATGGTGTC
Ce._parva_STE-U_373                 ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTTGACAG CAATGGTGTC
Ce._peruviana_IMUR_1843             ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC
Ce._peruviana_STE-U_395             ATTGGTGCTG CTTTCTGGCA GACCATCTCT GGCGAGCACG GTCTCGACAG CAATGGTGTC

                                                                                                  360
F._subglutinans_NRRL_22061          TACAACGGTA CCTCCGAGCT CCAGCTCGAG CGTATGAGTG TCTACTTCAA CGAGGTATGC
Ce._camelliae_STE-U_234             TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._camelliae_STE-U_277             TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._elegans_STE-U_518               TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTATGT
Ce._infestans_ATCC_44816            TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._infestans_IMI_299376            TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._infestans_STE-U_2319            TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._infestans_STE-U_708             TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._lageniformis_UFV_115            TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._microcylindrica_ATCC_38571      TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._microcylindrica_STE-U_683       TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._microcylindrica_STE-U_918       TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._novae-zelandiae_ATCC_44815      TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTATGT
Ce._parva_ATCC_28272                TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._parva_STE-U_373                 TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTGCGT
Ce._peruviana_IMUR_1843             TACAACGGCA GCTMTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT
Ce._peruviana_STE-U_395             TACAACGGCA GCTCTGAGCT CCAGCTCGAG CGCATGAGCG TCTACTTCAA CGAGGTACGT

                                                                                                  420
F._subglutinans_NRRL_22061          T-TT-A-XAC AGTC-A-AT- XGCCA-A-XG -AATTCC-CA A-G-XCTCAC ACA-ACTAGG
Ce._camelliae_STE-U_234             GACTG-XATG ATCT-A-ATC TTTCACA-XG -AGAATCACA GTG-ACTTAC GCCTATTAGG
Ce._camelliae_STE-U_277             GACTG-XATG ATCT-A-ATC TTTCACA-XG -AGAATCACA GTG-ACTTAC GCCTATTAGG
Ce._elegans_STE-U_518               GACTGACAAC CCTCGA-ATT TTCTACATCA GAGAATCACA GTGGACTTAC GCCCTATAGG
Ce._infestans_ATCC_44816            GACT-ATGGC ACTC-ACATT TGCTACACTG TGAAATCAGA ATGTACTCAC GCTCCGTAGG
Ce._infestans_IMI_299376            GACT-ATGGC ACTC-ACATT TGCTACACTG TGAAATCAGA ATGTACTCAC GCTCCGTAGG
Ce._infestans_STE-U_2319            GACC-ATAAC ACGC-ATATT TGCTACACTG TGAAATCGTA ATGTACTCAC GCTCCATAGG
Ce._infestans_STE-U_708             GACC-ATAAC ACTC-ATATT TGCAACACTG TGAAATCGTA ATGTACTCAC GCTCTGTAGG
Ce._lageniformis_UFV_115            GACC-AGAGC ACTC-TCATT TGC-XXXXTG TGAA-CGATA ATGTACTCAC GCTTCATAGG
Ce._microcylindrica_ATCC_38571      GACTG-XAAG ATCT-A-ATT TGCCACA-XG -AGAATCACA GTG-ACTTAC GCCTATTAGG
Ce._microcylindrica_STE-U_683       GACT-A-ATG ATCT-A-ATC TGTCACA-XG -AGAACCACA GTG-ACTTAC GCACAATAGG
Ce._microcylindrica_STE-U_918       GACT-A-ATG ATCT-A-ATC TG-CACA-XG -AGAACCACA GTG-ACTTAC GCACAATAGG
Ce._novae-zelandiae_ATCC_44815      GACTGACAAC CCTCGA-ATT TGCTACATCG GGGAATCACA GTGGACTTAC GCCCTATAGG
Ce._parva_ATCC_28272                GATT-ATAAC ACTC-A-TTT TATCACATTG AAGATTCTCA ATGTACTCAC ACATTCTAGG
Ce._parva_STE-U_373                 GATT-ATAAC ACTC-A-TTT TATCACATTG AAGATCCTCA ATGTACTCAC ACATTCTAGG
Ce._peruviana_IMUR_1843             GACT-A-ATG ATCT-A-ATC TGTCACA-XG -AGAACCACA GTG-ACTTAC GCACAATAGG
Ce._peruviana_STE-U_395             GACT-A-ATG ATCT-A-ATC TGTCACA-XG -AGAACCACA GTG-ACTTAC GCACAATAGG

                                                                                                  480
F._subglutinans_NRRL_22061          CCTCTGGCAA CAAGTATGTT CCCCGAGCCG TCCTCGTCGA TCTTGAGCCT GGTACCATGG
Ce._camelliae_STE-U_234             CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
Ce._camelliae_STE-U_277             CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
Ce._elegans_STE-U_518               CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTNCCATGG
Ce._infestans_ATCC_44816            CTTCTGGCAA CAAGTATGTC C-TCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._infestans_IMI_299376            CTTCTGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._infestans_STE-U_2319            CTTCTGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._infestans_STE-U_708             CTTCTGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._lageniformis_UFV_115            CTTCTGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._microcylindrica_ATCC_38571      CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTYGAGCCC GGTACCATGG
Ce._microcylindrica_STE-U_683       CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
Ce._microcylindrica_STE-U_918       CTTCTXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
Ce._novae-zelandiae_ATCC_44815      CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
Ce._parva_ATCC_28272                CTTCCGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._parva_STE-U_373                 CTTCCGGCAA CAAGTATGTC CCTCGCGCCG TCCTCGTCGA TCTTGAGCCC GGTACCATGG
Ce._peruviana_IMUR_1843             CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
Ce._peruviana_STE-U_395             CTTCTGGCAA CAAGTATGTC CCTCGCGCTG TCCTCGTCGA TCTCGAGCCC GGTACCATGG
```

						532
F._subglutinans_NRRL_22061	ACGCC-GTCC	-GAGCTGGTC	CCTTCGGTCA	NGCTCTTCCG	TCCCGACAAC	TT
Ce._camelliae_STE-U_234	ACGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	NGCTCTTTCG	CCCCGACAAC	TT
Ce._camelliae_STE-U_277	ACGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	AGCTCTTCCG	CCCNGACAAC	TT
Ce._elegans_STE-U_518	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	NGCTCTTNCG	CCCNGACAAC	TT
Ce._infestans_ATCC_44816	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	NGCTCTTTCG	TCCCGACAAC	TT
Ce._infestans_IMI_299376	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	AGCTCTTCCG	TCCCGACAAC	TT
Ce._infestans_STE-U_2319	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	NGCTCTTNCG	CCCNGACAAC	TT
Ce._infestans_STE-U_708	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	AGCTCTTCCG	CCCCGACAAC	TT
Ce._lageniformis_UFV_115	ATGCC-GTCC	-GTGCCGGTC	CTTTCGGTCA	NGCTTTTCCG	CCCCGACAAC	TT
Ce._microcylindrica_ATCC_38571	ACGCC-GTCC	-GTGCCGGTC	CTTTXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XX
Ce._microcylindrica_STE-U_683	ACGCC-GTCC	-GTGCTGGTC	CTTTCGGTCA	AGCTCTTCCG	CCCCGACAAC	TT
Ce._microcylindrica_STE-U_918	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XX
Ce._novae-zelandiae_ATCC_44815	ACGCC-GTCC	CGTGCCGGTC	CTTTCGGTCA	AGCTCTTCCG	CCCCGACAAC	TT
Ce._parva_ATCC_28272	ATGCCCGTCC	-GTGCCGGTC	CTTTTGGTCA	AGCTNTTTCG	CCCCGACAAC	TT
Ce._parva_STE-U_373	ATGCC-GTCC	-GTGCCGGNC	CTTTCGGTCA	NGCTCTTCCG	CCCCGACAAC	TT
Ce._peruviana_IMUR_1843	ACGCC-GTCC	-GTGCTGGTC	CTTTCGGTCA	NGCTCTTCCG	CCCCGACAAC	XX
Ce._peruviana_STE-U_395	ACGCC-GTCC	-GTGCTGGTC	CTTTCGGTCA	NGCTCTTCCG	CCCCGACAAC	TT